**Pipeline Review 2020 – Issues**

John Data Dump of Issues

* Orientation problem with Courtney and Sara’s data – we have a fix, but why did this occur? AtlasViewer issue?
* Need to document all the front-end decisions about wavelength-specific issues / extinction coeffs and whether extinction coeffs vary by age; also spatial dimension of SD distances (cm vs mm); where does SDgui come in and how precise does that have to be?
* Need imageRecon and RunGLM to run without aborting and write any problems to a log
* How deal with two session NIH data? Imagerecon for each run at present and then run GLM over multiple image recon files…but two runs should use light model for session 1 and two runs for session 2 light model
* Zscore design matrix for GLM? – see Adam’s email
* Input file is unwieldy – can we do anything there or just leave as is – do we need all those columns?
* Fix Vince’s file read; plays ok with my ‘unique’ code; when apply ‘unique’ code
* Set up GLM for Gates so I can do which analyses?
  + Load
  + First look change v nochange?
  + SLF
  + Others? Easy way to edit design matrix down the road?
* Fix code so single subject run works
* Some bits weren’t running first subject – why?
* Any way to streamline some of the AFNI code, or is that as is…
* Re-run Gates time series extraction from 0 – 18s.
* Set up code to extract time series without the average? E.g., from stim1 to stim2? Useful for plots and additional analyses like coherence
* Redo extract code so one file per clust\_order file; files will be smaller and can be added to git
* We used diff files for Y1 and Y2 tform to group space – is that all ok? Needs cleaning?
* Final template issue: can we pull the MNI labels into IndiaFinal and CustomMNI? Or put all Gates and NIH data into MNI as a final step?

Questions for Adam/Vince:

Sobana’s questions:

**In the ImageRecon code:**

1.

 params.lambda\_1=0.1;%range between 0.2-0.01--smoothness vs variance

params.lambda\_2=0.1;%range between 0.2-0.01--what is this??

params.gsigma=3;% standard deviation of Gaussian smoothing kernel in mm

Can you clarify where these values come from? I want to make sure that unlike the Extinction coefs, these are not numbers that will need to change for the NIRX system that I use.

2.

       if (endframe > size(procResult.s,1))

            endframe = size(procResult.s,1);

        end

It looks like with using these lines, the last stim marker info is excluded if padding is 0? So, in my case, I specify padding as 0, so my last stim marker gets chopped off. Is there a way to repair this?

3.

hrf=resample\_tts(hrf,infoHRF,newSamplingFreq,1e-3,1);

Do you anticipate the tolerance of 10^-3 to change as per machine?

4.

The script appears to work when I increase the number of %s at the very beginning to accept 15 fields in the .prn fille as the pipeline now expects. If I don’t do this, funky things get done withSubjectList and I get an error downstream. Can you clarify this?

5.

For the IC dataset, I plan to use the same HRF for HbO and HbR – simply because my collaborators and I are using latent change score models, and the interpretation of ‘change’ gets very complicated very quickly if there is more layers of signs one needs to keep in mind. Can you clarify that using the same HRF is fine – as long as we are clear on interpretation as detailed in the email correspondence between Adam, you and I?

6.

            cortex\_HbO = cortex\_HbO.\*1000;

            cortex\_HbR = cortex\_HbR.\*1000;

I notice you multiply this data with 1000, and you have a comment referring to Adam’s email. I was under the impression that this needed to be done at the back-end. Can you clarify what this 1000 does, and then, what the other 1000 is on top of this?

**In the RunGLM code:**

1.

        for j=1:numRegressors

            if ~isempty(info.paradigm.(['Pulse\_',num2str(regressorListND(j))]))

                doGLM = 1;

                runCt = runCt+1;

            end

        end

  b\_HbO = b\_HbO ./ runCt;

    b\_HbR = b\_HbR ./ runCt;

runCt gets calculated and then divides the final beta images to calculate the average beta map as specified by the lines above. However, upon running stuff line by line, I find that runCt is counting regressors instead of runs. For eg. for the subject from the IC data, we have 4 regressors, and 2 runs. When we get to the point where we have to calculate the average betamap (last two lines above), I ended up with runCt = 8. Something is off, I think?

2. Any fixes that are required for different machines?