

CS Accelerated qMT Mapping

I. Scanning Protocol

- 1) Turn on Console
 - username: sdw
 - password: adw2.0
- 2) Write a file for qMT sequence to read offset points
 - This must be done connected to the SFC network.
 - To set up an offset table:
 1. Plug computer into ethernet in console room.
 2. Terminal: `ssh -xy sdc@139.48.44.90`
 - password: adw2.0
 3. `cd /usr/g/research/UofC/mmacdon`
 4. Find the custom file and edit it:
 - `vi filename.txt` (or `gedit filename.txt`)
 - `x` to delete stuff
 - `i` to insert
 - `esc` to exit insert mode
 - `:wq` to save and exit
 - `:q` to close without saving
 - `dd` to delete line
 5. make a copy of the file to use later
 - `cp oldfile newfile`
 - The file you want the scanner to read should just be saved as **mem_qMT_parameters_custom.txt**
- 3) Consent + Screen Participant
 - Use ethics qMRI of MS. Forms can be found in Sinology share folder.
 - Protocol: QMRIMS_xxx
- 4) Scan Participant
 1. Console login:
 - sdc, adw2.0
 - Takes about 10 minutes.
 2. Create a new session and load protocol:
 - Last name: MM (initials)
 - Patient ID: QMRIMS_xxx
 - Weight:
 - Exam Description: QMRIMS??
 - Select protocol: Show all protocols - Other - **Pike Labs-MAM-qMT-2018_03_28**, accept
 - **Start Exam**
 - First Level - *First Level SAR* - No - Accept
 3. **Loc scan: 0:32 (1)**
 - Save and scan

4. **Calibration scan: 0:05 (2)**
 - Place the box
 - Save and scan
5. **T1-weighted Anatomical 4:31 (3)**
 - Click NOVA 32ch coil and unclick HNS
 - Center the brain, make sure nose is in.
 - NOT going to plan other scans off this one.
 - Save and scan
6. **multi_tr_b1-Mapping scan: 7:50 (4)**
 - Place the box very carefully. Try to get all of nose.
 - Save and scan
7. **AX ME SPGRE MPRI scan: 0:37 (5)**
 - Double click
 - Copy prescription from scan #4 (if not linked to 4 already)
 - Use Graphic RX toolbar
 - Rx to Rx symbol
 - Choose multi_tr scan
 - Keep checked: Match Field of View, Phase FOV, and Slice thickness.
 - Accept
 - Save (may take a couple seconds), and scan
 - qMT scan may change time when you do this
 - This is the one that can cause PNS!
8. **DESPOT 1 scan: 1:25 (6)**
 - Single click
 - Should be linked to scan 4, copy if not
 - Scan
 - Make sure this one isn't all noise (Subj 09 failed)
9. **IR SSFSE: 0:04 (7-20)**
 - Copy slice prescription from scan 6
 - Use Graphic RX toolbar
 - Rx to Rx
 - 3D dropdown menu
 - Choose DESPOT1 scan
 - Check scan coverage
 - Accept
 - Change the #slices back to 1
 - Save and scan
 - For scans 8-20:
 - Scan dropdown
 - **Manual prescan**
 - Done
 - Scan

10. qMT scan: 28:14 (21-32)

- Should be linked to other scans
- Details tab:
 - Freq + Phase = 128
 - Phase FOV = 0.75
 - TE = Minimum (29.7)
- Save and scan
- For scans 22-32:
 - Scan dropdown
 - **Manual prescan**
 - Done
- Scan
- Run again to get pulse timing graph (if needed)

11. End the exam.

- Top left
- “End”, “End Exam”

12. Push the data.

- Image icon, top left
- Select scan in top box - push ALL series
- Select node in bottom row. Push to node corresponding to exam description. Clicking the button pushes it automatically.
- **QUANT MR MS**
- To check data immediately:
 - Push to **QCWorkstation** node
 - View images on computer in room MR115

13. Fill out log book and QC form

14. System Restart - end of the day

- Tool icon - System Restart
- Takes about 10 mins

15. Fax copy of signed consent and screening to Fran

- **(403) 944-3622** (include research request number)
- Add participant to database (mricalgary) or let Kristen know so she can do it

5) Get K Space Data

1. Plug into SFC network.
 - Use ethernet cable with thunderbolt dongle in console room.
2. Find the pfile you're looking for (on Terminal).
 - [ssh sdc@139.48.44.90](ssh:sdsc@139.48.44.90)
 - yes
 - pwd: adw2.0
 - [cdraw](#)
 - [pwd](#)
 - /usr/g/mrraw
 - [ls -lrt P*](#)

- Find the file (based on date, time, and size).
 - Copy the name "P____.7"
 - `exit`
 - 3. Get the file.
 - `sftp sdc@139.48.44.90`
 - `pwd: MR114@3t`
 - `cd /usr/g/mrraw`
 - `get P117____.7`
 - wait for it to finish
 - `bye`
 - 6) Get DICOM Data
 - Push to node indicated by protocol (QMRIMS)
 - Check in **AcademicFS/PikeLab/INCOMING**
 - Takes about a day
 - Open and save data in HOROS so that it is in order for parameter map code
 - Save to **CSProject/SourceData/yyyy_mm_dd_qMRImS_xxx**
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II. Data Processing

- 1) Prepare Data
 - On Laptop:
 - Log into academic FS
 - Username (mamclean)
 - Password (6*****_Uc)
 - Open Osirix and import images from the server
 - Copy links
 - Export images to **AcademicFS/PikeLab/Melany/CSDData/SubjectID**
 - Get **all** the AX ME SPGRE and B1 files
 - Get P-file from computer and put it in **AcademicFS/PikeLab/Melany/CSDData/SubjectID**
 - On Linux:
 - Make a folder for data **1.9TB/Documents/CSProject/sourceData/SubjectID**
 - Make sub-folder **SPMData** and **DICOMS**
 - Log on to AcademicFS:
 - "Connect to Server"
 - mamclean
 - UC
 - 691266501Mel**
 - Put P-file into SubjectID folder
 - Put folders in **study** of the server into **DICOM** folder
 - There may be images that do not get copied over. Check the #items in the folder matches the highest image #.
- 2) Set up Undersampling Schemes
 - **Documents/CSProject/Undersample.m**

- Make sampling schemes for each matrix size and undersampling rate. You may also want to create multiple versions for each rate:
 1. Enter rate and version.
 2. Direct output to matrix size folder.
 3. Run.
- Saves the undersampling mask in **CSPreparedData/Masks/MatrixSize** as “**CSInputData_R_Vn_P1**”, “**mask1**”
- Matrices for data pipeline found in **CSProject/Subsample_Patterns/MatrixSize**.
- Text files for prospective sampling in **CSProject/Subsample_Lookup_Tables**.

3) Create Subject Field Maps

- **Documents/CSProject/ethanCode/qMT_Protocol_Analysis.m**
- In the first section, you can adjust the display settings.
- To create maps:
 1. Specify directory of DICOM data in 1.9TBVolume/Documents/CSProject/sourceData. Specify subdirectories.
 2. Add subjectID for output file name.
 3. Run. It will crash when T2* is called. (If there is an error, try restarting Matlab.)
 4. Check the mask and adjust thresholds if needed (lines 104-108)

4) Reconstruct P-files + Prepare Full K Space

- **Documents/CSProject/Orchestra/Examples/RunCartesian.m**
- This will convert p-files into a k-space matrix.
- Will take ~20 minutes.
- To prepare k-space:
 1. Make sure you are in the directory with the p-files. Desktop/Storage/Documents/CSProject/SourceData/SubjectID.
 2. Indicate the output filename. “SubjectID_Kspace” in Documents/CSProject/CSPreparedData/Data/
 3. Double check the location of the reference volume (i.e. 1 or 11)
 4. Indicate how many processing “chunks” you need.
 - Splits recon into multiple sets (chunks) of z-spectrum points. You could do each flip angle set separately or split them to save memory.
 - Set to 1 for CS project.
 5. Run.
- Saves the full K-space to “**CSProject/CSPreparedData/SubjectID_Kspace**” as data1 and refVol
- You may **run out of memory** when running this code. More can be available by turning **swap memory** on.
 1. In terminal: `sudo gparted`
 2. In GParted:
 - Devices
 - /dev/sdb
 - **Sdb2** (restart computer if this is not available)
 - Right click, ‘swap on’
- **Note: Make sure swap is on for 3D matrices!**

5) Retrospective K Space Reconstruction

- **Documents/CSProject/Archive/ReconQMT.m**
 - This will reconstruct k-space matrices with various sampling masks. Marc Lebel's code.
 - Time depends on rate; R = 16 takes ~20m, R = 0 takes ~18h
 - To reconstruct k-space:
 1. Make **SubjectID** folder in **Storage/Documents/CSProject/outputData** with **MTunscaled** folder inside.
 2. Enter subject ID, rate, and version.
 3. Run.
 - **Note:** Make sure that a filter of the correct size and roll off is in the **CSPreparedData/HammingFilters** folder if you want to do hamming filter. Filter called on line 72. For a new matrix size:
 1. **CSProject/HammingFilter.m**
 2. Enter matrix size. For 2-d use Z = 40 and save the middle slice after.
 3. Enter edge size, usually 15.
 - Reconstructed k-space gets taken from **CSPreparedData/Data**, reconstructed, and placed in **CSProject/outputData** folder.
 - You may run out of memory when running this code. Make sure you watch the **system monitor** while it is running.
- 6) Z-Spectrum Quick Check (Optional)
- Load previous results **OutputData/zSpectResults/zSpectResults.mat**
 - Make WM/GM masks
 - `maskcon = zeros(256);`
 - `maskcon(a:b,c:d) = 1;` Choose any WM rectangle
 - `maskwat = zeros(256);`
 - Load the fully sampled 'MTdata' you want to use (post-normalized)
 - Run **CSProject/zspect.m**
 - Save new responses
 - `WM0x = conditionerResponse;`
 - `stdWM0x = stdConditionerResponse;`
 - `save('file','var1','var2','-append')`
 - Run lines from **plotz.m**
- 7) Motion Correction and GM WM Segmentation
- Avery's SPM instructions are saved and documented in a Matlab script:
 - **Documents/CSProject/qMTCoregistration.m**
 - Change path names to correct locations.
 - Run 1st section.
 - Takes about 5 minutes
 - Crashes at some point (Undefined im_anat)
 - Should put **struct.nii** and others into SPM folder
 - Follow instructions in 2nd section.
 - Run following sections (3, 4, 5, remember to change paths!)
 - View the maps in ITK-SNAP.
 - **CSProject/itksnap-3.../bin**
 - You can add new images and decide where you want to threshold the maps.
 - Threshold using Contrast Inspector - min 0.9 - max 1 (90% or higher is included)
 - Go to the maps and remove skull from the mask or change size if you need to
 - Threshold mask:

- `Mask(find(Mask<=0.99))=0;`
- `Mask(find(Mask>=0.99))=1;`
- To strip the skull off the mask:
 1. Make sure there's no skull attached to main blob.
 - `figure, imshow (Mask2)`
 - Use cursor to find attached voxels (corners count).
 - `Mask2 (y , x) = 0`
 - ...
 2. Label "blobs"
 - `[Mask2 , #blobs] = bwlabel (Mask)`
 3. Set Mask to the correct blob
 - `MaskNew = ismember (Mask2 , 2)`
 - second blob
 - `Mask = MaskNew`
- Helpful mask adjustments you may need:
 - Resize maps:
 - `Map = resize (Map , x)` , where x is the scaling factor (usually 0.5).
 - Rotate maps:
 - `Map = rot90 (Map , n)` , where n is the number of 90 degree rotations.
 - Remove zeros:
 - `Map (find (Map == 0)) = 1` , or use this to replace any number with another.
 - Remove NaN or INF:
 - `Map (isfinite (Map)) = 0` , or use `isnan` to find NaN values.

8) Get Pulse Timing Variables

- Do this IF the scan parameters have changed from past settings
- Get info from pulse timing diagram collected during scan

9) qMT Mapping

- **Documents/CSProject/qMTLab-master/qMTLab.m**
- Map CS reconstructed data and zero-filled data found in **CSProject/outputData/SubjectID**
- Enter the protocol and click "**Build SF Table**" or **load a saved protocol**
- For CS data:
 - Use **MTdata_rate_Vn**
 - Study ID: **SubjectID_rate_Vn**
- For ZF data:
 - Use **MTdataZF_rate_Vn**
 - Study ID: **SubjectID_ZF_rate_Vn**
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10) Expected Values

- | | | |
|----------------------------------|---------------------------------|---------|
| • F wm - 0.13 | F gm - 0.07 | |
| • Kf wm - 4.12 | Kf gm - 2.5 | (1/s) |
| • T2f wm - 30 | T2f gm - 50 | (ms) |
| • B0 map - minus 30 to 70 | | (Hz) |
| • B1 map high - 1.1 | B1 map low - 0.9 | (ratio) |
| • T1 map wm - 904 | T1 map gm - 1059 to 1331 | (ms) |
| • R1 Map wm - 1.1 | R1 map gm - 0.9 to 0.75 | (1/s) |

- More literature values can be found on laptop in qMTLabStartParameters - Sheet 2
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III. Statistical Analysis

1) Figures

- **Documents/CSProject/outputData/Accel_qMT_Figures.m**
- Make single subject, side by side qMT parameter maps
 - Load F, kf, R1f, T2f, and T2r from the **FitResults** folder of the subject you want (R=0)
 - Input crop size params
 - Run section for Figure #1
- Make single subject accelerated and difference F maps
 - Load the F map for each rate and save as F0, F4, F8, ...
 - Run section for Figure #2

2) Accelerated Z-spectra

- This will generate images like the ones in the 2017 **ISMRM presentation**
- Go to folder with SPM data:
 - **CSProject/outputData/subjectID/SPMdata**
 - `WM = load_nii('rc2structural.nii')`
 - `GM = load_nii('rc1structural.nii')`
 - `WMroi = WM.img;`
 - `WMroi (find(WM<=0.99)) = 0;`
 - `WMroi (find(WM>=0.99)) = 1;`
 - `maskcon = rot90(WMroi(:, :, 30));`
 - `maskcon = fliplr(maskcon);`
- **It's a good idea to save the masks first!**
- Navigate to **outputData/SubjectID/Slice 30**
- Load the MTdata_R_Vn of the rate you want to work on
- Run Ethan's script (**zspect.m**) with the ROI lines commented out (15-21)
- Save the outputs:
 - Make a storage folder **outputData/subjectID/z-spectra_0.99Masks**
 - Save: `WMx = conditionerResponse`, `GMx = waterResponse`, `stdWMx = stdConditionerResponse`, `stdGMx = stdWaterResponse`
 - Stored in: **WMResponses[WM0,WM2,...]**, **GMResponses[GM0,GM2,...]**, **Masks[maskcon,maskwat]**, **WMSDev[stdWM0,stdWM2...]**, **offsets**, ...
 - Repeat for next rate/ version
- How to get z-spectra images like the ones in the **ISMRM abstract**:
 1. Place ROI in WM and GM
 - Run Ethan's script
 - **SCProject/zspect.m**
 - Place first cursor to choose ROI in WM. Right click, create mask.
 - Place second cursor to choose ROI in GM. Right click, create mask.
 - Override other ROI's using:
 - `maskcon = roipoly;` Place in WM
 - `maskwat = roipoly;` Place in GM

2. Save WM and GM responses (for rate x)
 - `GMx = waterResponse; WMx = conditionerResponse;`
 - `stdGMx = stdWaterResponse; stdWMx = stdConditionerResponse;`
 - Repeat for each rate, using original ROI's
 - Comment out roipoly lines
 3. Run graphing script
 - **CSProject/Z-spectra/Plotz2.m**
 4. Calculate goodness of fit measures (for rate x)
 - `NMSEgmx = sum ((GMx - GM0) .^2) / sum (GM0 .^2)`
 - `NMSEwmx = sum ((WMx - WM0) .^2) / sum (WM0 .^2)`
- 3) NMSE Bar Graph
- **Documents/CSProject/outputData/Accel_qMT_NMSEtable.m**
- 4) Bland-Altman Plots
- **Documents/CSProject/outputData/ThesisFiguresData/BAplots2.m**
 - Follow instructions in script
 - Save workspace as "BAdataSubject__"
 - **Documents/CSProject/outputData/ThesisFiguresData/BAplotsAllSubjects**
 - Enter all subjects you want included
 - Enter Rate
 - Repeat for all rates