July 8, 2014

1. Q: xnat2loc doesn’t work.   
   A: make sure session label, server name, your user name, password, project label and subject label are all spelled correctly. This may take a little practice.
2. Q: What is that dot “.” in the command “sfind\_4dfp . -g" in the ppt? Is this a typo?  
   A: This dot actually represents current directory. Many of the HOF scripts take root directory where processing is done as first argument. Thus, this dot “.” should be separated by spaces from both sides when you run the command. You should do all your processing in the session directory:  
   xnat2loc <session> …  
   cd <session>  
   sfind\_4dfp . -g  
   …
3. Q: How do I know which scans do I need for the analysis?  
   A: Typically, we’d recommend to include all available T1 (can tell by the number of files in the series), T2, FLAIR, DTI and DSC sequences. Unless intentional, do not include tractography, FA, TRACE, and other images that don’t look like raw scans.
4. Q. How do I know how to match scan number and scan type in the manual configuration file?   
   A: Just to clarify: scan type is a special notion used by HOF to classify scans. Scan type is derived from series description (also called scan description or scan type in XNAT) stored in DICOM metadata. Each image processed by HOF has to be assigned a scan type. You can run the following command:  
   slist li  
   to list all recognized HOF scan types.   
   Generally, you select scan types that are the closest match to the image in question. To have a better idea, you can list all DICOM series descriptions that are associated automatically by the HOF with this scan type by running:  
   slist qi <Scan type>  
   e.g. slist qi DSC gives:   
   15 DSC perf 4 PERFUSION,PWI,TRAPERFUSION,AXEPIPERFUSION,AXEPIPERFUSION#2,EPI2DPERFUSION,TRAPERFUSION++NOANGLE++,TRAPERFUSION++NOANGLE++,TRAPERFUSION+NOANGLE+,TRAPERFUSION--NO\_ANGLE--,TRAPERFUSION--NOANGLE--,TRAPERFUSION++STRAIGHT+++,AXEPIPERFUSIONTPEN,AXEPIPERFUSIONSTPN

Where sample series descriptions are separated by comma.

1. Q: How do I re-generate images using sfind\_4dfp? Do I need to delete images generated before?  
   A: After you’ve created scan configuration file (named, say, sfind.params),  just rerun sfind\_4dfp with -o option:  
   sfind\_4dfp . -o -g  
   This will re-generate all necessary configuration to run subsequent processing.
2. Q: Running fimproc takes too much time. Is this normal?  
   A: Generating  DTI maps takes about 10 minutes. Generating perfusion maps can take up to an hour. You can rerun fimproc repeatedly if it was interrupted. You can also generate only diffusion or only perfusion maps (e.g. for testing) by running fimproc -noperf or fimproc -nodiff.
3. Q: Running the condr\_qc script does not generate the pdf QC file. What’s wrong?  
   A: Try the following:  
   xvfb\_wrapper.sh condr\_qc .
4. Q: I’ve processed a study with HOF. How do I start measuring ROI’s?   
   A: After running HOF pipeline, you can download co-registered images on your local computer and do ROI analysis. You’d want to do analysis that involves images on your local machine, because it’s the most tedious task and takes a lot of time as it is. You can use any ROI analysis tool you’re comfortable with, to generate masks and simple statistics. Simple tools include ImageJ or MRICron. If you want something more advanced and integrated, try Analyze or 3D Slicer.

There are two scripts (still in development) available on NRG cluster that recognize HOF configuration files and output, calcstats and calcroi. Calcstats uses a spherical ROI for measuring mean and standard deviation on all HOF coregistered images. Calcroi will take a custom binary mask to calculate mean and standard deviation for that mask.