Running MCs for NIH

10 July 2019

# Rotation and segmentation

## Rotation

* We use the *sub\_neurologicalHighRes.nii* files for each subject
* This first needs to be rotated so that it lands on close to an axial orientation for NIH – not true for Gates - Vince’s script does the final rotation after that.
* *MRI\_Rotate.sh* does this first rotation, but you need to change three things:
  1. The subject list
  2. The working directory
  3. The -rotate x y z amount. It can be negative to allow rotation the other direction.
* This will need to be done on an individual basis for all participants, then we can move to the next step.

## Segmentation

* We need to do this in two steps (for NIH) - one is to remove the background noise, the other is to strip the skull
* These can be run as a group
* Turn to the *MRI\_cleanup\_May18.sh* (in the same folder as *autoSegment20190428.sh*) – if running India Gates data the script just has step 6 in it, ignore the in-between ones.
  1. Subjects need to be put in the subject list
  2. Change the working directory
  3. First argument changes the step amount. We probably want step(a-350), but this can be adjusted if needed.
  4. The next two arguments shouldn’t need adjustment - they remove the outside noise, and create ${subj}\_final\_Masked.nii.
  5. We then multiply the image by itself. Check this with Sam - it should be necessary for all NIH kids where resolution is poorer, but this is not necessary for Gates phase 2.
  6. The last line then needs adjustment - shown below. Make sure the wd is correct, then there are two changes you can make: One is the 0.7 below can be adjusted up or down - this is the segmentation parameter. The other is you can add a -a at the end - this uses the other segmentation method (useful if the first one is leaving skull in).

autoSegment20190428.sh -t /Users/administrator/Desktop/test/${subj}\_enhanced.nii -o  
//Users/administrator/Desktop/test/${subj}/ -s 0.7 -c 3 -b -m

autoSegment20190428.sh -t /Users/administrator/Desktop/test/${subj}\_enhanced.nii -o  
//Users/administrator/Desktop/test/${subj}/ -s 0.6 -c 3 -b -m -a

* The end result of this should have no skull, and needs to be checked that it has not cut away part of the brain. Equally there needs to be padded skull all around the brain (although Vince’s script should take care of that). Check previous examples so you know what this means.

# Photon migration simulation preparation

## Individual anatomy

* Once segmented you need to open MATLAB, and navigate to the folder with all the segmented images for that one participant in. You do not need a NIRS or a digpts at this stage.
* Open *AtlasViewerGUI* (by typing the same into MATLAB)
* It will popup with a dialogue box - just hit close or cancel.
* When it opens AV, hit file -> import MRI anatomy
* By default, it should populate the fields - make sure hseg is with segmented head, WM is with white matter, brain is with grey matter, and CSF is with CSF.
* Hit import
* Once this is done, it will ask you to select reference points - hit yes
* These should be the same as for a digitization - NZ, IZ, CZ, LP, RP
* You *MUST* check during this step that the head is aligned with the cardinal left right as given. If not, the rotation and segmentation was not right.
* When this is done it will ask if you want the 10-20 EEG points, hit yes
* When this is done, you can close AV

## Move files

* If you already have an atlas or anatomical (ie template), start here.
* Make a new subfolder for the participant entitled *digitization*
* Copy the anatomical folder, the digpts, the NIRS file, and the HeliumScripts folder into there.
* Use the digpts from that session - if it doesn’t exist, use the template with the same capsize
* NIRS does not need to be from that subject, just the right number of sources/detectors. You need to check if this is right regarding short sources as well.

## Set up probes

* In MATLAB navigate to the digitization folder and open AV
* Go to tools -> register atlas to Digpoints
* Then at the bottom Register Probe to Surface
* Go to Forward model -> set MC Parameters
* Check scattering values with John before going ahead with defaults. These are found in the optical properties excel sheet and can be copied across for NIH and Gates. Change these to what’s specified in the right hand columns.
* Number of photons: 100000000 (thats *8* zeros - count them!)
* Forward model -> Generate MC Input
* Then cancel (don’t run locally on your computer)
* This gives fw …..inp files within the fw folder - check you have the right number
* IF you are running locally to test, you can say ‘file exists, try running now,’ and wait for it to finish. Once that is done you can move to complete steps, below.

# Running MCs

## Transfer files to HPC

* This is only relevant if running on the HPC. Make sure Homer2 versions on HPC match what you have on the computer.
* Copying folder from local destination to HPC, using your ID:

scp -r /Users/administrator/Desktop/sub1002  
taw15kfu@hpc.uea.ac.uk:/gpfs/home/taw15kfu/

* I would then advise using the linux to see them directly (open the HPC app, and hit files). If you prefer to do it remotely, you sign in with:

ssh -XY (id)

* After copying homer2 over, (if not there already - make sure version is the same as the setup computer), set permissions, this allows homer to access the tMCimg file for monte carlo:

chmod 700 /gpfs/home/taw15kfu/homer2/PACKAGES/tMCimg/bin/Linux/tMCimg

* You may also need to make the tMCimg first for the HPC

## Changing paths in files

* We have the fw folder and the HeliumScripts folder (again for HPC use).
* Make changes to the pathnames with the two files, and the subject lists (can do multiple).
* Every single inp file the path needs to be changed
* HeliumScripts folder will be there with all the bsub files
* Also in HeliumScripts, the bsub files need paths to the Headvol to be updated
* *change\_inp.sh* does this, use the backslash vs forward slashes to separate out words, and the second part tells you what each one gets replaced with
* *change\_bsub.sh* does the same thing for the bsub files
* Check that everything is right before proceeding
* If working remotely - use nano to see it in editor instead of bash
* Run these two scripts and check the output.

bash change\_bsub.sh

bash change\_inp.sh

## Running MC

* To run, first edit the subject list in *sub\_job.sh*

bash sub\_job.sh

* Check bjobs, if it has run suspiciously quickly then there is a problem
* Once it’s done, bjobs will show no active jobs
* Then we can transfer everything back to the local destination

## Move back and complete steps

* Once everything finishes, copy folder from HPC to local destination (reverse of the above):

scp -r taw15kfu@hpc.uea.ac.uk:/gpfs/home/taw15kfu/NIRS\_Project/  
/Users/administrator/Desktop

* Do the register atlas to digpts and register probe to surface again.
* After that, you need to cd to the *digitization/fw/* folder of that participant in the terminal and run the following (unless run locally):

touch \*

* This updates the files so they are modified recently. Without this it might say input is newer than output, and wipe the output, or ask you to rerun it.
* If you try to run with Forward model -> Generate MC Input, it will say there is already an input, so hit OK
* *IMPORTANT* if it says anything else hit cancel and check that the fw folder contains the new MC files
* Tick Forward model -> enable sensitivity matrix volume
* Then go to Forward model -> Generate load sensitivity profile
* These will take a while to load. It may ask if the head needs downsampling, if it asks, say yes, and accept the downsampled head.
* This generates a coloured picture which is your sensitivity profile
* Before closing, check that the *Adot* files are in the *digitization/fw* folder

**Creating sensitivity profiles in niftii format in preparation for image construction**

* Run **transformSensProfileToAnat.sh**.
* This script takes a subject list file that contains the following information in columns, one row per subject, and spaces in-between input columns:
  + Subject-Id
  + Full path to sample NIRSFile (e.g., IND.nirs or NIHVWM.nirs)
  + Full path to the location of the subject-specific MC results (the folder with the fw folder…)
  + Full path to the location of the .nirs files that have been processed through Homer2 (see below). Note that this script doesn’t do anything with these files – this column is in the input file for subsequent steps.
  + Full path to the location of the Image Recon output (create by createfNIRSBetaImages below). **NOTE: if you created a separate digitisation for a second session, be sure to create a ‘SecondSession’ sub-folder within the image recon folder and point this line of output to this folder. Otherwise, the second session output will overwrite the first.**
  + Full path to the headvol.vox file used when creating the MC results. This will either be in the anatomical folder within the subject-specific MC results or in the template folder used for the MCs.
  + NOTE: line 71 of this script specifies the threshold for the resultant sensitivity volumes. Any values < the threshold (currently 0.0001) will be trimmed from the output files (see Wijeakumar et al., 2015).
* To run the script, do the following:
  + Navigate to Data folder in terminal
  + Link in the Github scripts: export PATH=${PATH}:/Users/nfb15zpu/Documents/GitHub/MRI-NIRS\_Pipeline/scripts
  + Link in matlab: export PATH=${PATH}:/Applications/MATLAB\_R2018b.app/bin
  + Run: transformSensProfileToAnat.sh {filename}
  + Example: transformSensProfileToAnat.sh SubjectList30mo\_NIHVWM\_ICPipe\_1Subj204a.prn

**NIRS Processing in EasyNIRS / Homer2:**

* First step in NIRS processing is to sort the stim marks. This is done in some variant of NIRS\_Pro1.m
* To make sure there are no Infinity values in the .nirs file, the following scripts can be run. Note that this was observed with the NIRS machine in India, but not at UEA.
* FindVal.m : it creates a text file with first and last time points with Infinity values.
* Examine these text files. For those .nirs files that have Infinity values only at the end – I remove the cells with ReplaceVal.m
* What is left are files with Infinity values in the middle of the recording. Two things needs to be done to these .nirs files. First, the Infinity values have to be replaced with interpolated values. For this, first run FinalValues.m to create text files that show the timepoints for all the Infinity values. You need to use this to change values (check comments to know whether you need to replace 25 points or 50 points or more) in Inter\_val.m for each file manually.
* After interpolation, the stim triggers within 10 timepoints of these segments need to be turned off. Run Turnstim.m to do this.
* After correcting the NIRS files, they need to be analysed using EasyNIRS to obtain beta values for each condition, channel, chromophore and subject. This is done using a configuration file in EasyNIRS (.cfg file) that loads the specific processing options desired.

**NIRS Processing post-EasyNIRS:**

* Run script to extract and average the beta values…
  + Open matlab
  + Navigate to the Data folder
  + Make sure the Github ‘scripts’ folder is linked into the matlab path
  + Run **BetasExtractAndAverage** for each set of NIRS data to process
  + Input to this function is the same input file used above (in transformSensProfileToAnat.sh)
  + Example: BetasExtractAndAverage('SubjectList30mo\_NIHVWM\_ICPipe\_1Subj204a.prn')
* **After running this function**, navigate to the .nirs processing folder and delete all Final\_O and Final\_D .csv files that have all zeros in the design matrix (i.e., there were not enough trials for this subject to estimate the GLM). Deleting these files will save lots of time in the next step because these subjects will be skipped.

**Image Reconstruction:**

* Open matlab
* Navigate to Data folder
* Make sure the Github ‘scripts’ folder is linked into the matlab path
* Run **createfNIRSBetaImages.m** in matlab
* Example: createfNIRSBetaImages('SubjectList30mo\_NIHVWM\_ICPipe\_Subj204a.prn')
* **After running this function**, navigate to each Image Recon output folder and delete any extra conditions from the output. For instance, in terminal, navigate to the Image Recon folder and type ‘rm \*\_cond1\_\*’ to delete the first condition. Sometimes, we have included extra stims in the .nirs files that we don’t care about for the GLM. Every regressor in the GLM gets an output file; so in this step, we are just trimming down to the specific regressors we care about.
* **Once the regressors are trimmed, run ‘AverageImages\_Example.sh’ as relevant to average the Beta Images across multiple sessions for the same participant.**
* NOTE: after running AverageImages, move the original files to a ‘OrigImages’ folder (‘cp \*\_orig.nii OrigImages’). It is also important to check for any ‘fatal’ errors during the run of this script (which can occur, for instance, if the two beta images for a participant are different sizes…)

**Move to Group Space (e.g., CustomMNI) as needed:**

* Navigate to Data folder in terminal
* Link in the Github scripts: export PATH=${PATH}:/Users/nfb15zpu/Documents/GitHub/MRI-NIRS\_Pipeline/scripts
* Link ANTS tools: export PATH=${PATH}:/Applications/ANTS/bin
* An example ‘Transform\_18mo\_FirstHalf.sh’ is in the Github ‘files’ folder.
* This file needs the following:
  + A subject list
  + The base T1 in subject space
  + The base segmented brain image in subject space
  + The template group space
  + The segmented template in group space
  + A lower-resolution template as desired
  + A lower-resolution segmented template as desired
  + A list of subject-specific images to register to the group space

**Create a Group Mask as needed:**

* Github ‘scripts’ has an example called ‘NIRS\_Mask\_ANOVA\_Example.sh’ that can be edited. The goal of this script is to sum up how many subjects contribute at least some data (across any condition) to each voxel. This can then be thresholded in the final step based on a percentage of subjects (e.g., 60-70%).
* Once the mask has been created, it can then be multiplied with all the group-level images to filter out any ‘fringy’ voxels with sparse data.

**Group ANOVA:**

* Sample script: Load\_MVM.txt.

**Concatenate ANOVA results:**

* Sample script: Load\_MVM.txt.

**ROIStats on ANOVA results:**

* Sample script: Load\_MVM.txt.