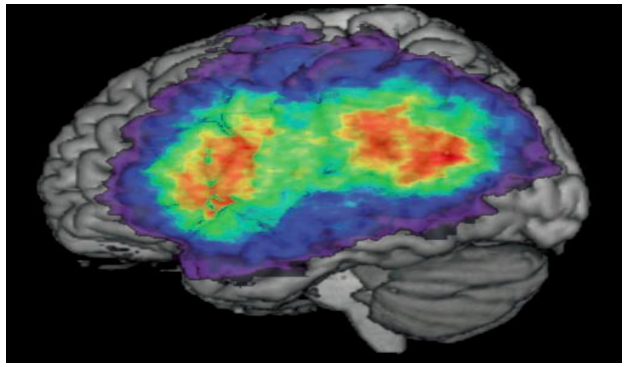
MRRI
MOSS REHABILITATION RESEARCH INSTITUTE

Lesion-Symptom Mapping Workshop



<u>Speakers:</u>

Frank Garcea

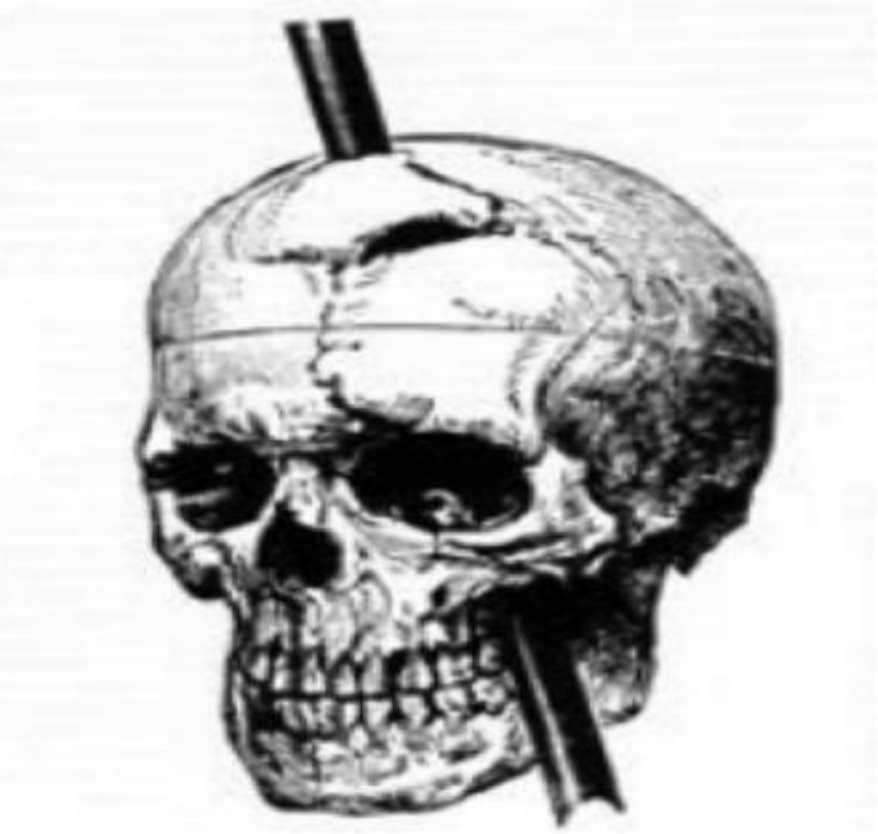
Harrison Stoll

Austin Wild

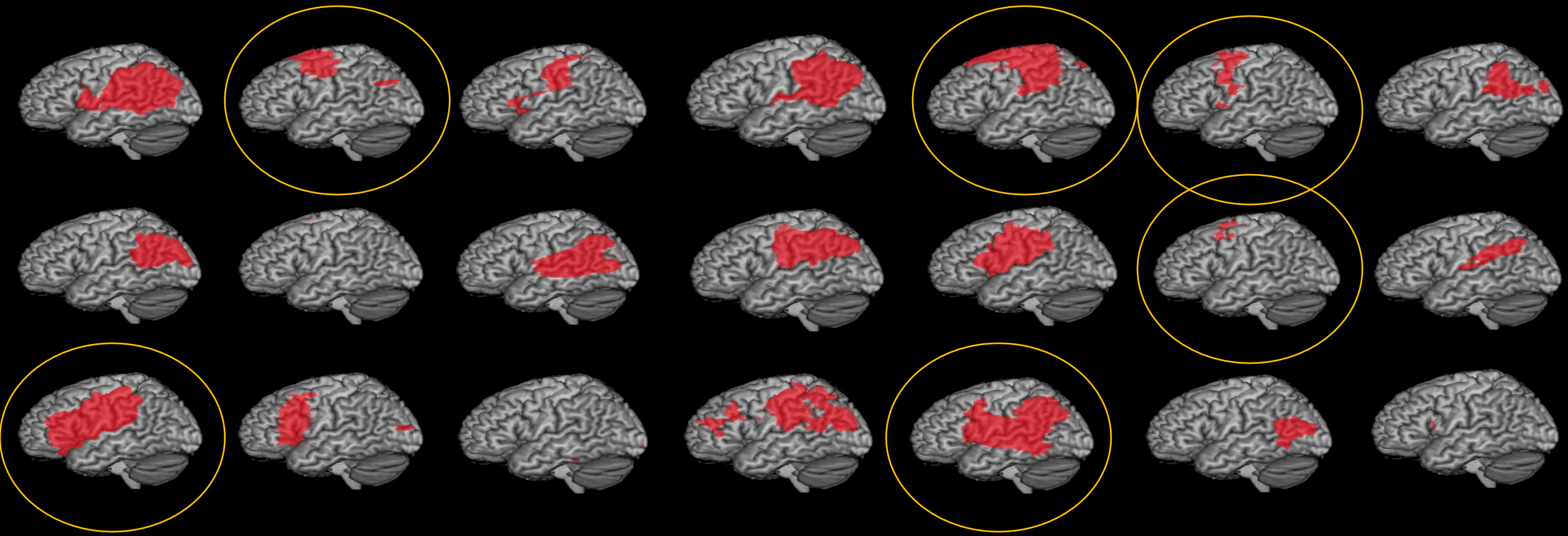
<u>Organizer:</u>

Aaron Wong

Case studies: powerful but incomplete



Which area is responsible?



Why Lesion-Symptom Mapping

- Relates behavioral impairments to the lesioned brain locations that likely caused those impairments
  - Insight into the function of particular brain regions
  - Allows us to connect work in patients to that of other neuroanatomical methods (e.g., fMRI)

Workshop Agenda

Goal: Learn the lesion-symptom-mapping pipeline, from a single MRI scan to the group aggregate result (assuming you already measured behavior)

Session 1: Scanning, Lesion-Drawing, and Basic Analyses

Session 2: Lesion-Symptom Mapping (SVR-LSM) and Post-Processing

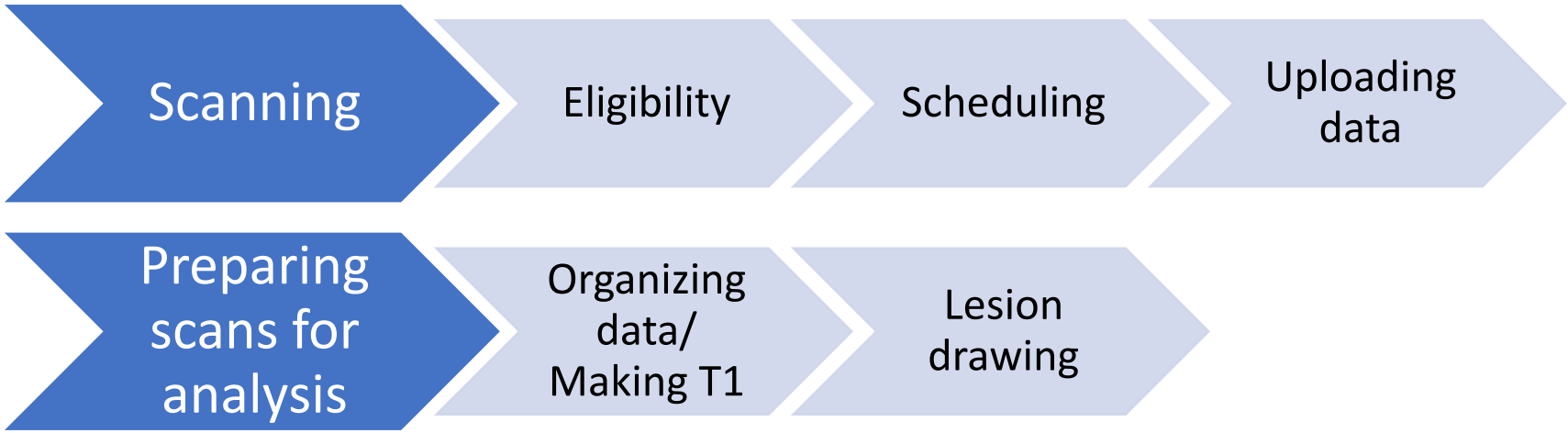
Session 3: Variations and Methodological Considerations

To follow along:

- MRIcron: https://www.nitrc.org/frs/?group_id=152
- Materials: https://mrri.org/lesion-symptom-mapping-workshop-series/

Intro to Scanning, Lesion Drawing, and Basic Analysis

Objectives


Scanning
Eligibility
Scheduling
Uploading data
Preparing scans for analysis
Organizing data/ Making T1
Lesion drawing

Eligibility

- Go through a MRI screening form with the participant
  - Examples:
    - Have you had an MRI before?
    - Are you claustrophobic?
    - Do you have any metal or electronic implants?
- If participant has a metal or electronic implant, it is important to check with a MRI tech
  - If still unsure, contact the participant's doctor or obtain the medical records for the implant surgery

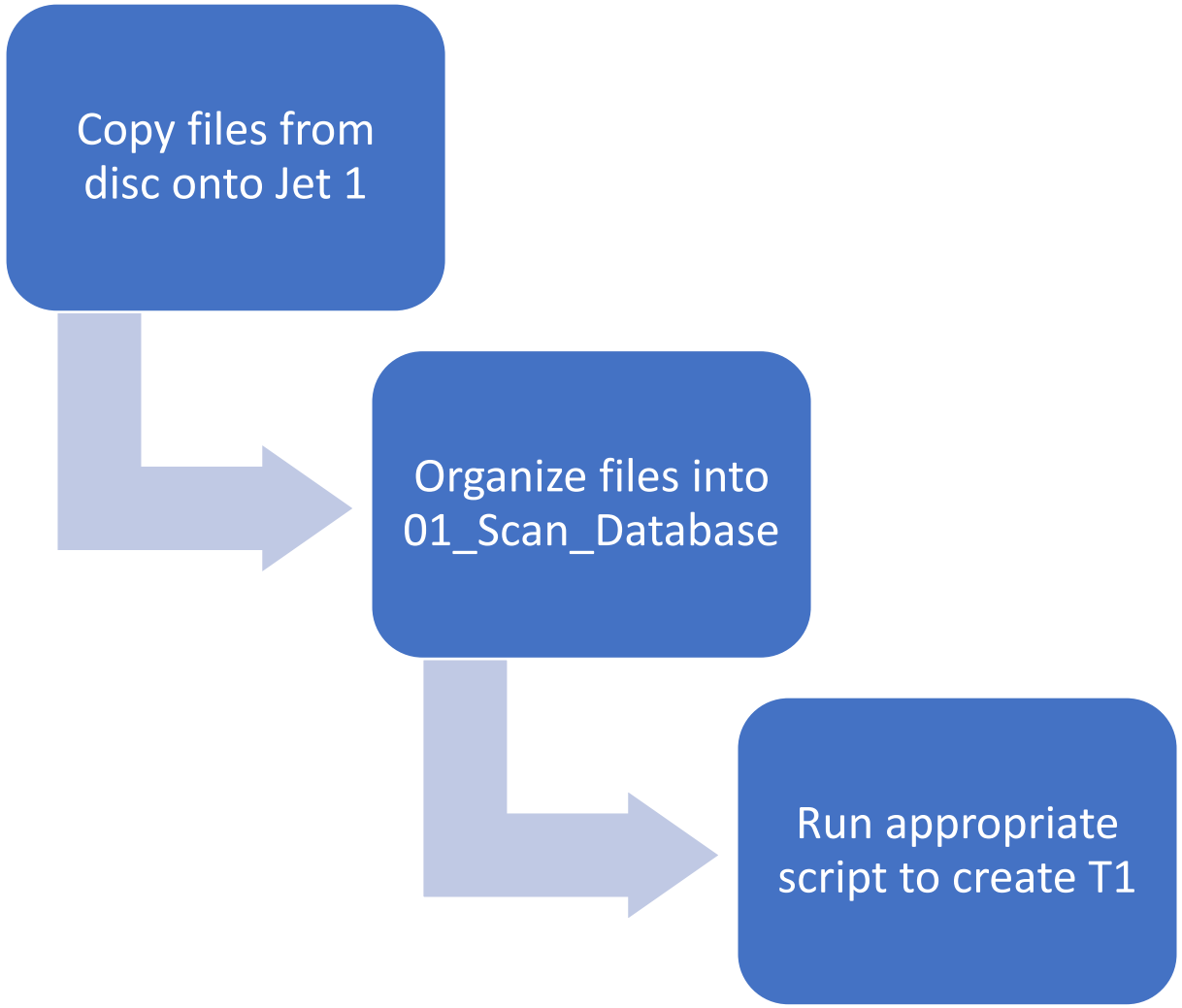
Scheduling

- Need to schedule slots at least 3 weeks in advance
- Email Branch's RA with appropriate information a week before the scan
- If you have not filled a scan slot at least 3 days in advance, you should cancel it
  - You can be charged for dropping scans late
- Call radiology and the precertification team to confirm

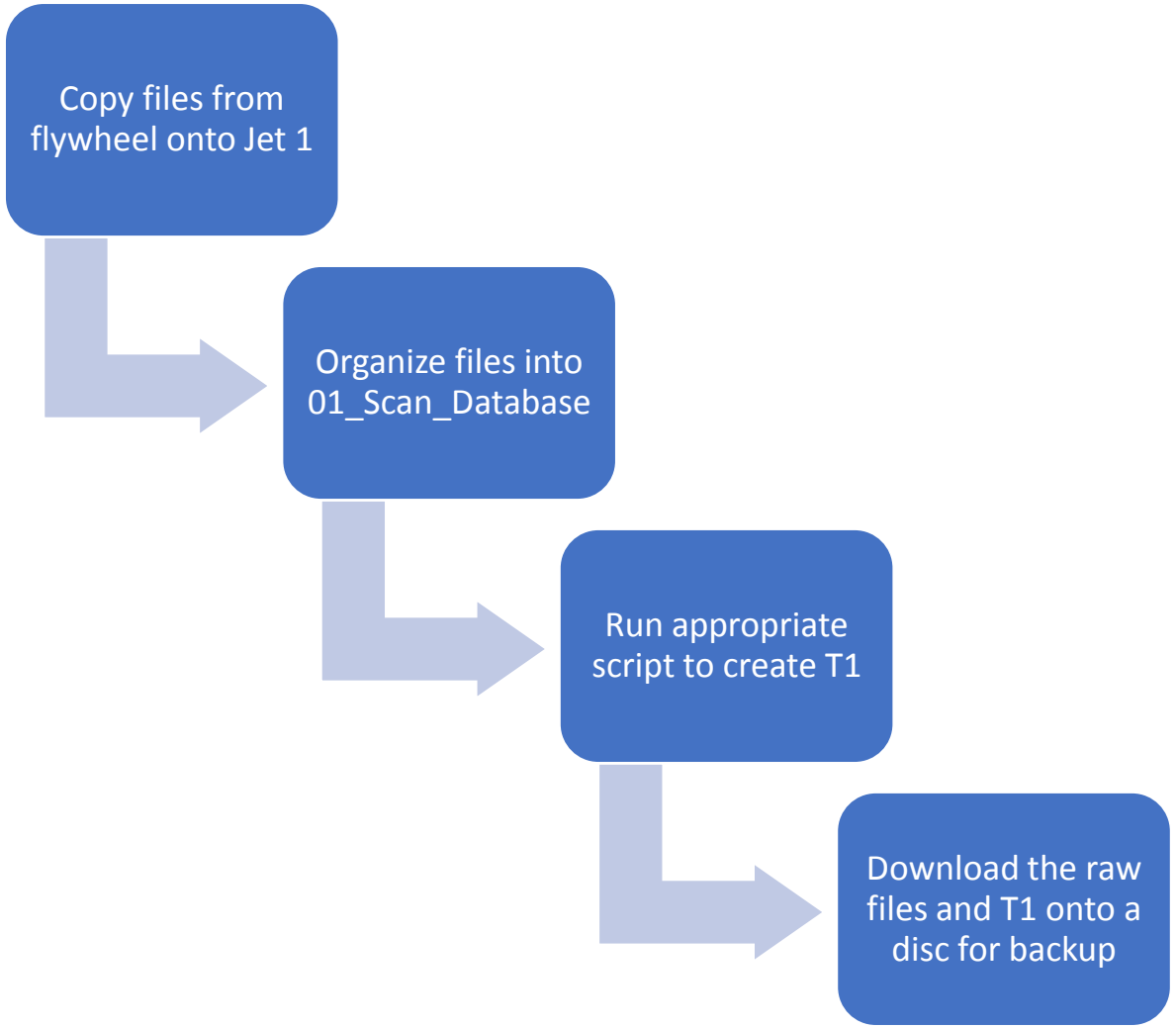
Scanning

- Schedule participants a hour before your scan slot to-
  - Go over your labs consent form & what your participant will do while in the scanner
    - Example sequences:
      - Breathing localizer, MPRAGE (T1), DTI
- Important things to remember:
  - Use Ridehealth whenever possible
  - You can only schedule 1 hour slots
  - Use the metal detector before the participant enters the MRI
  - Be malleable

Uploading & organizing files (Current)

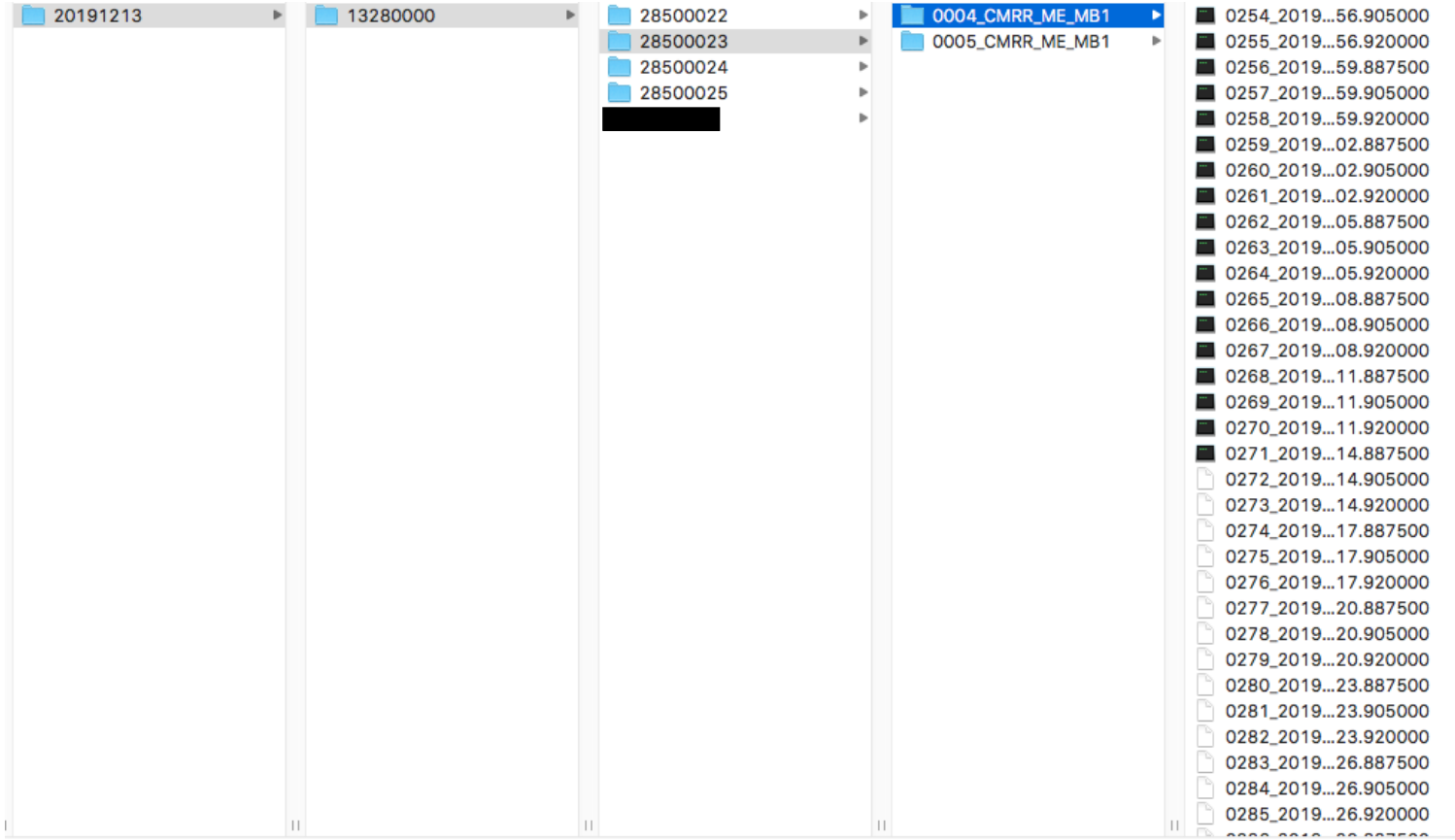


Uploading & organizing files (Future)



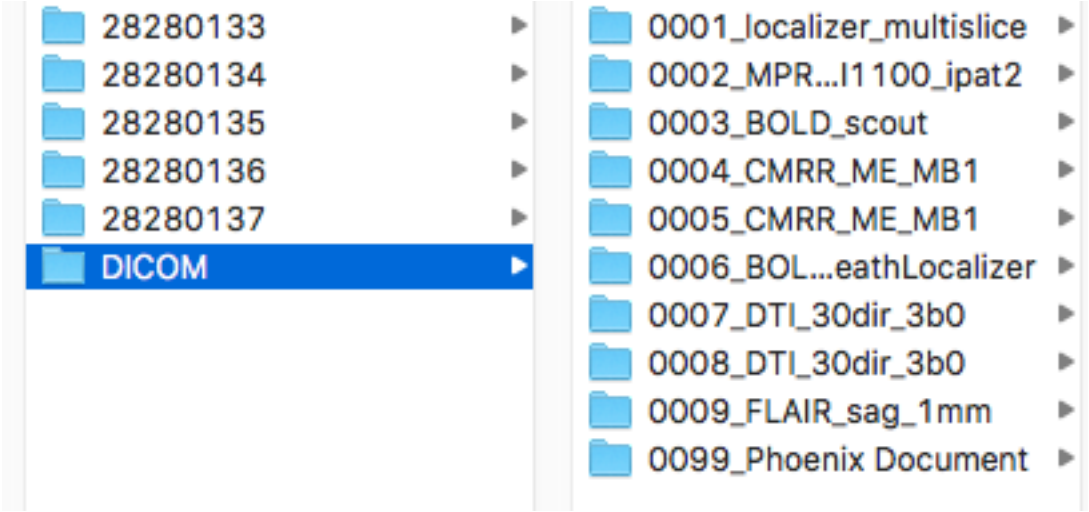
Downloading raw DICOM files

- When you download the files onto the disc, it will look something like this:



Processing raw DICOM files

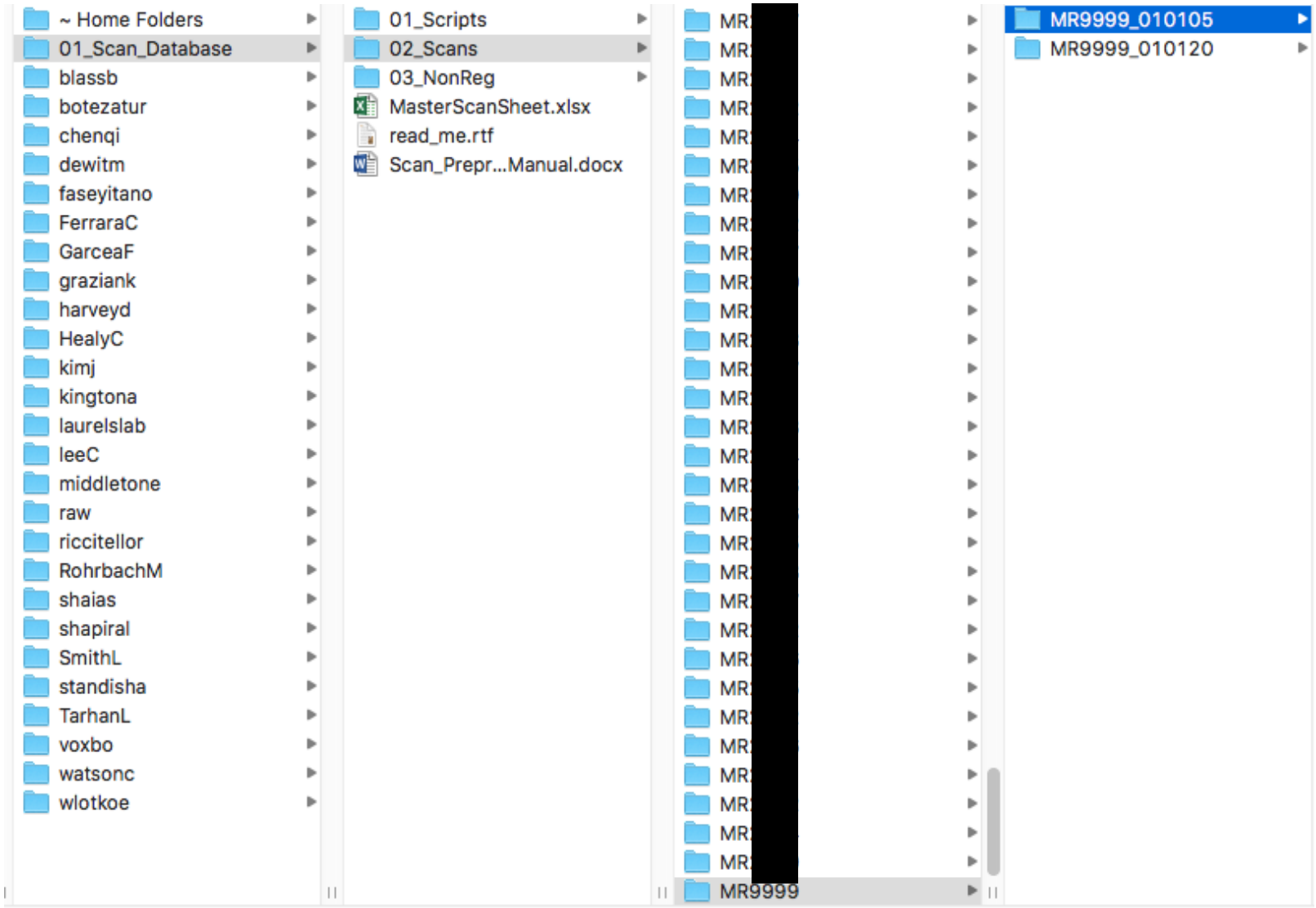
- Depending on how your files are formatted, you'll want to run one of two pre-processing scripts.
  - This will organize the files into a single DICOM parent folder, where all of the different sequence data will be sorted



Creating the T1 for drawing

- Run dcm2niix_afni on the 0002_MPRAGE folder to create a T1
  - There are other programs, such as voxbo that can compile these images into a T1 as well
- Before jumping into drawing, be sure to organize all of the files onto Jet 1, and update the MasterScanTracking sheet

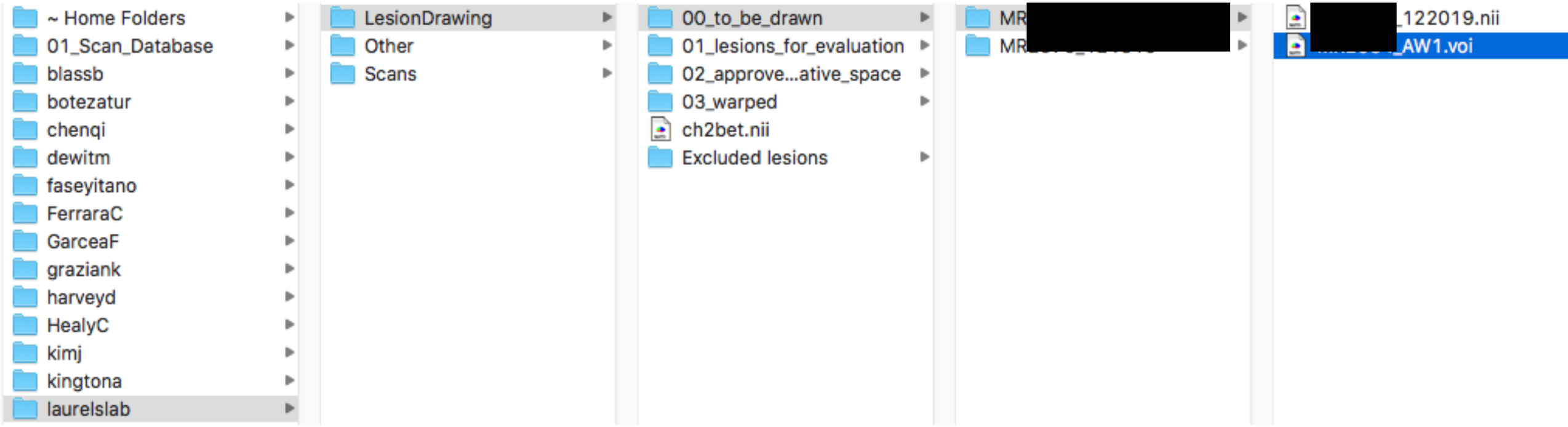
Organizing files on Jet 1



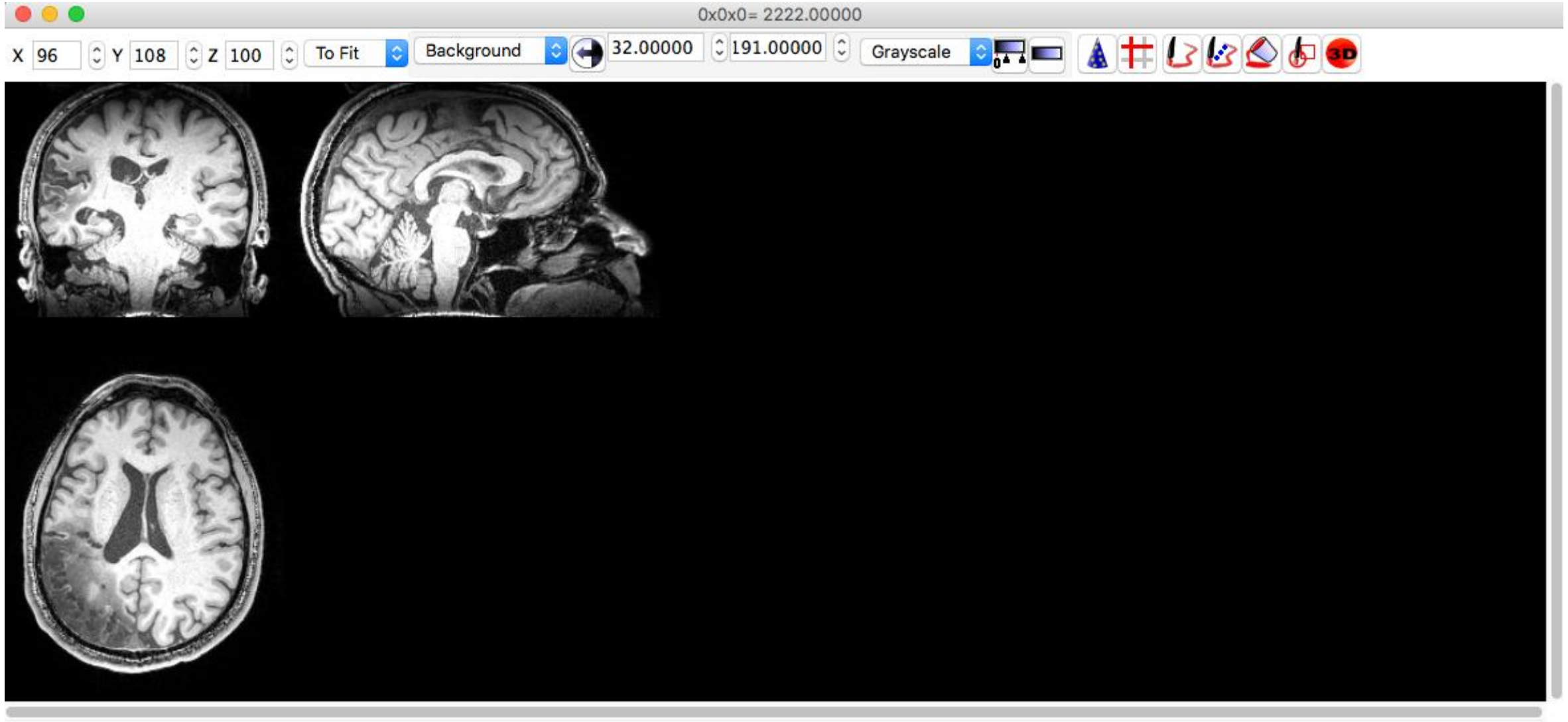
Updating the Master Scan Sheet

MR#	Lab	Date of Scan	# of discs	Type of Sc	Localiz	T1 MPRA	boldSCO	Resting BOLD	fairest_UI_1200ms (	fairest_UI_m0 (p	D	Resting BOLD (	FLA	Arteri	Breat	Full Sequence List	Notes
MR2		8/27/15	1 (extra is a	MRI	1	1	1	1	1	1	1					Localizer, T1 MPRAGE, fairest_UI_1200_ep2_max_bold, pcasl_PHC_1200ms, DTI_12dir	disc 2 is a copy of disc 1
MR2	Myrna	2/5/15	1	MRI	1	1	1	1	1	1	1		1			Localizer, T1 MPRAGE, pcasl_PHC_1500ms_scen_90mm, fairest_UI_1200ms, DTI_preordered30+5b0, ep2d_max_bold, flair	date unsure (binder note: 11/5/
MR2	Myrna	12/21/2012; 12/24	2	MRI; CT												brain multislice, T1 SAG, diffusion 128 RES, 2D CAR RAW DATA, 3D GRE COW SOURCE DATA, T2 AXIAL, T1 AXIAL, FLAIR AXIAL, 3D	Penn Scan code: XMR9190 ; date
MR2	Myrna	4/30/15	1	MRI	1	1	1	1	1	1	1		1			Localizer, T1 MPRAGE, pcasl_PHC_1500ms_scen_90mm, fairest_UI_1200ms, DTI_preordered30+5b0, ep2d_max_bold, flair	
MR2		9/26/16	1 (extra is a	MRI	1	1	1	1	1	1	1	1	1		1	Localizer, T1 MPRAGE, fairest_UI_1200_ep2_max_bold, pcasl_PHC_1200ms, DTI_12dir	disc 2 is a copy of disc 1
MR2	Myrna	5/4/16	1	MRI	1	1	1	1	1	1	1		1			Localizer, T1 MPRAGE, pcasl_PHC_1500ms_scen_90mm, fairest_UI_1200ms, DTI_preordered30+5b0, ep2d_max_bold, flair	
MR2	Myrna	4/7/15	1	MRI	1	1	1	1	1	1	1		1			Localizer, T1 MPRAGE, pcasl_PHC_1500ms_scen_90mm, fairest_UI_1200ms, DTI_preordered30+5b0, ep2d_max_bold, flair	
MR2	Eddie		1	MRI, CT													clinical MRI and CT; dates unsur
MR2	Buxbaum	1/6/16	1	MRI	1	1	1	1	1		1		1	1		Localizer, T1 MPRAGE, max_boldSCOUT, max_BOLD, fairest_UI_1200ms, Flair, DTI, ep2d_max_bold, pcasl, PHC_1500ms	repeat with Myrna's lab
MR2		10/16/16	1	MRI	1	1	1	1	1		1		1	1		localizer, t1 mprage, flair axial 320 4mm, ep2d_casl_AM_1500MS, ep2d_fairist_UI_1000ms, DTI	
MR2	Buxbaum	6/20/19	1	MRI	1	1	1				1	1	1		1	localizer, T1 MPRAGE, BOLD_scout, CMRR_ME_MB1, BOLD_breathLocalizer, DTI, FLAIR	
MR2		8/26/16	1	MRI	1	1	1	1	1		1		1	1		localizer, t1 mprage, flair axial 320 4mm, ep2d_casl_AM_1500MS, ep2d_fairist_UI_1000ms, DTI	
MR2	Myrna	7/31/15	1	MRI	1	1	1	1	1	1	1		1			Localizer, T1 MPRAGE, pcasl_PHC_1500ms_scen_90mm, fairest_UI_1200ms, DTI_preordered30+5b0, ep2d_max_bold, flair	
MR2		10/27/16	1 (extra is a	MRI	1	1	1	1	1	1	1					Localizer, T1 MPRAGE, fairest_UI_1200_ep2_max_bold, pcasl_PHC_1200ms, DTI_12dir	disc 2 is a copy of disc 1
MR2		9/14/16	1	MRI	1	1	1	1	1		1		1	1		localizer, t1 mprage, flair axial 320 4mm, ep2d_casl_AM_1500MS, ep2d_fairist_UI_1000ms, DTI	
MR2		9/19/16	1	MRI	1	1	1	1	1		1		1	1		localizer, t1 mprage, flair axial 320 4mm, ep2d_casl_AM_1500MS, ep2d_fairist_UI_1000ms, DTI	
MR2	Myrna	12/8/15	1	MRI	1	1	1	1	1	1	1		1			Localizer, T1 MPRAGE, pcasl_PHC_1500ms_scen_90mm, fairest_UI_1200ms, DTI_preordered30+5b0, ep2d_max_bold, flair	
MR2	Buxbaum	1/25/19	1	MRI	1	1	1				1	1	1		1	Localizer, T1 MPRAGE, pcasl_PHC_1500ms_scen_90mm, fairest_UI_1200ms, DTI_preordered30+5b0, ep2d_max_bold, flair (no boldscout)	
MR2	Buxbaum	10/13/17	1	MRI	1	1	1				1	1	1		1	localizer, T1 MPRAGE, BOLD_scout, CMRR_ME_MB1, BOLD_breathLocalizer, DTI, FLAIR	
MR2	Myrna		1	MRI	1	1	1	1	1	1	1		1			Localizer, T1 MPRAGE, pcasl_PHC_1500ms_scen_90mm, fairest_UI_1200ms, DTI_preordered30+5b0, ep2d_max_bold, flair	disc already processed; dates on
MR2	Buxbaum	5/17/19	1	MRI	1	1	1				1	1	1		1	localizer, T1 MPRAGE, BOLD_scout, CMRR_ME_MB1, BOLD_breathLocalizer, DTI, FLAIR	
MR2	Jax?	5/14/15	1	MRI	1	1	1	1	1		1		1	1		localizer, t1 mprage, flair axial 320 4mm, ep2d_casl_AM_1500MS, ep2d_fairist_UI_1000ms, DTI	
MR2		7/23/15	1	MRI	1	1	1	1	1		1		1	1		localizer, t1 mprage, flair axial 320 4mm, ep2d_casl_AM_1500MS, ep2d_fairist_UI_1000ms, DTI	
MR2	Buxbaum	8/28/17	2	MRI	1	1	1				1	1	1		1	localizer, T1 MPRAGE, BOLD_scout, CMRR_ME_MB1, BOLD_breathLocalizer, DTI, FLAIR	Sequences spread across both d
MR2		4/16/16	1	MRI	1	1	1	1	1		1		1	1		localizer, t1 mprage, flair axial 320 4mm, ep2d_casl_AM_1500MS, ep2d_fairist_UI_1000ms, DTI	
MR2		6/24/16	1	MRI	1	1	1	1	1		1		1	1		localizer, t1 mprage, flair axial 320 4mm, ep2d_casl_AM_1500MS, ep2d_fairist_UI_1000ms, DTI	
MR2	Buxbaum	6/14/19	1	MRI	1	1	1				1	1	1		1	localizer, T1 MPRAGE, BOLD_scout, CMRR_ME_MB1, BOLD_breathLocalizer, DTI, FLAIR	localizer, T1 MPRAGE, BOLD_sc
MR2	Myrna		1	MRI	1	1	1	1	1	1	1		1			Localizer, T1 MPRAGE, pcasl_PHC_1500ms_scen_90mm, fairest_UI_1200ms, DTI_preordered30+5b0, ep2d_max_bold, flair	disc already processed; dates on
MR2	Buxbaum	11/10/18	1	MRI	1	1	1				1	1	1		1	localizer, T1 MPRAGE, BOLD_scout, CMRR_ME_MB1, BOLD_breathLocalizer, DTI, FLAIR	
MR2	Myrna		1	MRI	1	1	1	1	1	1	1		1			Localizer, T1 MPRAGE, pcasl_PHC_1500ms_scen_90mm, fairest_UI_1200ms, DTI_preordered30+5b0, ep2d_max_bold, flair	disc already processed; dates on
MR2	Myrna	3/7/17	1	MRI	1	1	1	1	1	1	1		1			Localizer, T1 MPRAGE, pcasl_PHC_1500ms_scen_90mm, fairest_UI_1200ms, DTI_preordered30+5b0, ep2d_max_bold, flair	
MR2	Buxbaum	5/17/19	1	MRI	1	1	1				1	1	1		1	localizer, T1 MPRAGE, BOLD_scout, CMRR_ME_MB1, BOLD_breathLocalizer, DTI, FLAIR	
MR2	Buxbaum	9/29/17	1	MRI	1	1	1				1	1	1		1	localizer, T1 MPRAGE, BOLD_scout, CMRR_ME_MB1, BOLD_breathLocalizer, DTI, FLAIR	
MR2		11/9/16	1 (extra is a	MRI	1	1	1	1	1	1	1					Localizer, T1 MPRAGE, fairest_UI_1200_ep2_max_bold, pcasl_PHC_1200ms, DTI_12dir	disc 2 is a copy of disc 1
MR2	Buxbaum	5/23/19	1	MRI	1	1	1				1	1	1		1	localizer, T1 MPRAGE, BOLD_scout, CMRR_ME_MB1, BOLD_breathLocalizer, DTI, FLAIR	
MR2	Buxbaum	8/25/17	1	MRI	1	1	1				1	1	1		1	localizer, T1 MPRAGE, BOLD_scout, CMRR_ME_MB1, BOLD_breathLocalizer, DTI, FLAIR	
MR2	Myrna	12/16/15	1	MRI	1	1	1	1	1	1	1		1			Localizer, T1 MPRAGE, pcasl_PHC_1500ms_scen_90mm, fairest_UI_1200ms, DTI_preordered30+5b0, ep2d_max_bold, flair	Penn scan code: XMR9192
MR2	Buxbaum	3/27/17	1	MRI	1	1	1	1	1	1	1		1	1		Localizer, T1 MPRAGE, max_boldSCOUT, max_BOLD, fairest_UI_1200ms, Flair, DTI, ep2d_max_bold, pcasl, PHC_1500ms	n/a
MR2	Buxbaum	10/23/17	1	MRI	1	1	1				1	1	1		1	localizer, T1 MPRAGE, BOLD_scout, CMRR_ME_MB1, BOLD_breathLocalizer, DTI, FLAIR	
MR2	Buxbaum	7/25/18	1	MRI	1	1	1				1	1	1		1	localizer, T1 MPRAGE, BOLD_scout, CMRR_ME_MB1, BOLD_breathLocalizer, DTI, FLAIR	not sure where disc is, lost to fo
MR2	Buxbaum	11/13/17	2	MRI	1	1	1				1	1	1		1	localizer, T1 MPRAGE, BOLD_scout, CMRR_ME_MB1, BOLD_breathLocalizer, DTI, FLAIR	Sequences spread across both d
MR2	Eddie	10/5/17	1	MRI, CT												BRAIN ROUTINE JH, radiologist, MRA NECK WO NEW	clinical CT and clinical MRI; proc
MR2	Buxbaum	5/10/18	2 (See notes	MRI	1	1	1					1			1	Localizer, T1 MPRAGE, CMR_ME_MB1, BOLD_BreathLocalizer	Disc 2 has the remainder of the
MR2	Eddie	11/26/17	1	MRI												5A1C2BE40, Brain - Routine	clinical MRI
MR2	Buxbaum	9/16/19	1	MRI	1	1	1				1	1	1		1	localizer, M1 MPRAGE, BOLD_scout, CMRR_ME_BBI, BOLD, DTI, Flair	one of the sequences had to be
MR2	Middleton	9/3/19	1	MRI												Apparent diffusion coefficient, Ax DWI, Flair, SWAN, T2 (FRFSE) F_S, AXIA BRAVO REFORMAT, COR BRAVO FORMAT, COR PD, FI	clinical MRI 9/3/19 Jeanes; erro
MR2	Buxbaum	4/5/19	1	MRI	1	1	1				1	1	1		1	localizer, T1 MPRAGE, BOLD_scout, CMRR_ME_MB1, BOLD_breathLocalizer, DTI, FLAIR	
MR2	Middleton	8/10/18	1	CT												HEAD AXIAL, BRAIN PERF 8CM RAPID_Head, BRAIN W_O HX_Head	clinical CT Abington health
MR2	Middleton	10/10/17	1	MRI												BRAIN ROUTINE, radiologist	clinical MRI from Temple; errors
MR2	Erica	2/8/18	1	CT												5A8B63550, BRAIN HELICAL IDOSE 1 HEAD, Brain WO Head	clinical CT
MR2	Buxbaum	5/31/19	1	MRI	1	1	1				1	1	1		1	localizer, T1 MPRAGE, BOLD_scout, CMRR_ME_MB1, BOLD_breathLocalizer, DTI, FLAIR	

Lab pipeline



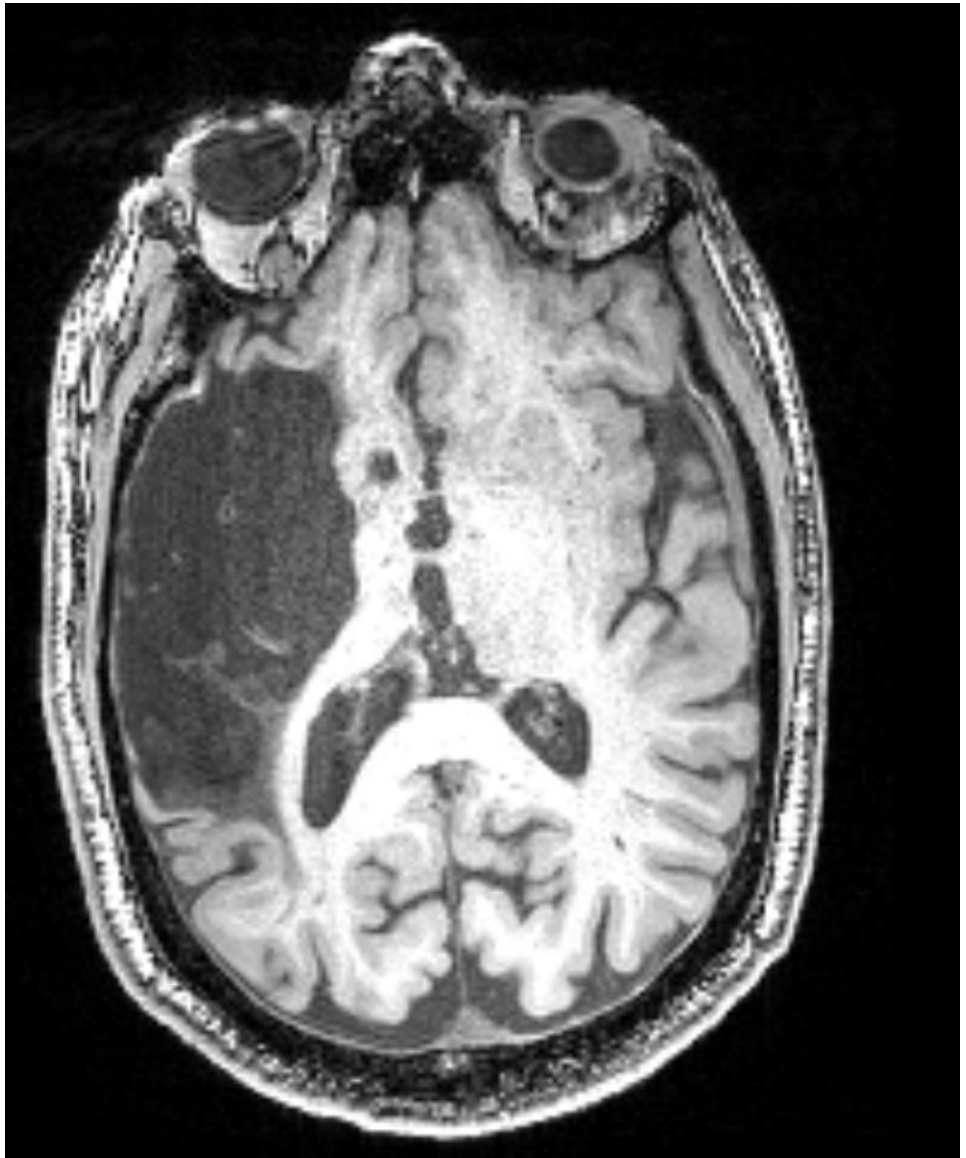
Lesion drawing

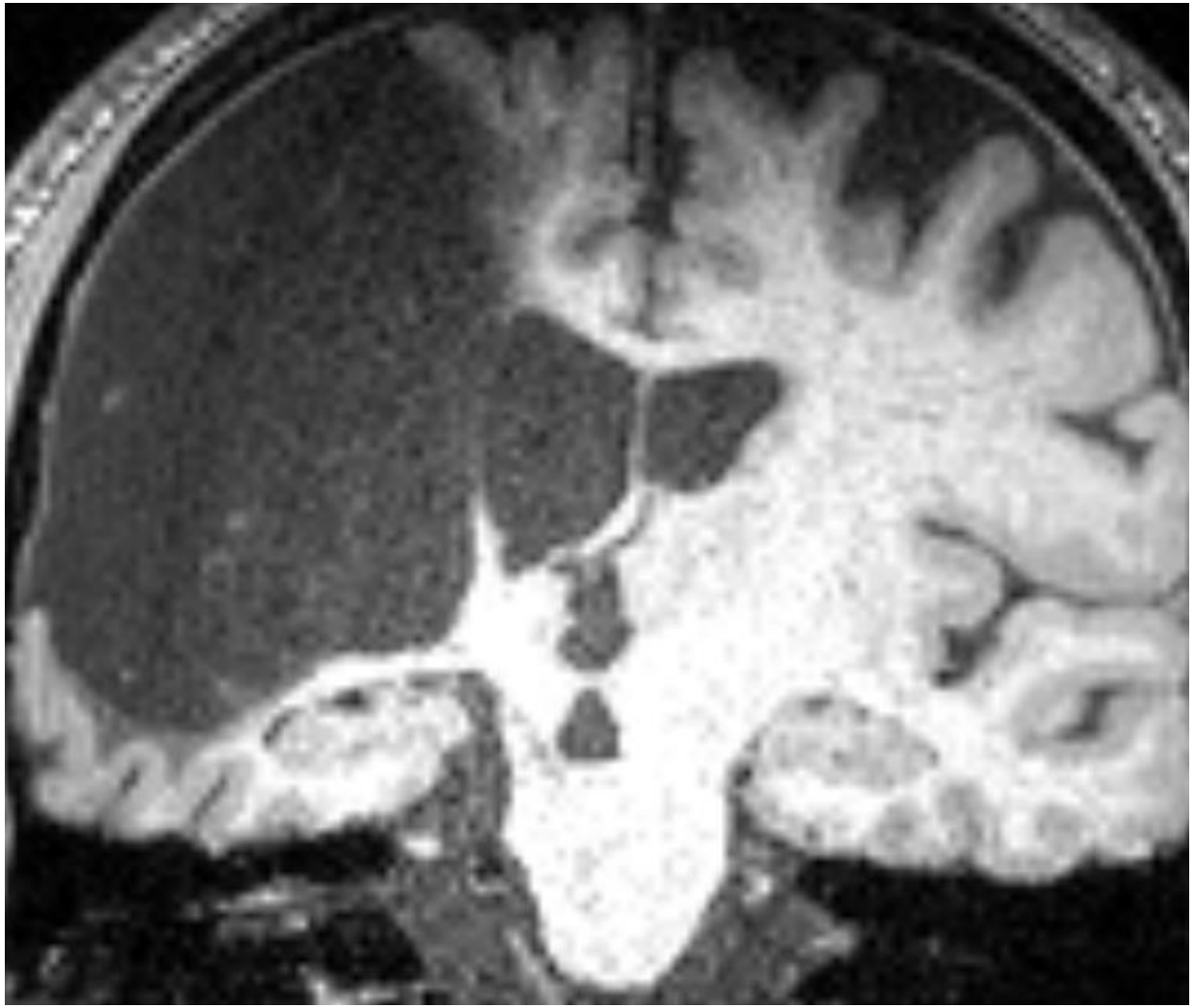


Lesion drawing

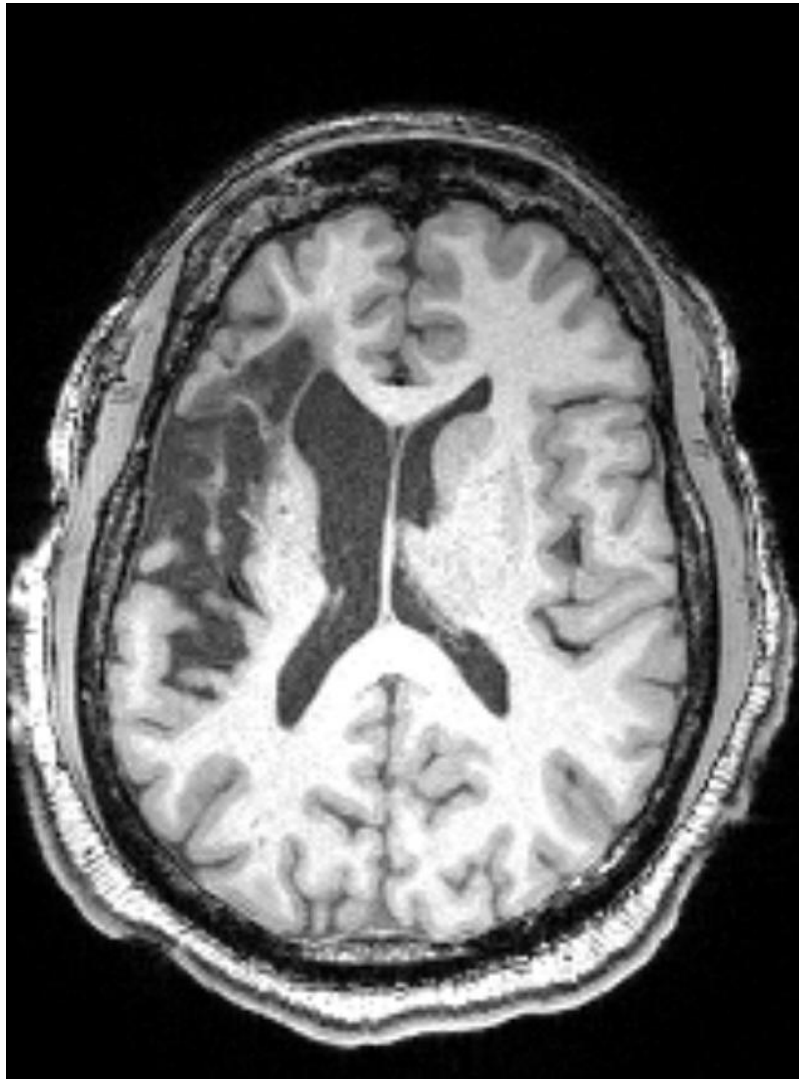
- Drawing can take 4-10 hours based on a myriad of variables
  - Things to be aware of when drawing:
    1. Lesion size
    2. Lateral sulcus
    3. Ventricles
    4. Atrophy
    5. Bi-lateral
    6. Multiple events

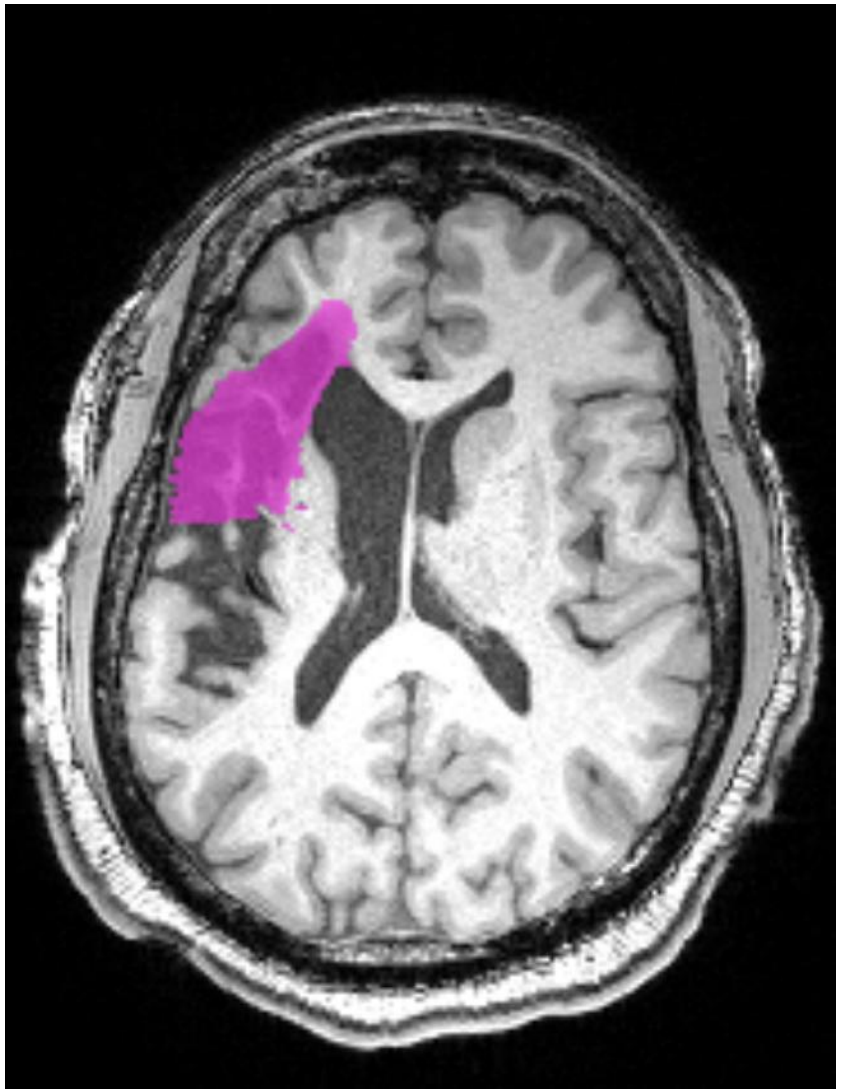
Variable 1: Lesion size



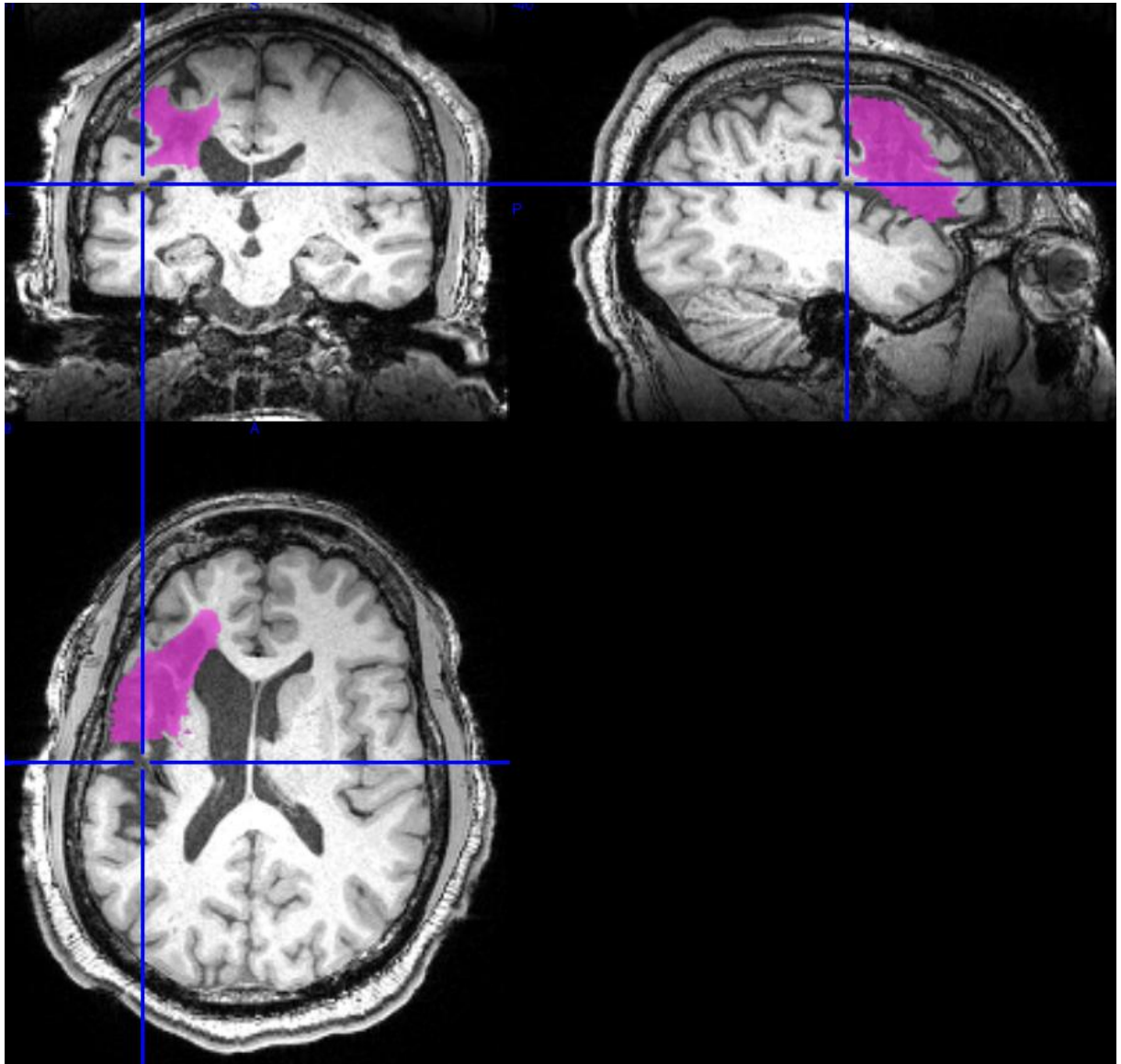


Variable 2: Lesions in the lateral Sulcus

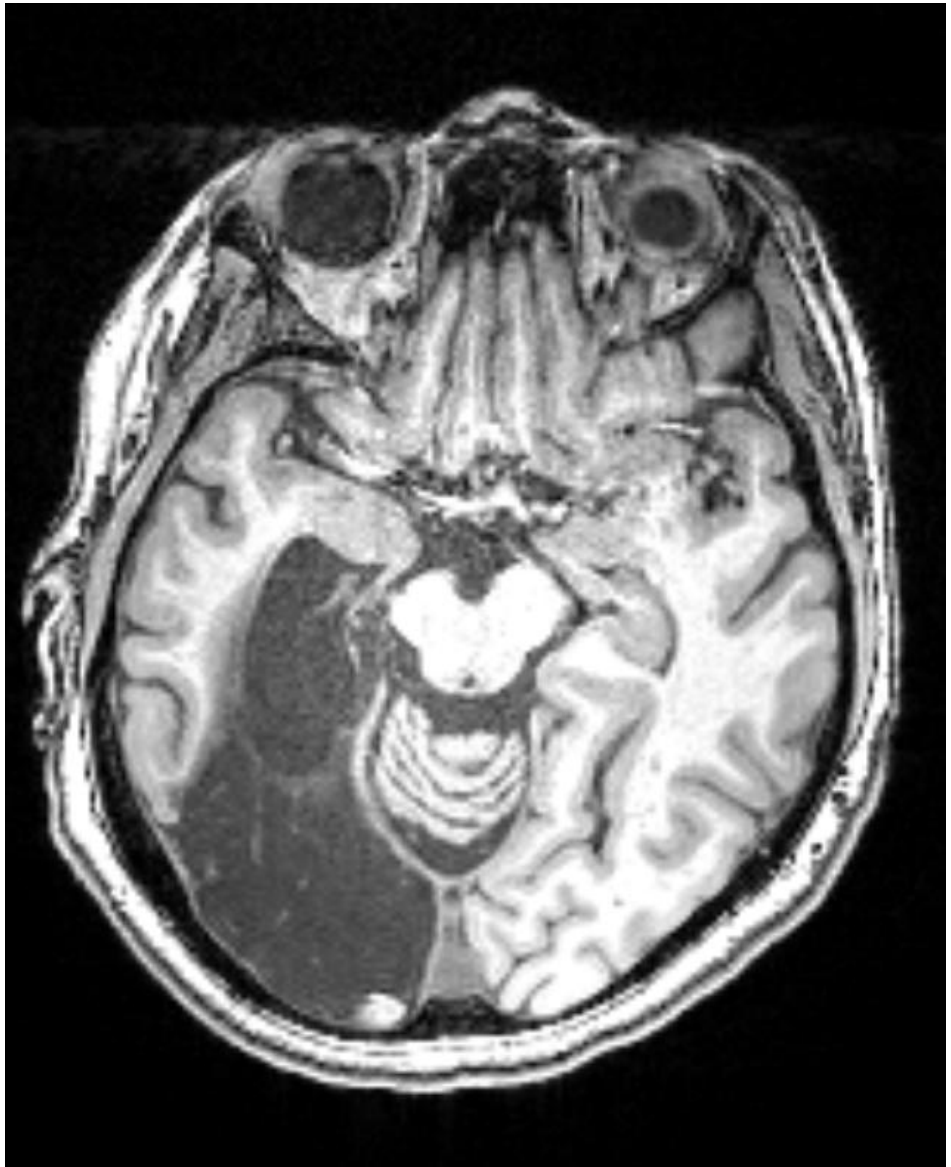


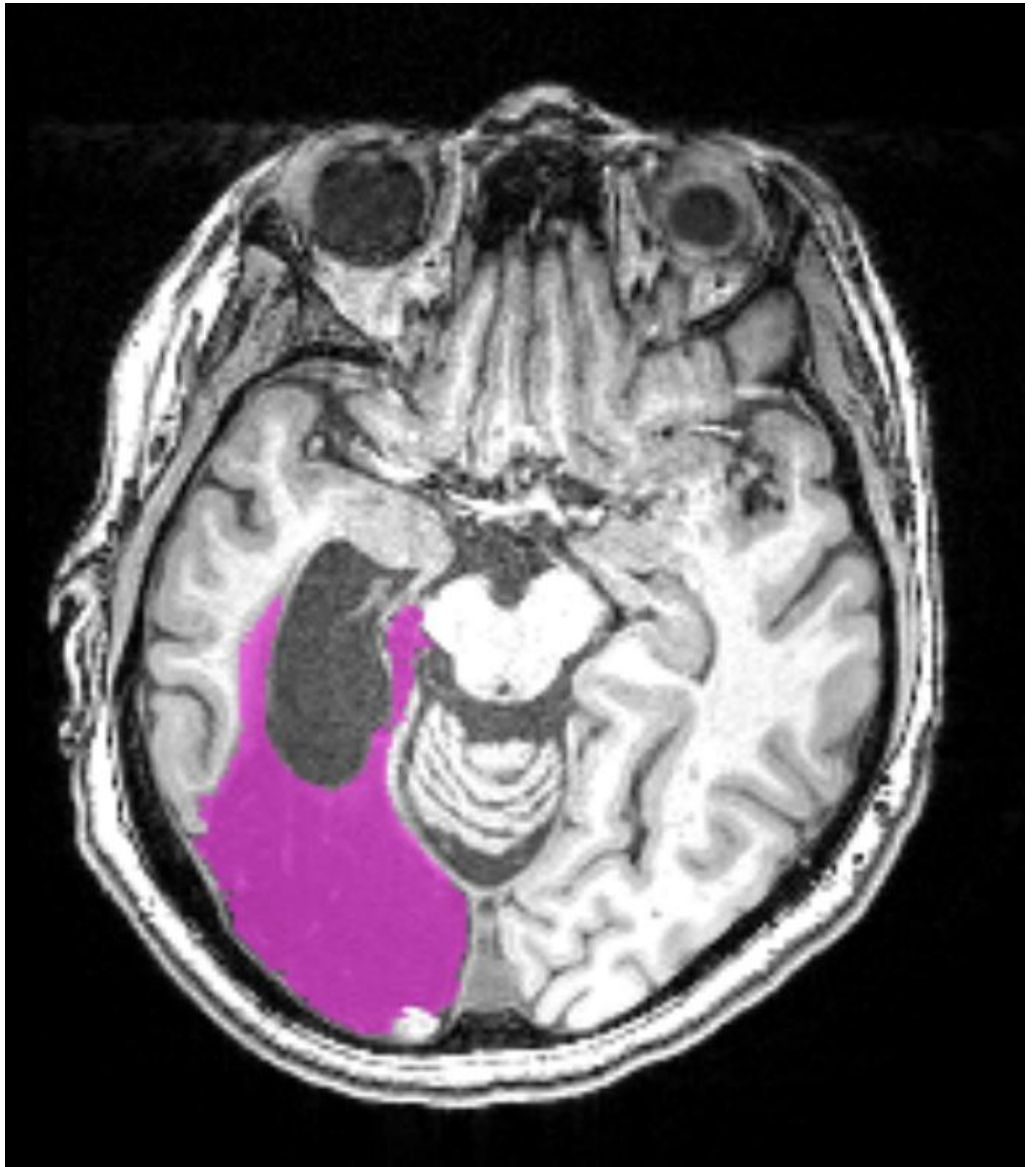


Variable 2: Lesions in the lateral sulcus

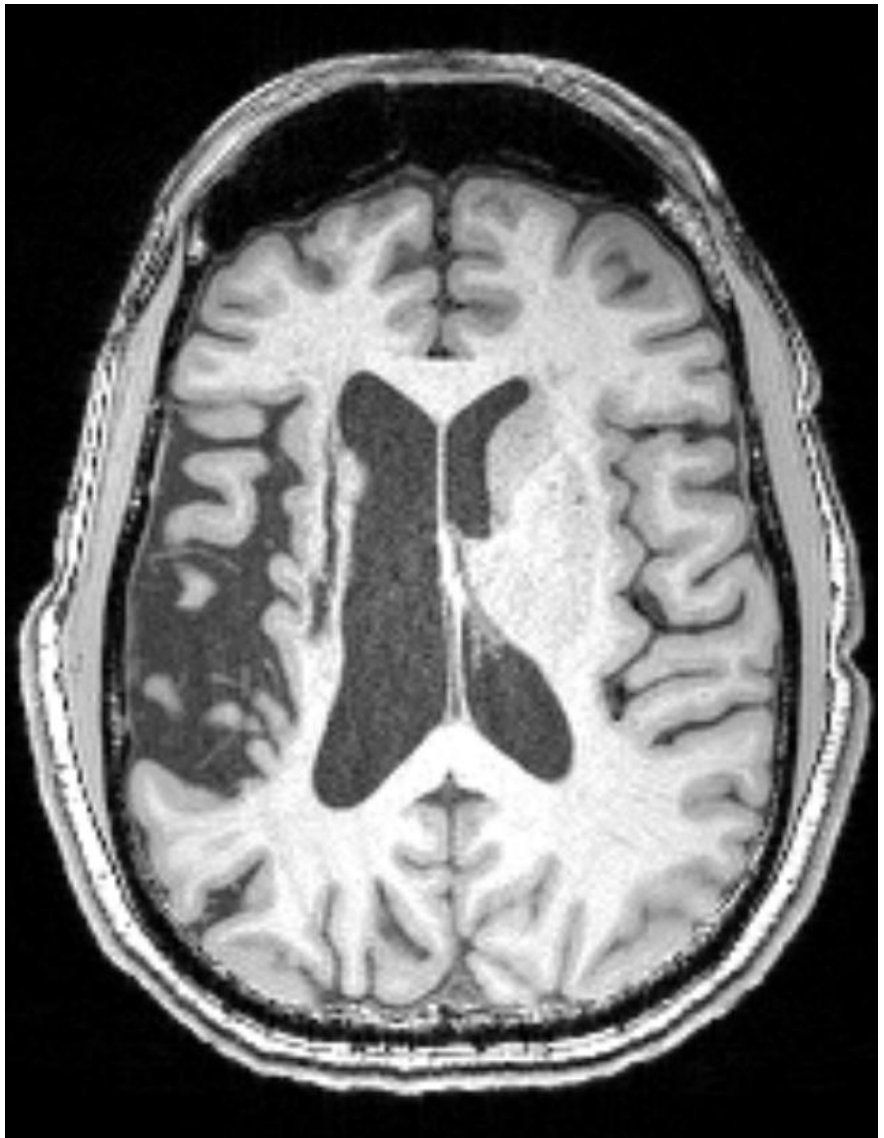


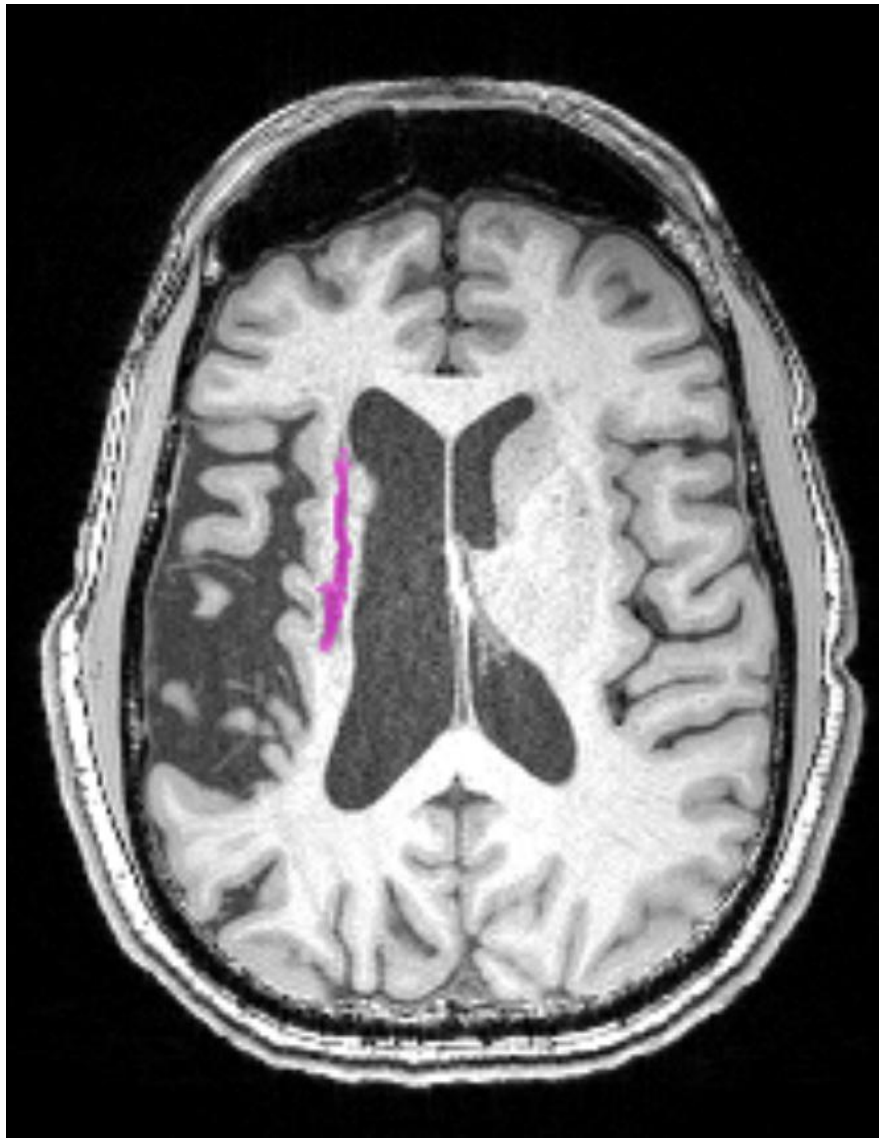
Variable 3: Lesions in the ventricles



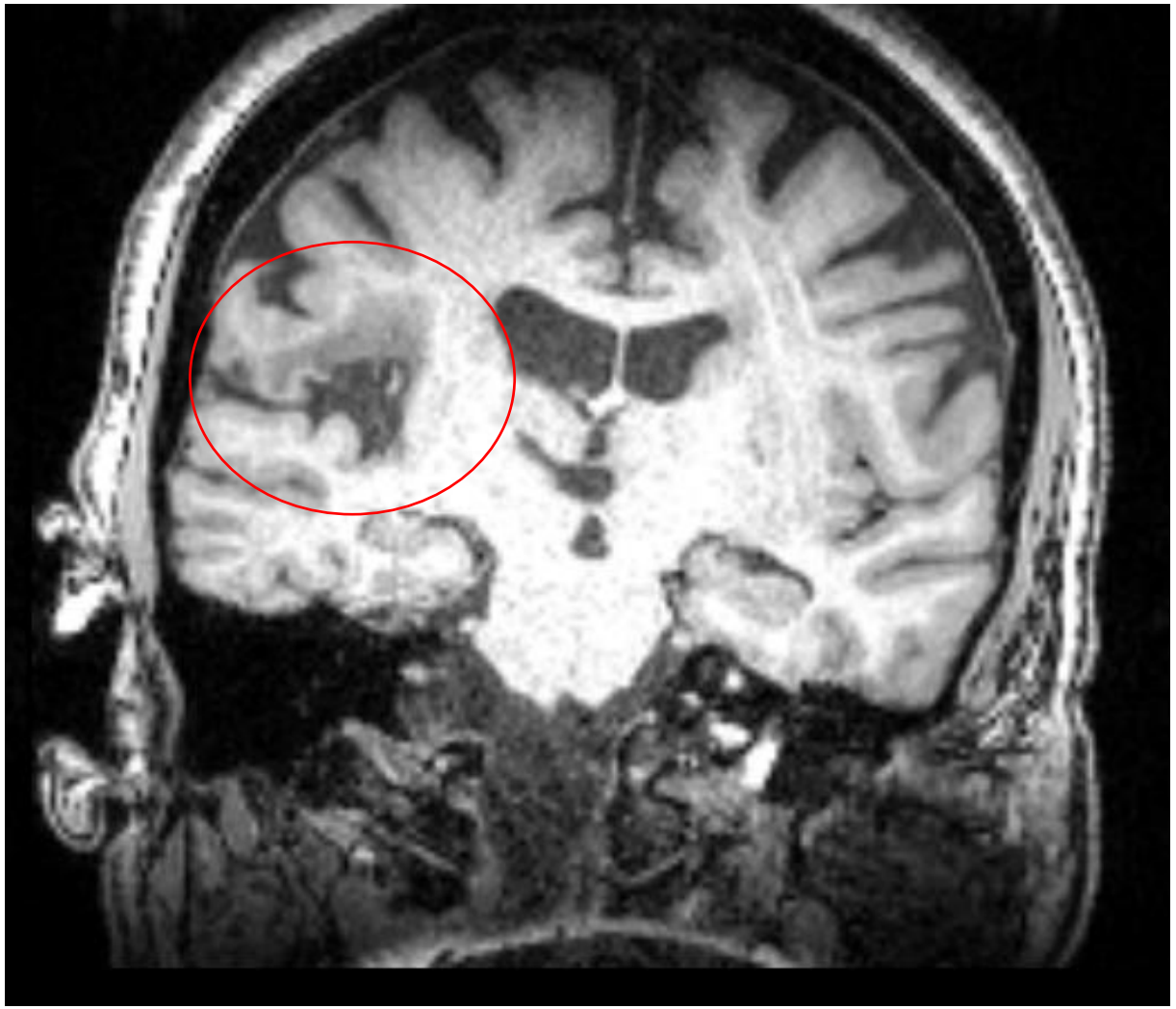


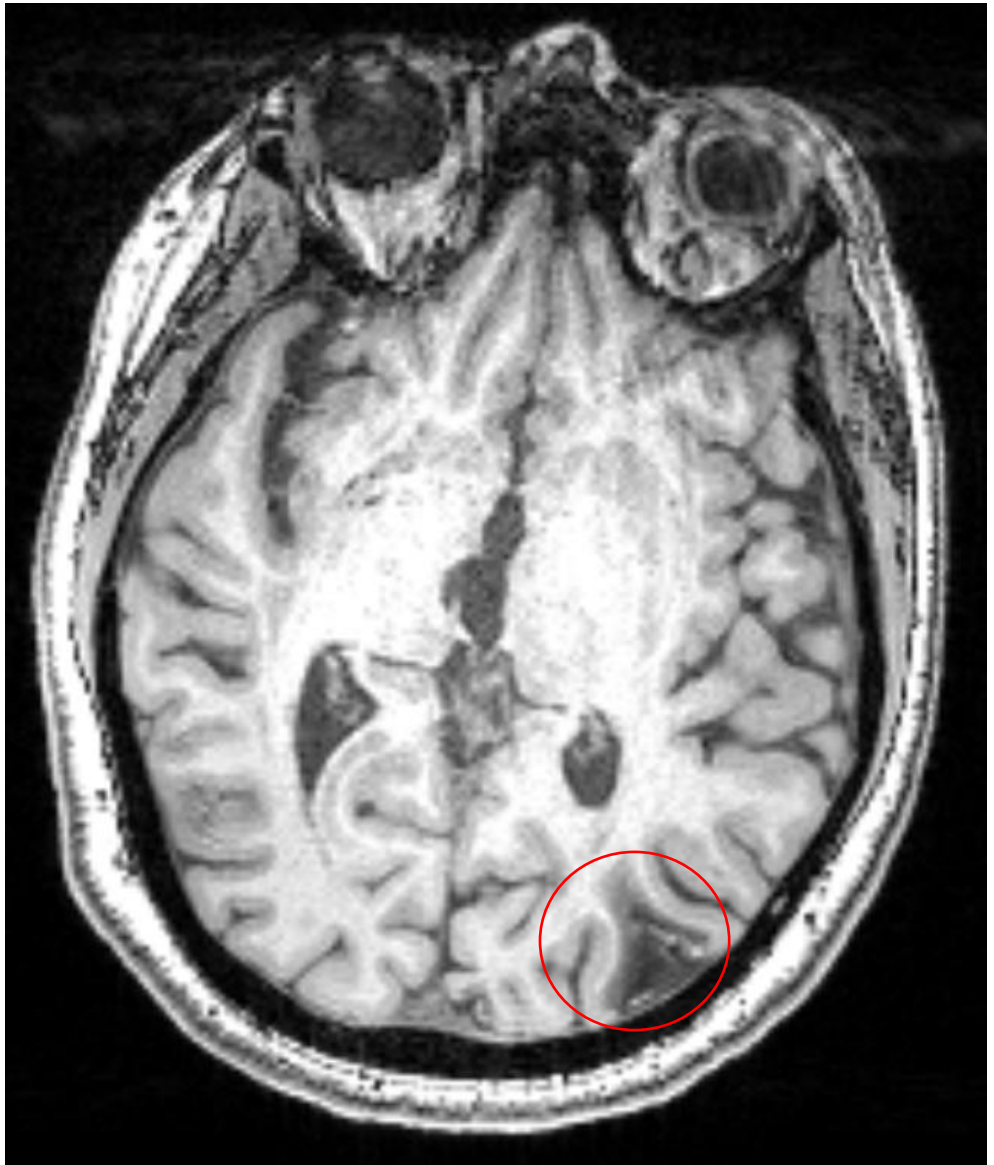
Variable 4: Atrophy

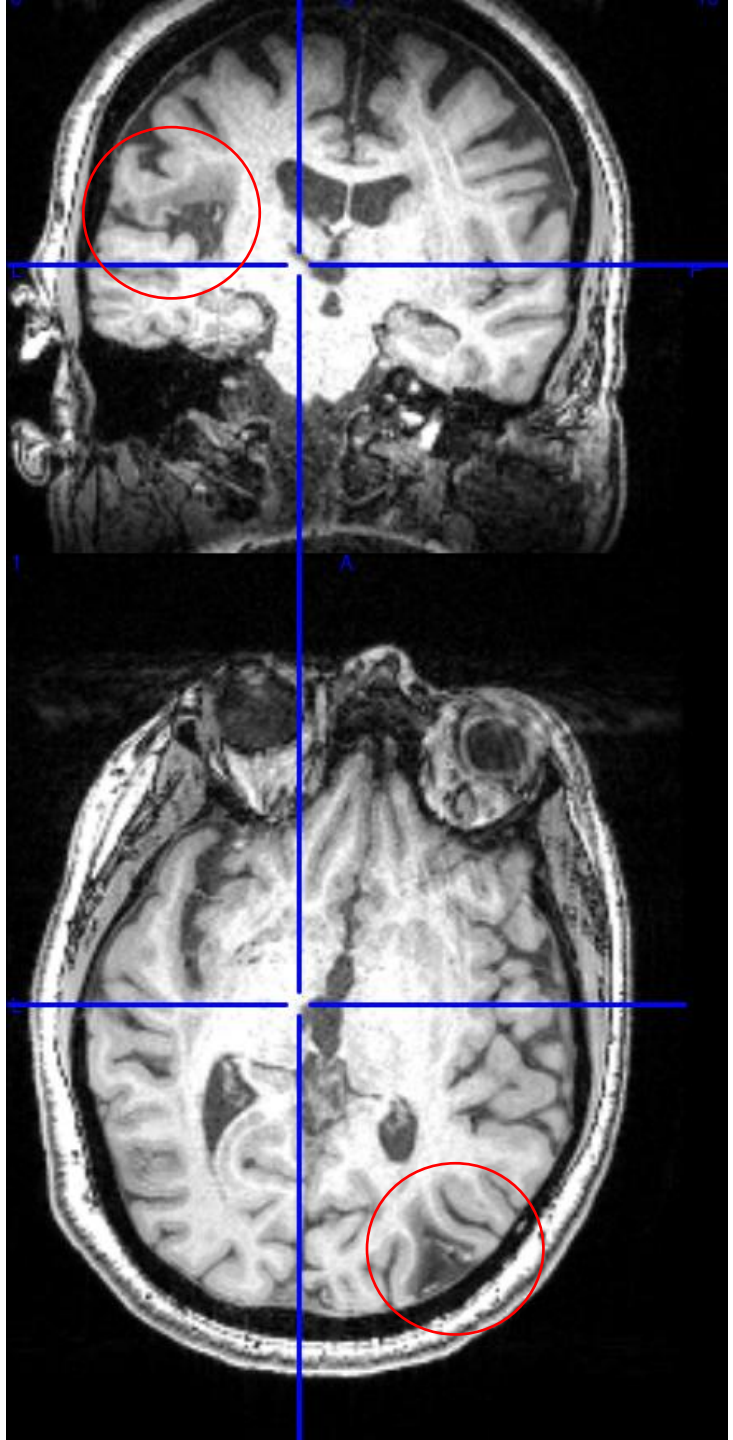




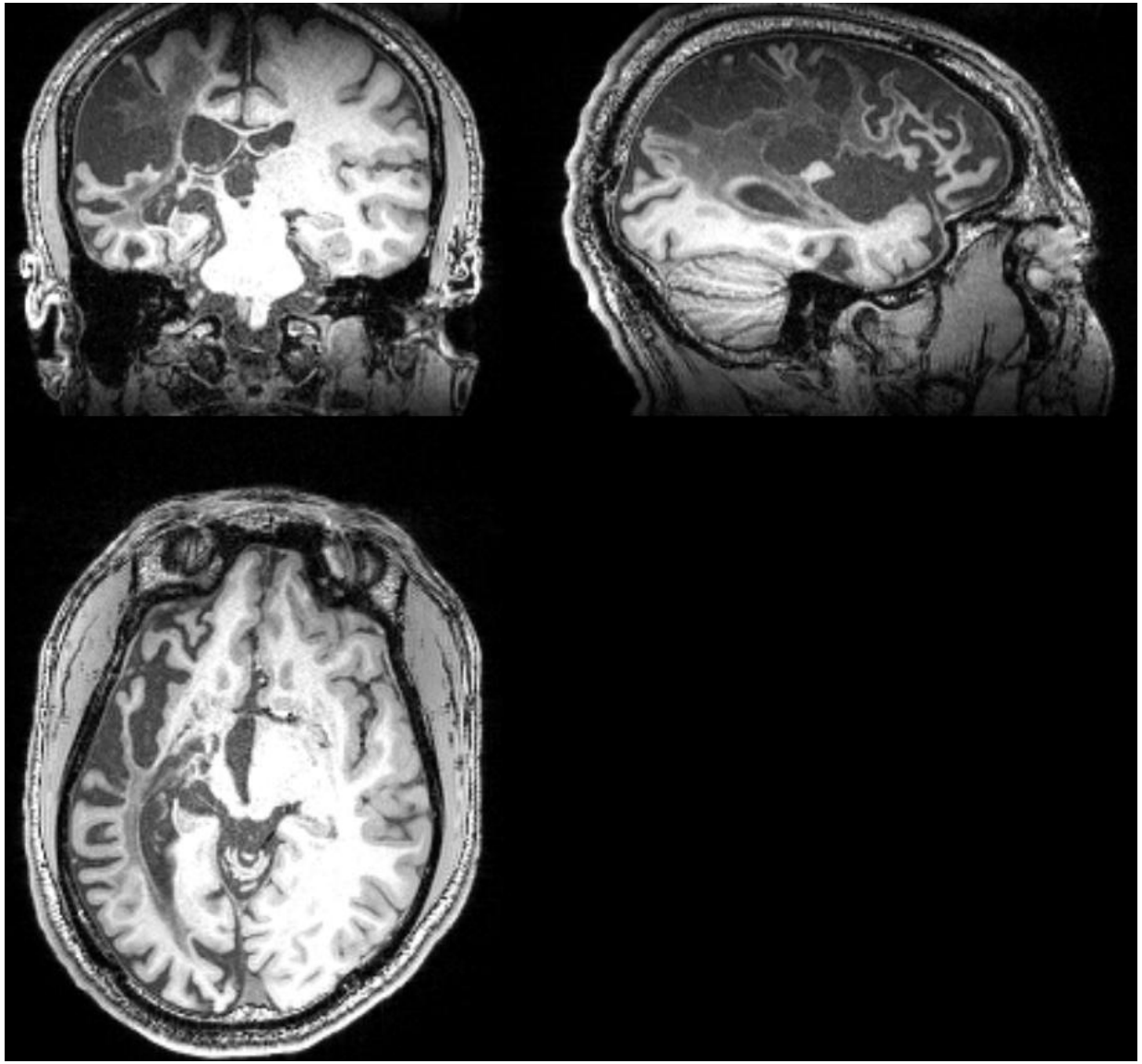
Variable 5: Bi-Lateral/Multiple events





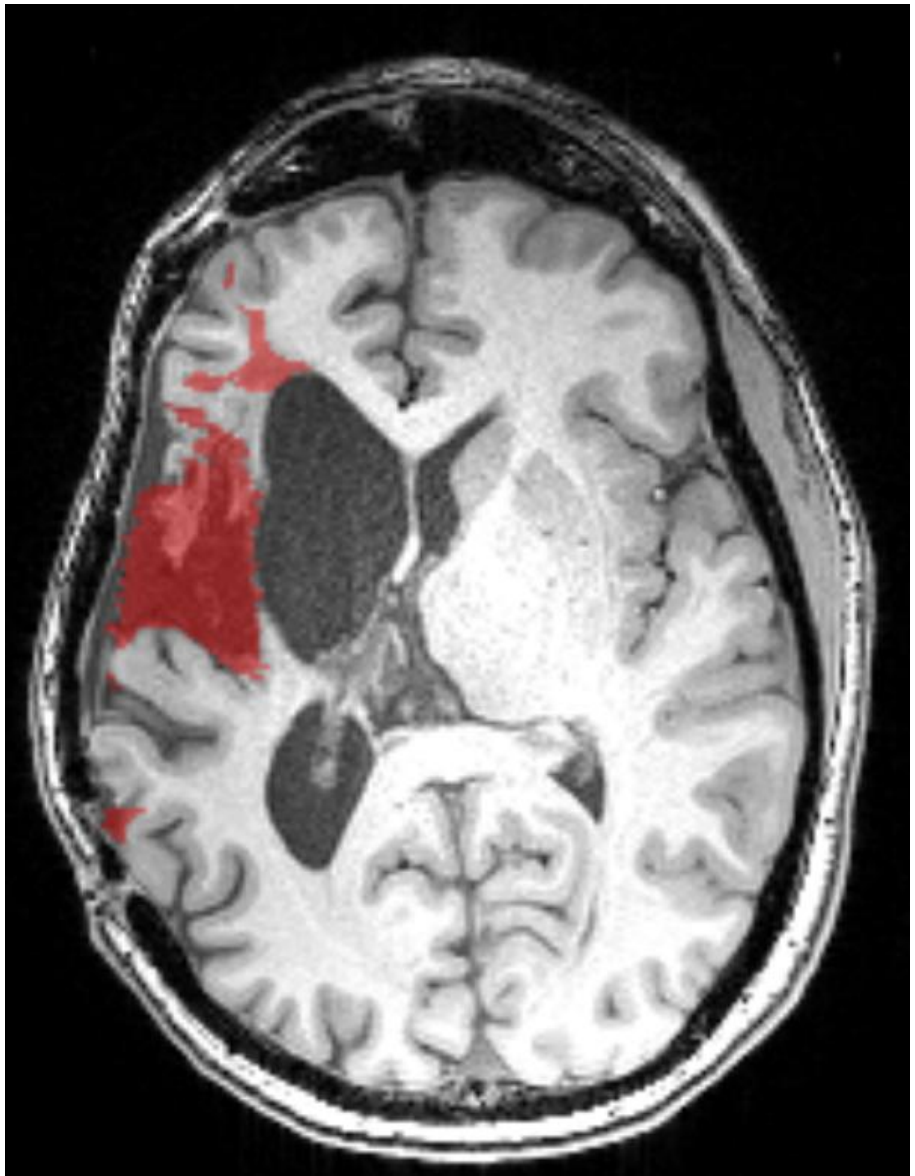


All of the above

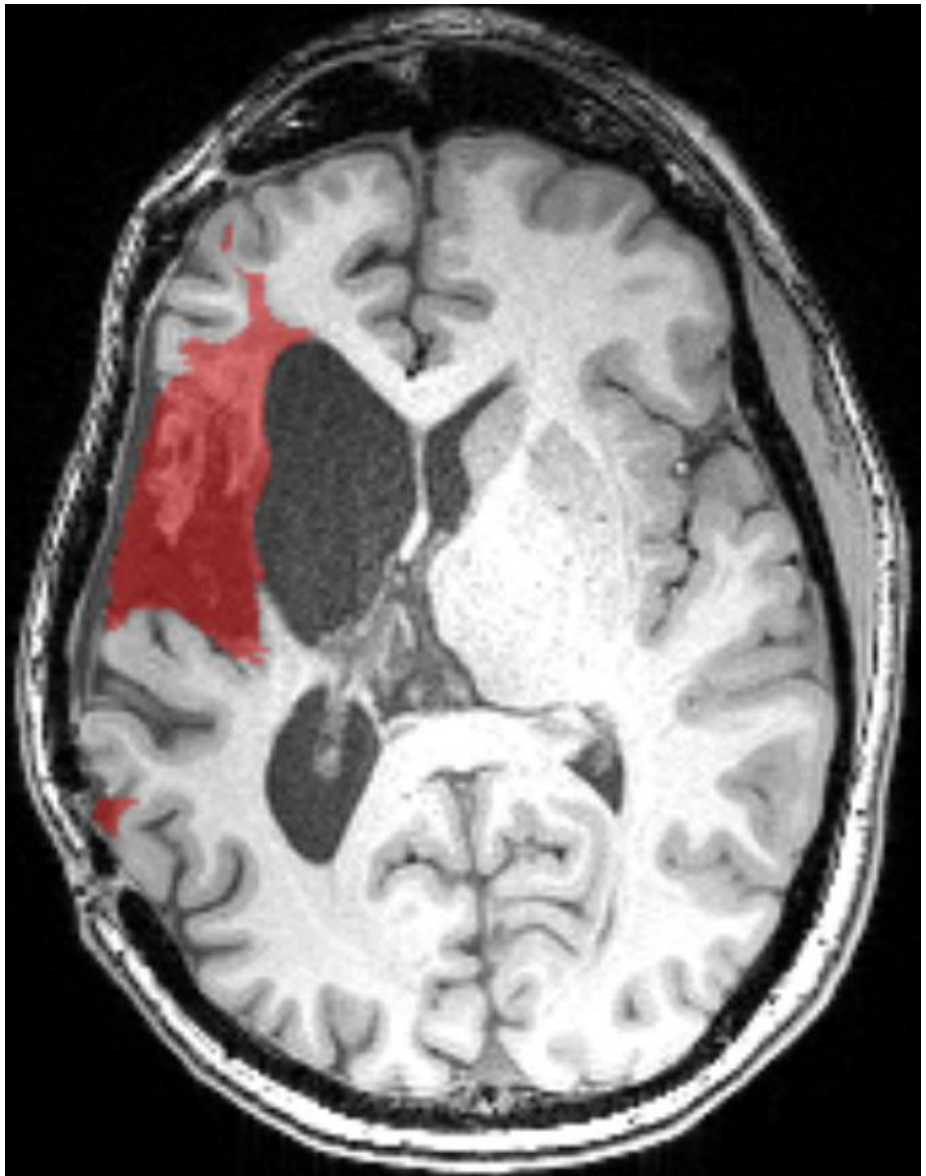


Checking the drawn lesion

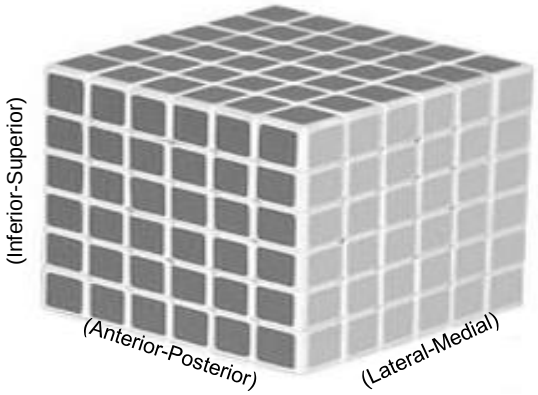
First draft



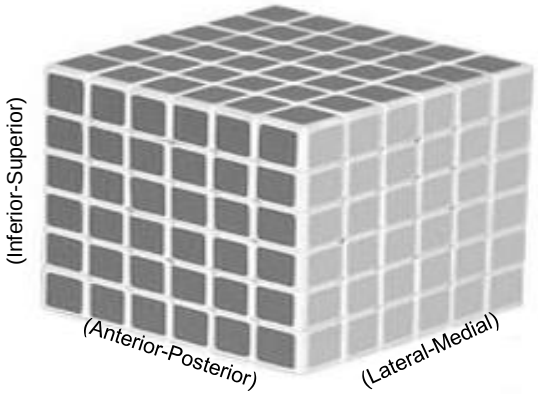
Edits after meeting with Branch



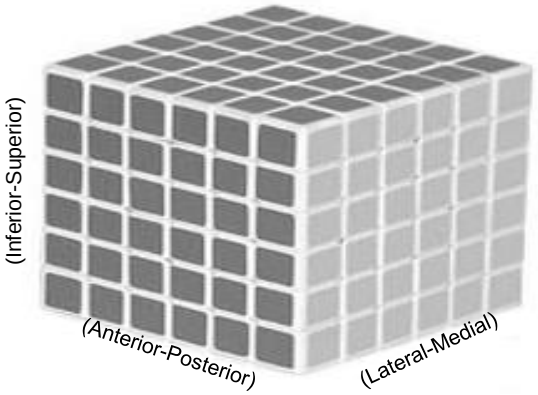
What are scan files?



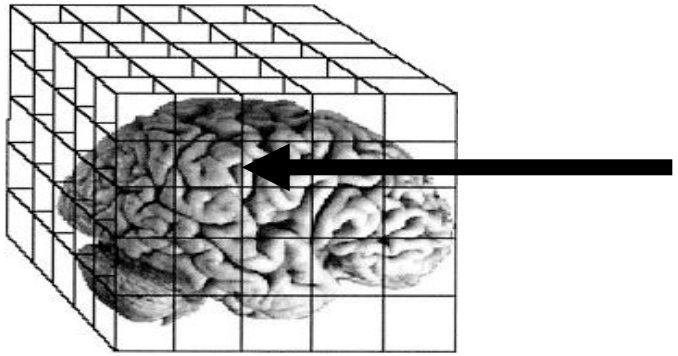
TR_1



TR_2

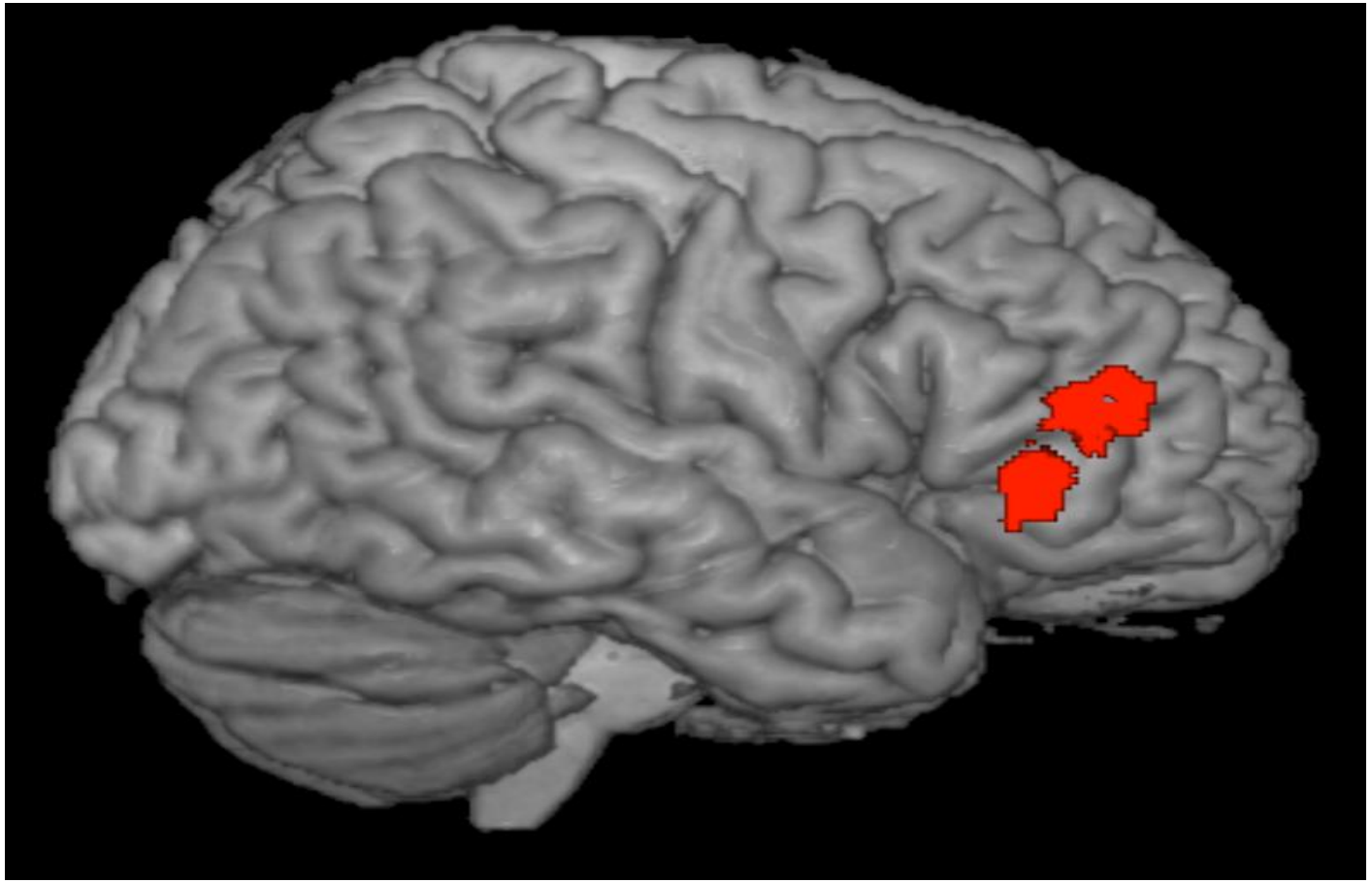


TR_3 ……TR_n

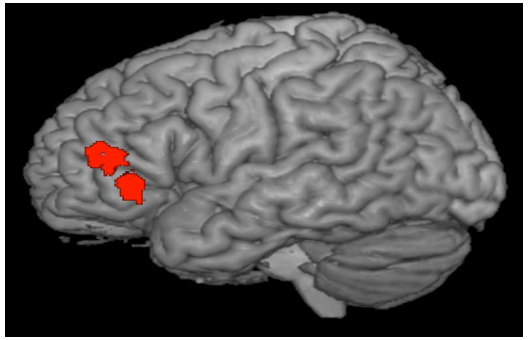


Voxel = basic unit of measurement.

What are **lesion** files?



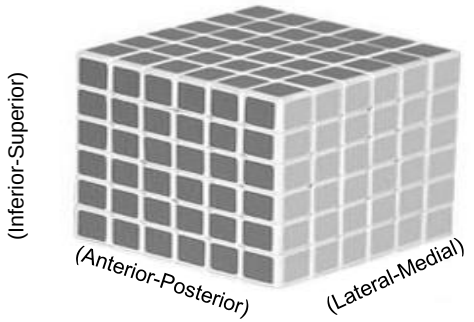
What are **lesion** files?



- Lesions drawn on native T1 or T2 structural image.
- Warped by neurologist who has expertise in identifying the accuracy of the lesion drawing.
- Final product is a lesion file in a template space (typically MNI space).
- Permits group-level analyses because all lesions are in the same coordinate space.

Coordinate Space

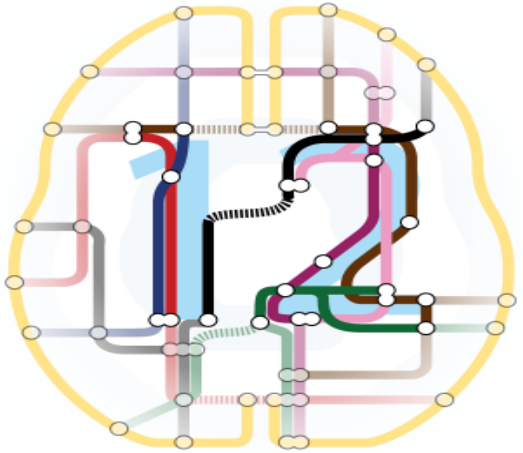
- Lesions files are three-dimensional arrays that are binarized.
- Voxels labeled with 0 = healthy tissue; voxels labeled with 1 = lesion tissue.
- Typical lesion in coordinate space is a binarized array of 181x217x181 voxels (> 7 million voxels).
- Try it yourself using mricron.



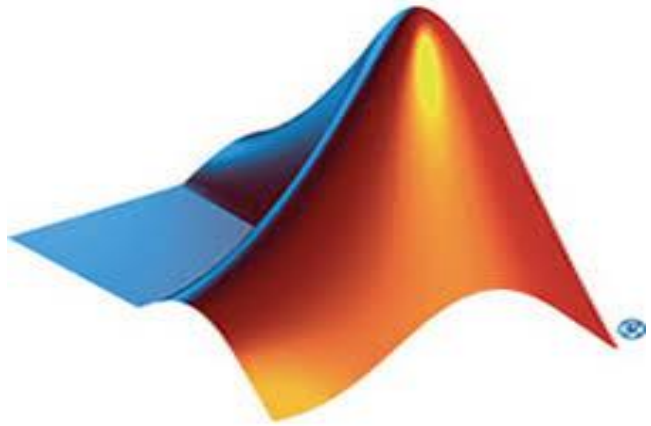
Coordinate Space

- Statistical Parametric Mapping Toolbox and Matlab computing software.

SPM



Matlab



For an SPM tutorial, see:
https://andysbrainbook.readthedocs.io/en/latest/SPM/SPM_Overview.html

Coordinate Space

- Statistical Parametric Mapping Toolbox and Matlab computing software.

SPM Matlab

- Using indexing functions in Matlab, we can find voxels equal to a specific value (e.g., lesions voxels = 1; statistical values > 1.96).

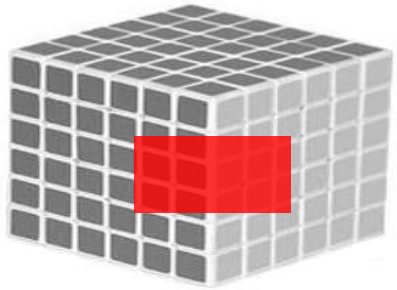
- Use indices to perform a range of statistical operations (e.g., overlap with predefined BA; subtracting voxels; compute the mean value in a subset of voxels).

For an SPM tutorial, see:
https://andysbrainbook.readthedocs.io/en/latest/SPM/SPM_Overview.html

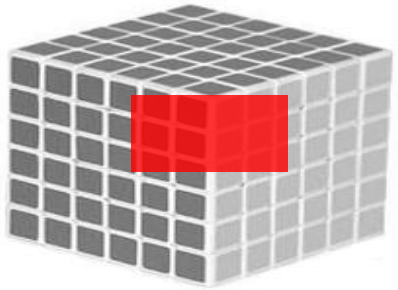
Lesion File Statistics

- Summing lesion overlap at each individual voxel.

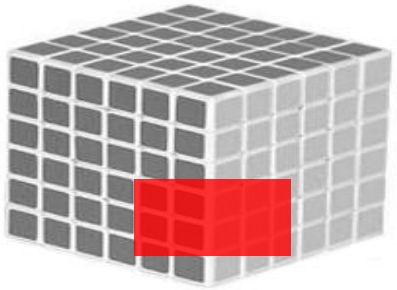
Subject 1



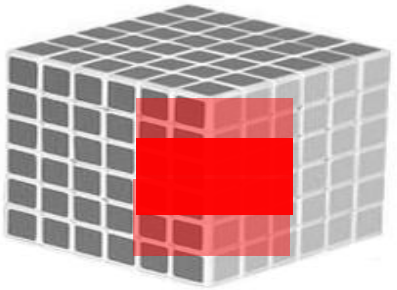
Subject 2

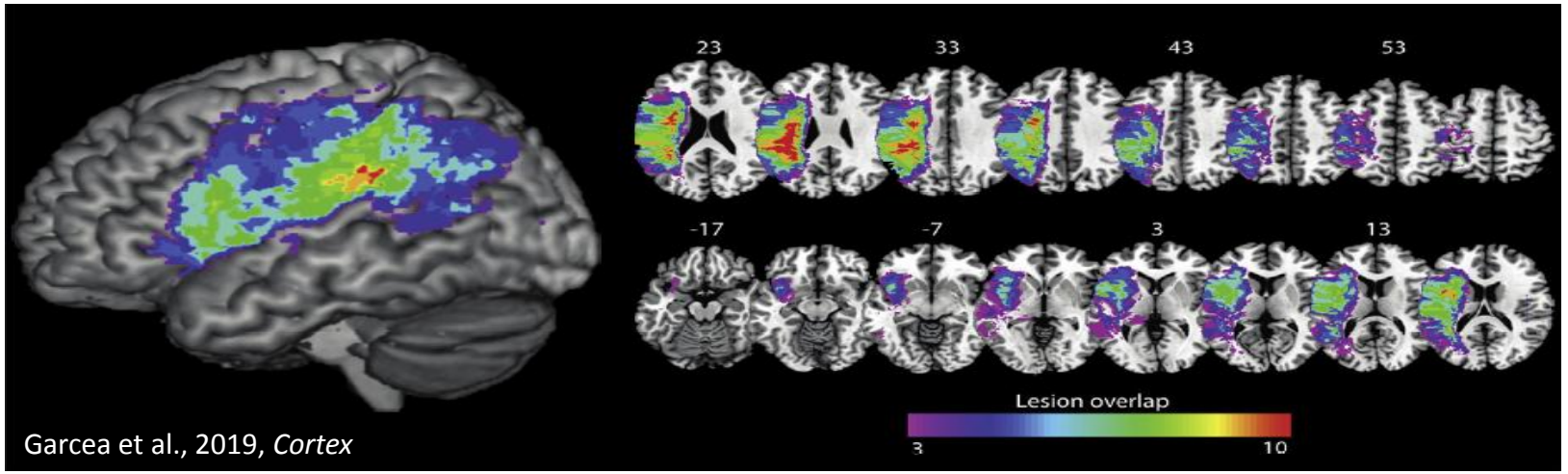


Subject 3



Lesion Overlap





Garcea et al., 2019, *Cortex*

Lesion File Statistics

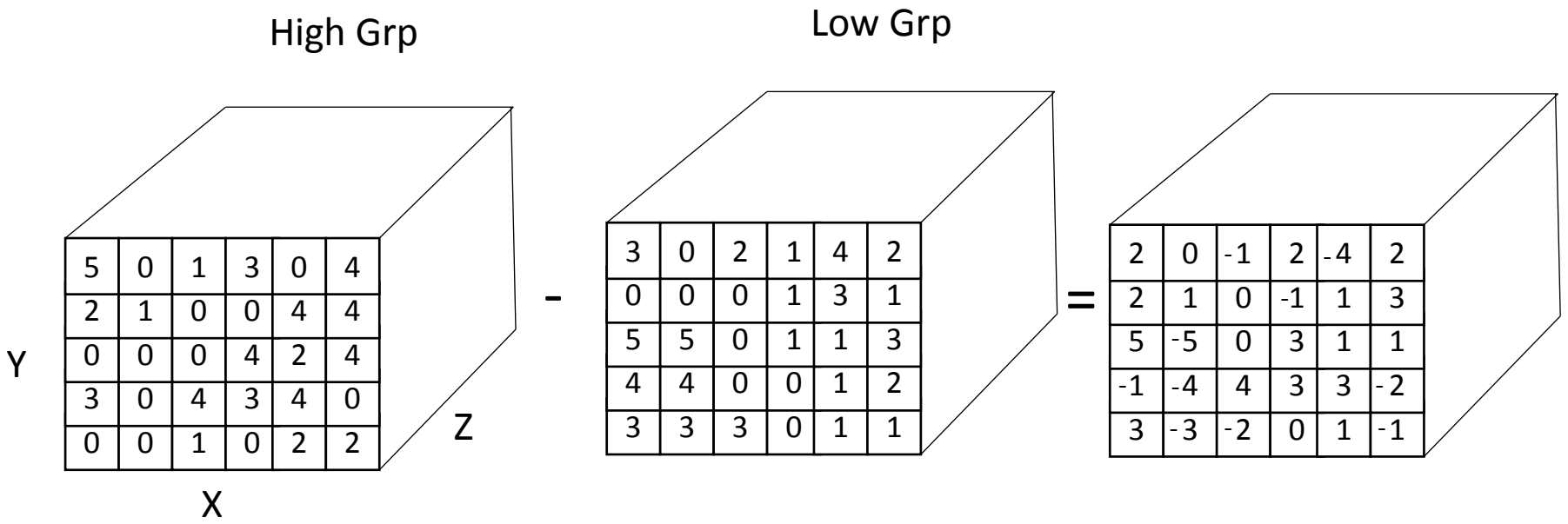
- Summing lesion overlap at each individual voxel.

- Other applications of this approach:
  - Subtracting subsets of participants who are impaired relative to those who are not impaired.

  - Identifying voxels with maximal overlap and performing secondary analysis on those voxels only (ROI approach).

  - Flexible approach to address your research question.

Subtraction map



Subtraction Map Steps

1) Divide Ps into a high and low group based of behavioral score
   - If using median split, consider cutting out middle (10-20%) of sample so its less arbitrary
2) Make overlap map for each group
3) Subtract high group from low group (and vice versa)
   - Done with VoxBo in Terminal
4) Reset template
5) Plot both maps onto template brain

Subtraction Map Voxbo Commands

- vbim -i [Map A] -sub [Map B] -o [Name of output map]
- vbim -i High_Grp.nii -sub Low_Grp.nii -o High_sub_Low.nii

- vbim -i [Input Map] -setspace [Template] -o [Name of output map]
- vbim -i High_sub_Low.nii -setspace ch2bet.nii -o High_sub_low_setspace.nii

Terminal output Subtraction Map

Matlab-Mini-3:~ mrri$ cd ~/Desktop/Lesion_Practice/Subtraction_Map/. **Setting CD to where analysis files are located**

Matlab-Mini-3:Subtraction_Map mrri$ vbim -i High_Grp/HighGrp.nii.gz -sub Low_Grp/LowGrp.nii.gz -o High_sub_Low.nii.gz **Subtracting high group from low group**

[I] vbim: reading file High_Grp/HighGrp.nii.gz

[I] vbim: wrote file High_sub_Low.nii.gz

Matlab-Mini-3:Subtraction_Map mrri$ vbim -i Low_Grp/LowGrp.nii.gz -sub High_Grp/HighGrp.nii.gz -o Low_sub_High.nii.gz **Subtracting low group from high group**

[I] vbim: reading file Low_Grp/LowGrp.nii.gz

[I] vbim: wrote file Low_sub_High.nii.gz

Matlab-Mini-3:Subtraction_Map mrri$ vbim -i High_sub_Low.nii.gz -setspace ch2bet.nii.gz -o High_sub_Low_setspace.nii.gz **Setting output to ch2bet template**

[I] vbim: reading file High_sub_Low.nii.gz

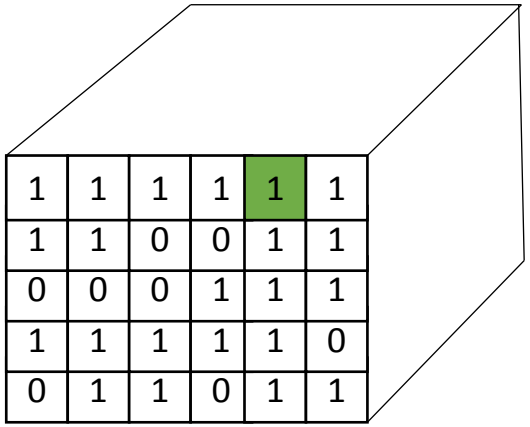
[I] vbim: wrote file High_sub_Low_setspace.nii.gz

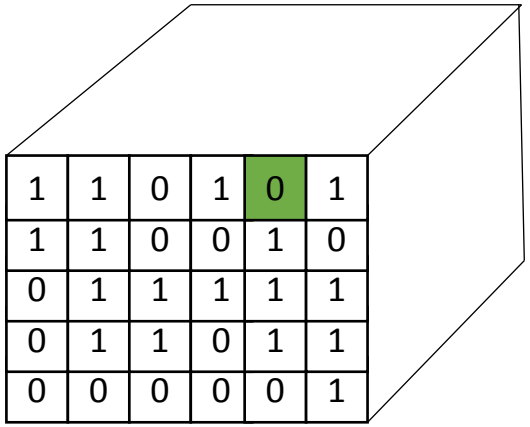
Matlab-Mini-3:Subtraction_Map mrri$ vbim -i Low_sub_High.nii.gz -setspace ch2bet.nii.gz -o Low_sub_High_setspace.nii.gz **Setting output to ch2bet template**

[I] vbim: reading file Low_sub_High.nii.gz

[I] vbim: wrote file Low_sub_High_setspace.nii.gz

Matlab-Mini-3:Subtraction_Map mrri$





Score with Voxel Lesioned	Score with Voxel Not Lesioned
10	3
15	4
12	7
13	6
8	1
16	5
19	4

t = 5.64

VLSM Basics

- Do this in each voxel of the brain
- Need to correct for # of tests
- Several ways to do this, in VoxBo we use false discovery rate (FDR)
- Other things to consider before running analysis:
  - Lesion Threshold # (10% of sample)
  - Correcting for total lesion volume

VLSM Steps

1. Make 4d map
   - Map of all lesions in one .nii file
2. Create document with behavioral scores
   - Make sure behavioral scores are in the same order as lesion files
   - VoxBo does not read .txt or .xls files; can make
3. Run VLSM Analysis
   - Consider parameters (lesion threshold, direction of scores, etc.)
4. Reset output to template

VLSM VoxBo Code

- vbim [Lesion Files] -write4d [Output File Name]
- vbim Lesions/*.nii -write4d VLSM_Prac_4d.nii

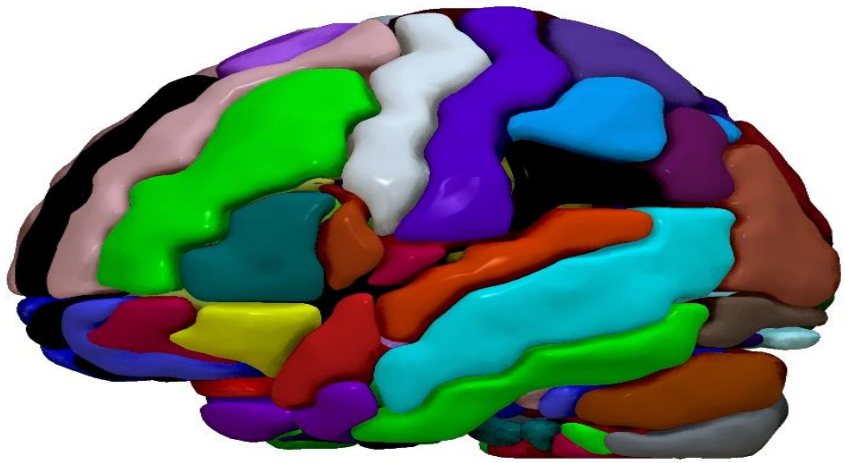
- vbtmap [4d File] [Score File] [Output File Name] -q [Threshold of FDR Correction] -n [Lesion Threshold #]
- vbtmap VLSM_Prac_4d.nii behavior VLSM_Prac_Output.nii -q 0 -n 3
  - Adding -z flag will transform output into z values instead of t
  - Adding -f flag will flip scores depending on direction you are interested in
  - VoxBo assumes you are interested in higher scores

Terminal output of VLSM

- Matlab-Mini-3:~ mrri$ cd ~/Desktop/Lesion_Practice/VLSM/ **Setting CD to where analysis files are located**
- Matlab-Mini-3:VLSM mrri$ vbim Lesions/*.nii -write4d VLSM_Prac_4d.nii **Making 4d file**
- [I] vbim: wrote file VLSM_Prac_4d.nii
- Matlab-Mini-3:VLSM mrri$ emacs behavior **Making file to read behavior scores (copy paste scores then hit ctrl + X, Y)**
- Matlab-Mini-3:VLSM mrri$ vbtmap VLSM_Prac_4d.nii behavior VLSM_Prac_Output.nii -q 0 -z -f -n 13 **Running VLSM**
- [I] vbtmap: FDR calculation included 317218 voxels with p values from 0.0000 to 0.9237
- [I] vbtmap: FDR threhsold for q=0.01 is 2.6231
- [I] vbtmap: FDR threhsold for q=0.02 is 2.2649
- [I] vbtmap: FDR threhsold for q=0.03 is 2.0552
- [I] vbtmap: FDR threhsold for q=0.04 is 1.9031
- [I] vbtmap: FDR threhsold for q=0.05 is 1.7806
- [I] vbtmap: FDR threhsold for q=0.10 is 1.3737
- [I] vbtmap: FDR threhsold for q=0.15 is 1.1088
- [I] vbtmap: FDR threhsold for q=0.20 is 0.9001
- [I] vbtmap: FDR threhsold for q=0.40 is 0.2844
- [I] vbtmap: unique lesion patterns: 175383
- [I] vbtmap: wrote stat map to VLSM_n128.nii
- Matlab-Mini-3:VLSM mrri$ vbim -i VLSM_Prac_Output.nii -setspace ch2bet.nii -o VLSM_Prac_Output_setspace.nii **Setting output to ch2bet template**

Post-analysis Statistics

- Now that we have a whole-brain map, let’s identify peaks, clusters, and voxel coordinates.
- Matlab scripts take as input a statistical map, an atlas map, and ask for a threshold of significance.



Post-analysis Statistics

- Now that we have a whole-brain map, let's identify peaks, clusters, and voxel coordinates.
- Matlab scripts take as input a statistical map, an atlas map, and ask for a threshold of significance.

```
function [VoxelStats] = ExtractVoxelStats
%% set up parameters
thresh = input('what is your voxel threshold to determine significance?');
%% first map
[file,path] = uigetfile('*.nii','select run1 map 1');
Volume1 = spm_vol(fullfile(path,file));
[SubMap1,XYZ] = spm_read_vols(Volume1);
statmap = reshape(SubMap1,[size(SubMap1,1)*size(SubMap1,2)*size(SubMap1,3),1]);
statmap = abs(statmap);
%% second map
[file,path] = uigetfile('*.nii.gz','select run1 map 2');
Volume2 = spm_vol(fullfile(path,file));
[SubMap2,XYZ] = spm_read_vols(Volume2);
broadmanmap = reshape(SubMap2,[size(SubMap2,1)*size(SubMap2,2)*size(SubMap2,3),1]);
```

Post-analysis Statistics

- Now that we have a whole-brain map, let’s identify peaks, clusters, and voxel coordinates.
- Matlab scripts take as input a statistical map, an atlas map, and ask for a threshold of significance.
- Then identify the peak voxel in the statistical map (strongest supra-threshold value) in every subregion of an atlas map.

```
%% let's loop through brodmann areas to get coordinates
brodmanregions = unique(broadmanmap);
counter = 0;
VoxelStats = [];
% main loop
for broadmani = 1:length(brodmanregions)
    if brodmanregions(broadmani)>0
        %% get voxelwise coordinates for each brodmann area
        %counter = counter + 1;
        tmpvoxindices = find(broadmanmap==brodmanregions(broadmani));
        if size(find(statmap(tmpvoxindices)>thresh),1) > 0
            counter = counter + 1;
            VoxelStats.broadman(counter).data = statmap(tmpvoxindices);
            %% let's get the peak coordinate in each broadman ROI.
            tmpdata = VoxelStats.broadman(counter).data;
            descendingpeaks = sortrows(tmpdata,'descend');
            peakvalue = descendingpeaks(1);
            voxelindex = find(statmap(tmpvoxindices) == peakvalue);
            [I,J,K] = ind2sub([size(SubMap2,1),size(SubMap2,2),size(SubMap2,3)],tmpvoxindices(voxelindex));
            peakvox = [I,J,K];
            %% simple transformation from voxel space to coordinate space
            mnicoord(:,1) = peakvox(:,1) - 90;
            mnicoord(:,2) = peakvox(:,2) - 125;
            mnicoord(:,3) = peakvox(:,3) - 71;
            mnicoordsize = size(mnicoord,1);
            if size(mnicoord,1) > 1; mnicoord = ceil(mean(mnicoord)); end
            %% Now calculate stats that we need for our excel file.
            VoxelStats.ROIStats(counter,1) = size(VoxelStats.broadman(counter).data,1);
            VoxelStats.ROIStats(counter,2) = size(find(VoxelStats.broadman(counter).data>thresh),1);
            VoxelStats.ROIStats(counter,3) = brodmanregions(broadmani);
            VoxelStats.ROIStats(counter,4) = mnicoord(1);
            VoxelStats.ROIStats(counter,5) = mnicoord(2);
            VoxelStats.ROIStats(counter,6) = mnicoord(3);
            VoxelStats.ROIStats(counter,7) = peakvalue;
            VoxelStats.ROIStats(counter,8) = mnicoordsize;
            clear tmpvoxindices mnicoord mnicoordsize
```

Identifies all unique subregions within an atlas map

Identify all voxels in stat map that overlap with subregion in atlas map.

Find peak voxel within the subset of voxels in subregion

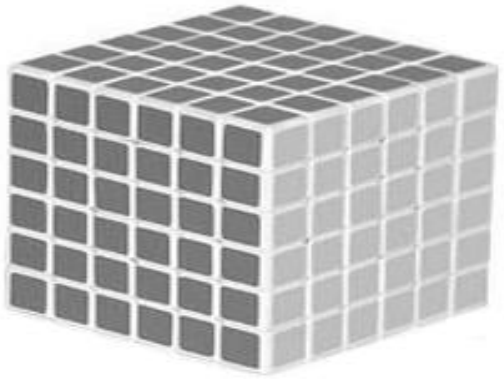
Convert the peak voxel to MNI coordinates.

Give us information about peak values (cluster size, peak voxel value, XYZ coordinate).

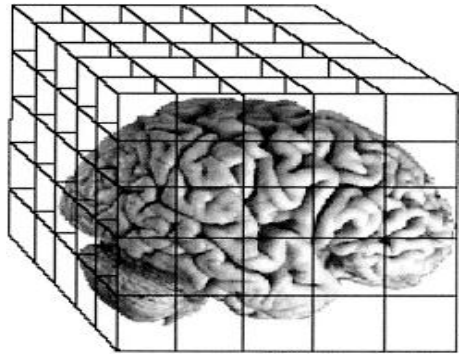
```
% write out data in excel
xlswrite(['VoxelStats with ' num2str(thresh) ' threshold.xlsx'],VoxelStats.ROIStats);
```

Public Service Announcement

- This assumes that both maps are in the same coordinate space.



Higher resolution



Lower resolution

- Always know the dimensions of your lesions, statistical maps, and atlases used for analysis.