# Neuroimaging: basic workflow, visualisation & clinical tractography

Klinik für Neurochirurgie

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File formats

DICOM vs NIfTI

.dcm
- What the scanner generates
  - Clinical standard
  - 1 file = 2D slice
- NOT compressed/ cannot be compressed
  - Big data file
- Works with PACS and RIS
- Metadata = contain personal info!

.nii/.nii.gz
- Research standard
- Stores entire 3D/4D volumes in ONE file
- Easier for processing and sharing
- Metadata = orientation + voxel size
- Allows for lossless compression (.nii.gz)
- NOT compatible with PACS
- But with every other neuroimaging software

File formats

How do I find T1/T2/DWI??
The best way is to look at the **number of slices/files.**

Given our current protocol…

T1 (without KM) = 176 slices
T1 (with KM) = 176 slices
T2 = 30
T2 FLAIR = 35

File formats

File formats

Converting between .dcm and .nii

There are scripts that you can run:
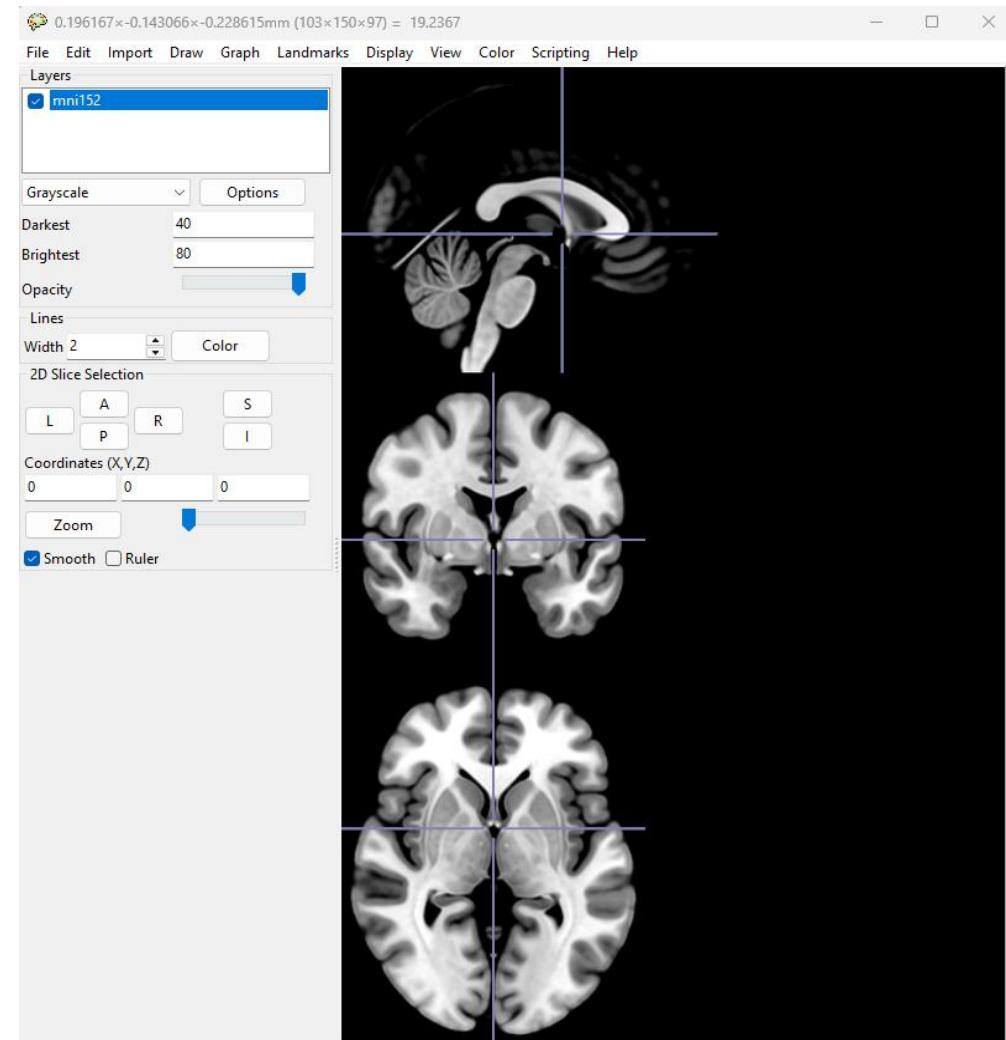
Python workflow:
import dicom2nifti
dicom2nifti.convert_directory('/path/to/dicom_folder', '/output/folder')

Bash workflow (comes with FSL, SPM, etc.):
dcm2niix -o /output/folder -f pat01_T1 /path/to/dicom_folder

GUI version (essentially runs dcm2niix):
MRIcroGL (https://www.nitrc.org/projects/mricrogl/\)

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MRIcroGL
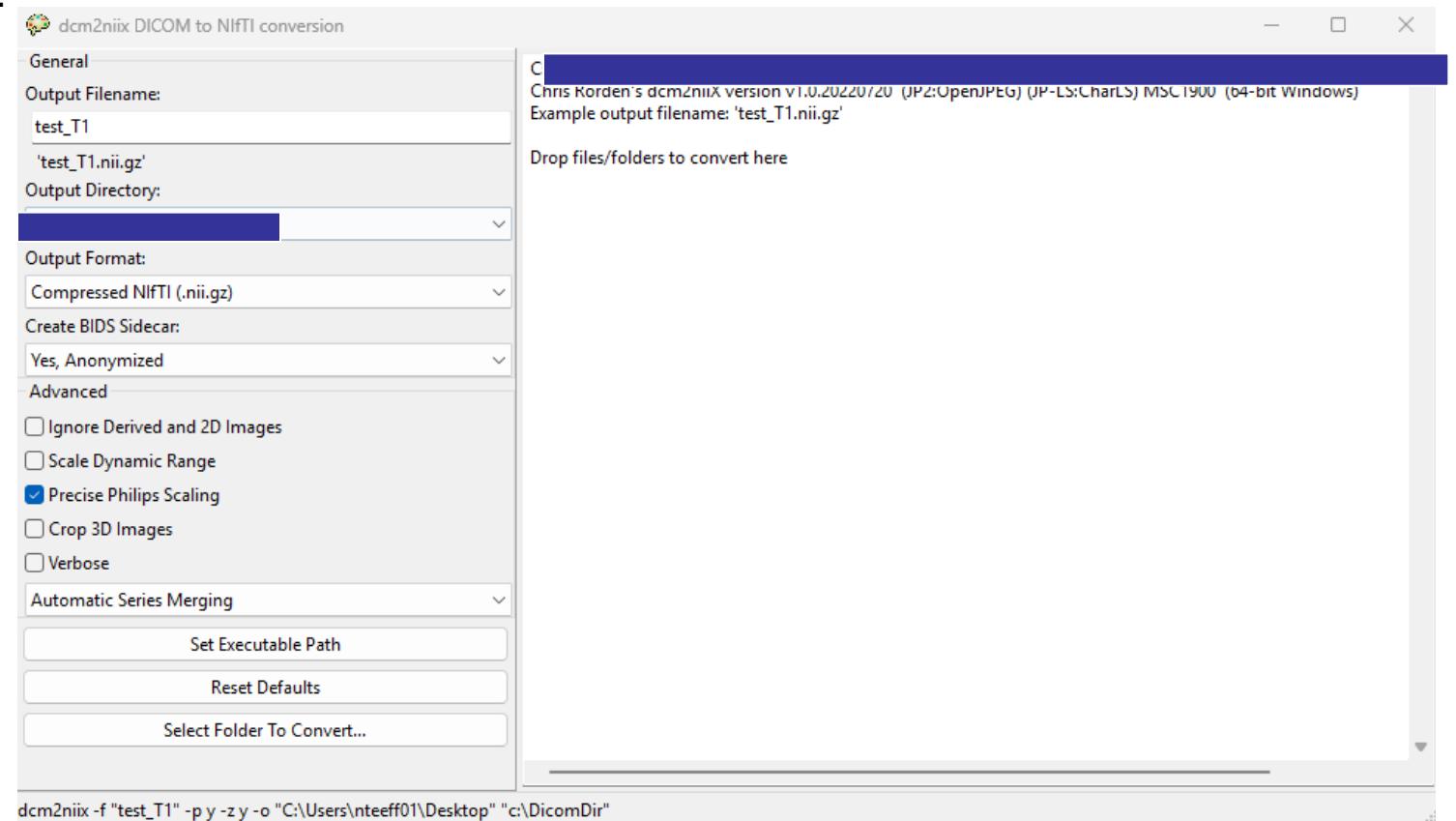
If you write your thesis with me, this program will likely become one of your best friends.

It has everything a "good friend" should have:
- It is free and open-access
- It is user-friendly and comes with a GUI
- It is great for visualization
- It runs on every OS
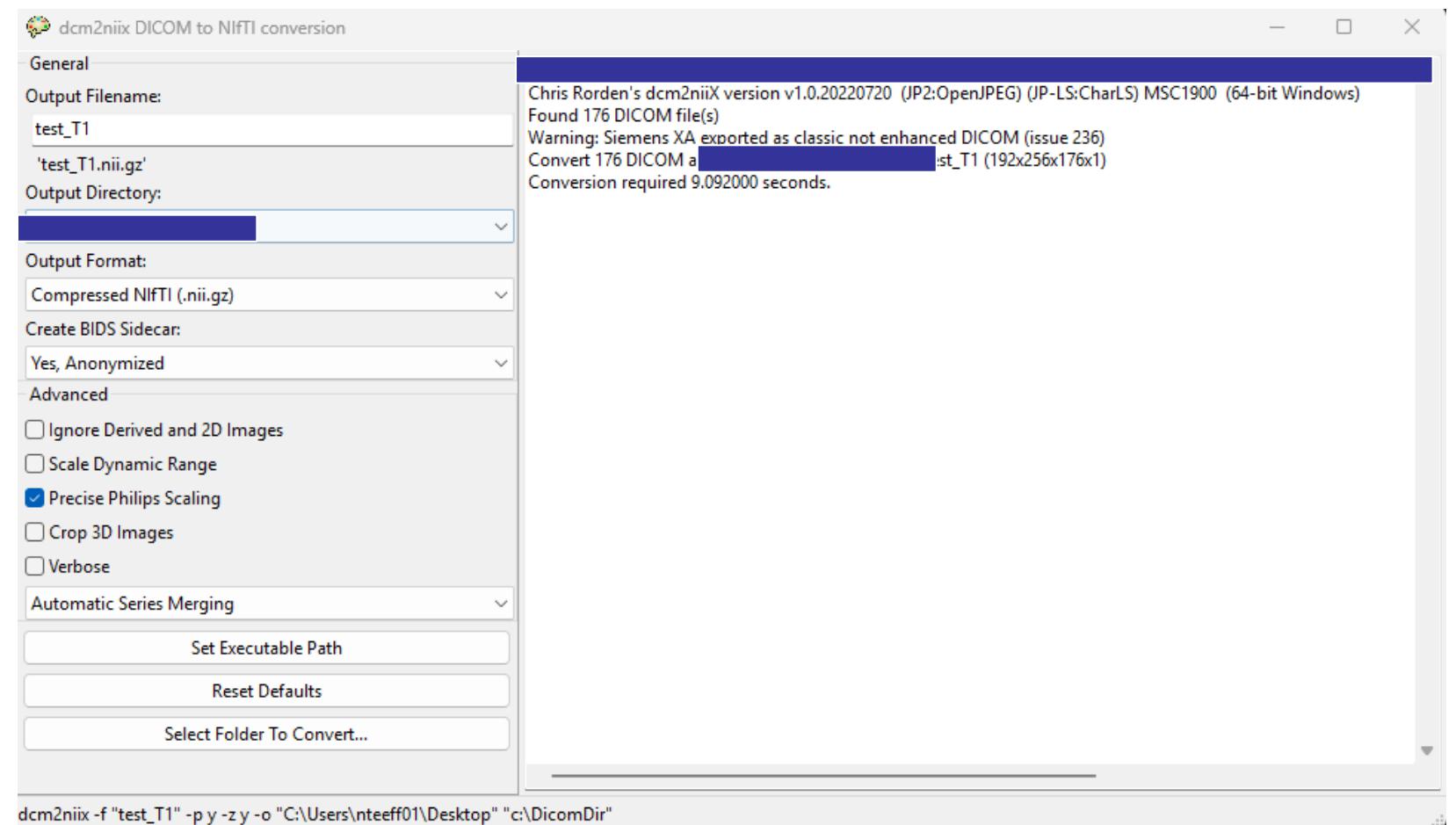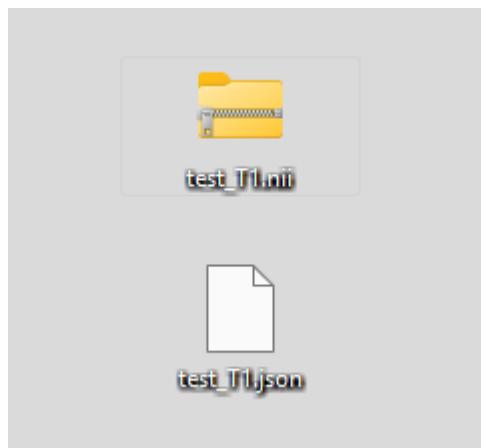
To convert a .dcm to .nii:

- "Import"
- "Convert DICOM to NIfTI"
- You should get something like this
- Take the folder that contains all DICOMs you want to convert and drag and drop it in this window

dcm2niix -f "test_T1" -p y -z y -o "C:\Users\nteeff01\Desktop" "c:\DicomDir"

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MRIcroGL

If it worked properly, you should see something like this.
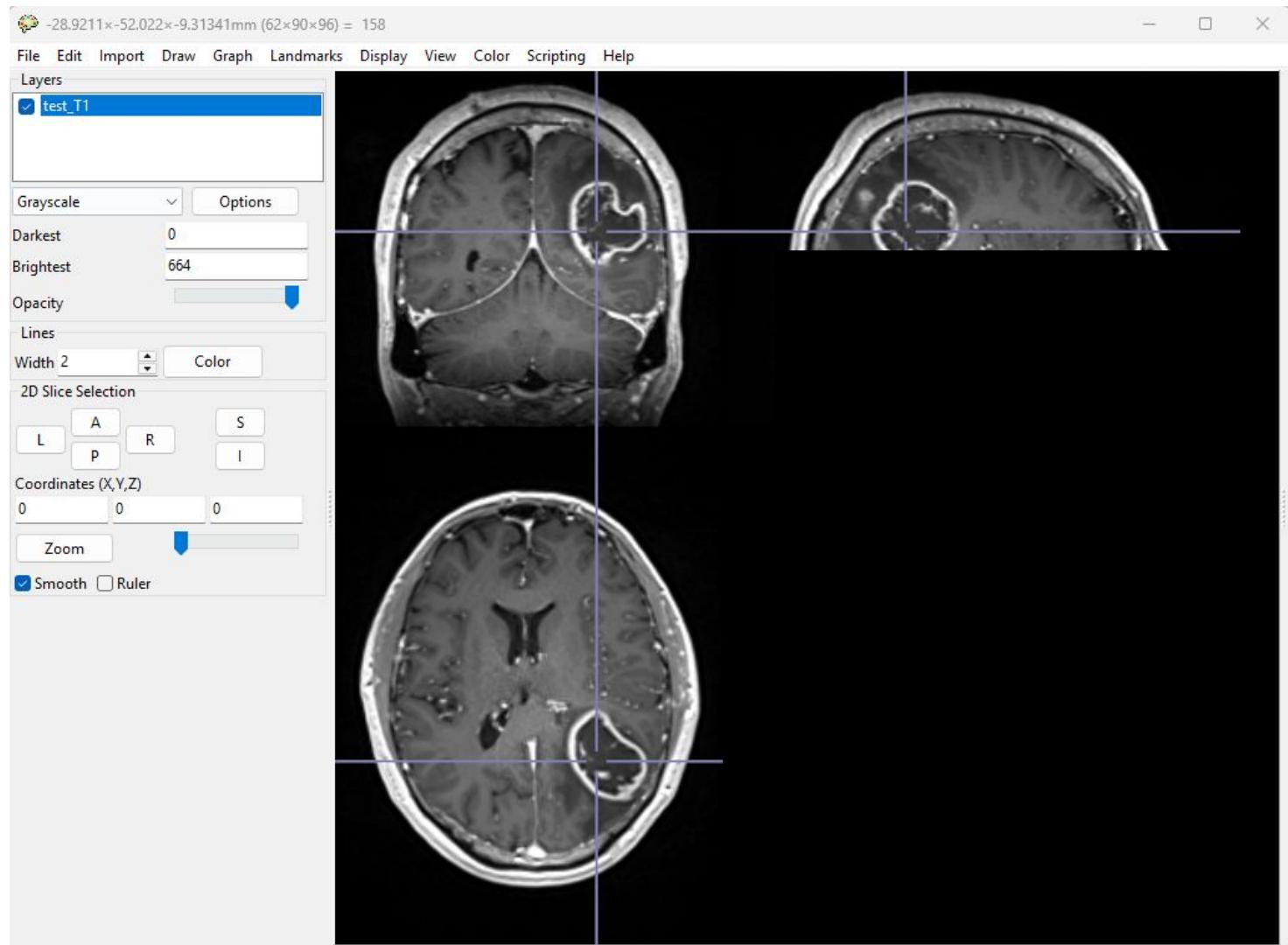
MRIcroGL

You can now open your nifti by going to "File → Open".

The goal now is to **segment** the lesion.
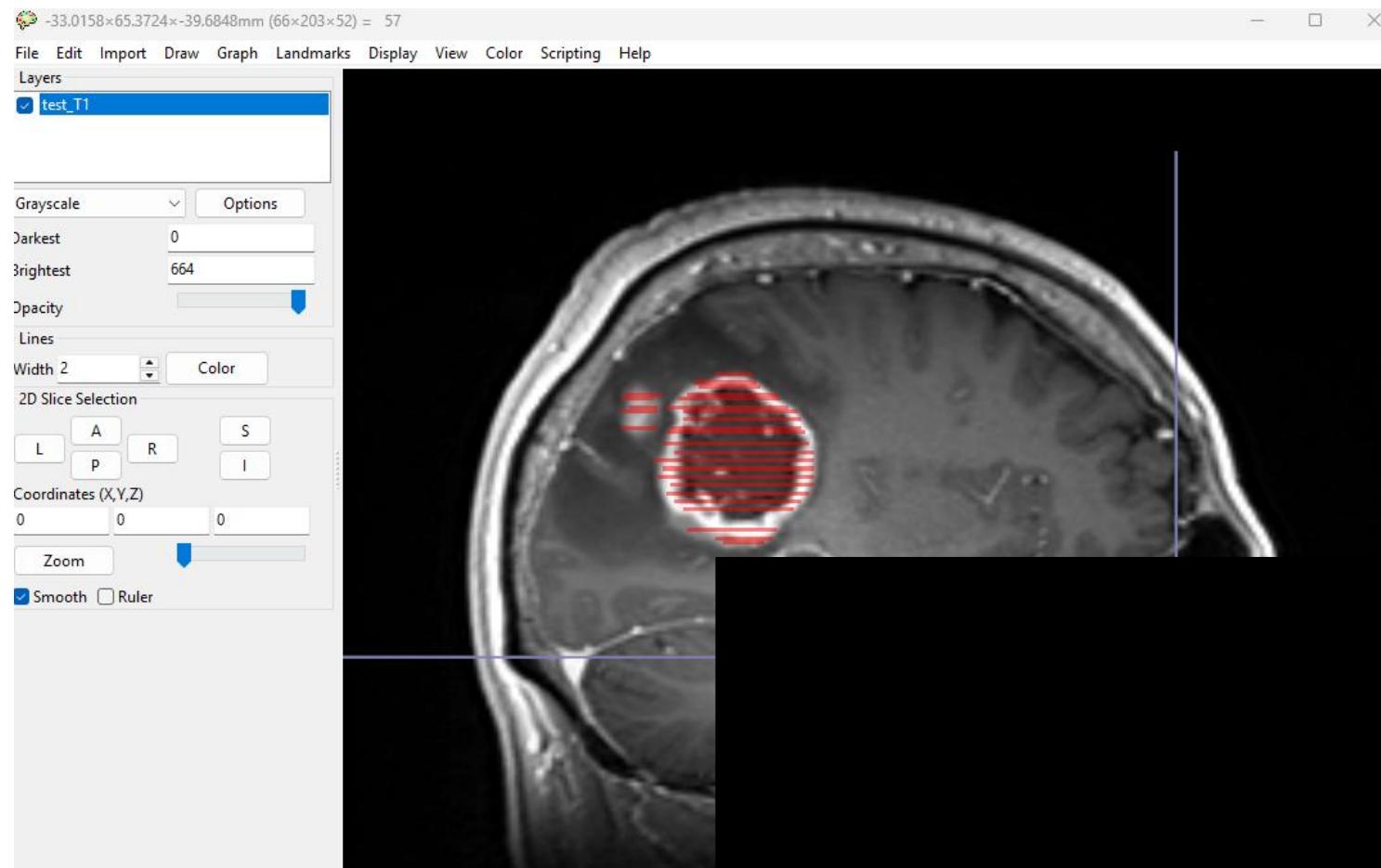
To do this, we need to "Draw" the lesion.

What does this segmentation really create??

Semi-automatic lesion segmentation with MRIcroGL

- If you segmented the lesion every 2 slices, the sagittal plane should look like this.

- **Beginning** and **end** are very important.

- Now we need to turn this into a mass and that's why we need to interpolate.

- Draw > Advanced > Interpolate between slices > All axial gaps

- Now you shouldn't see any gaps along the axial plane.

- Sometimes, lesion edges are rather "sharp" → smooth
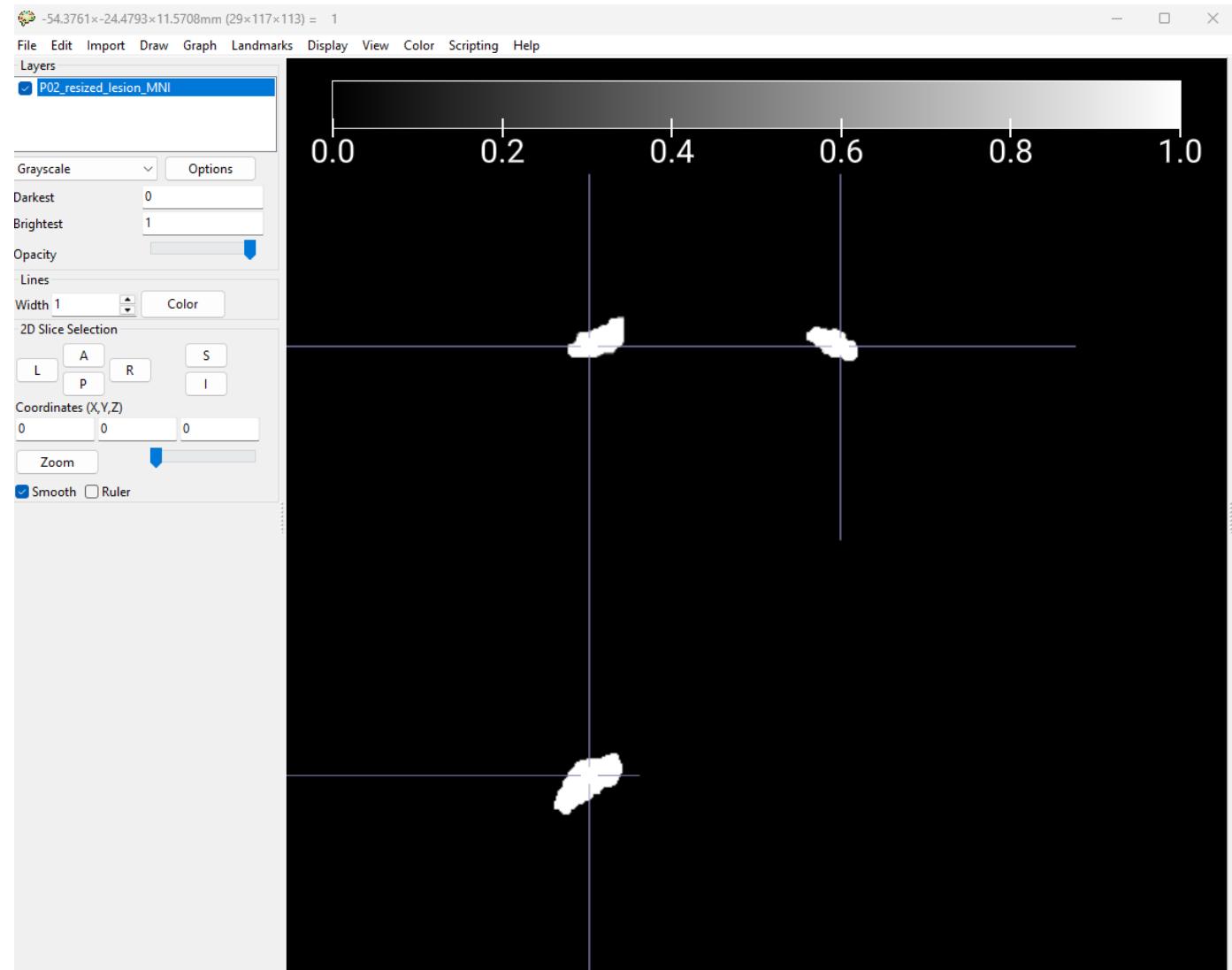
Semi-automatic lesion segmentation with MRIcroGL

To save your wonderful creation:
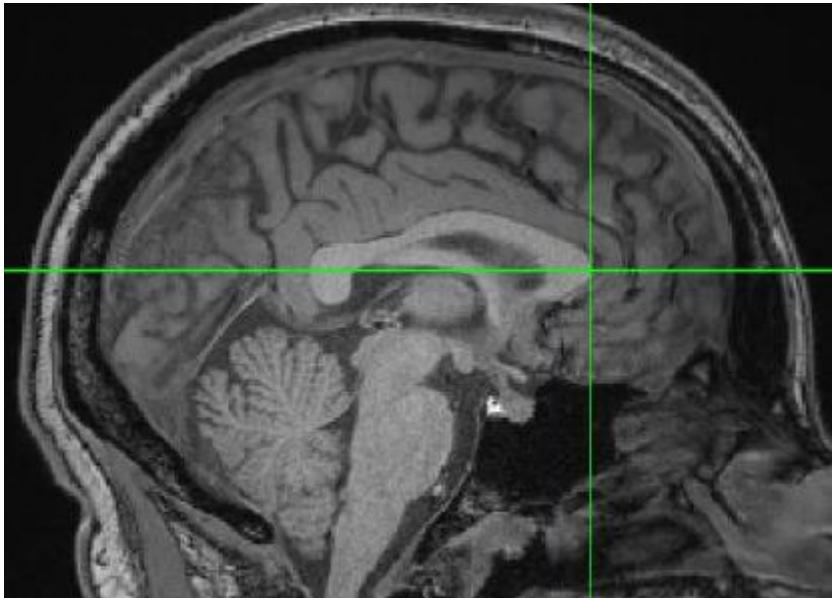
Draw > Save VOI > save it as .nii or .nii.gz

If we open the lesion file using MRIcroGL (as the main image), what will it look like?
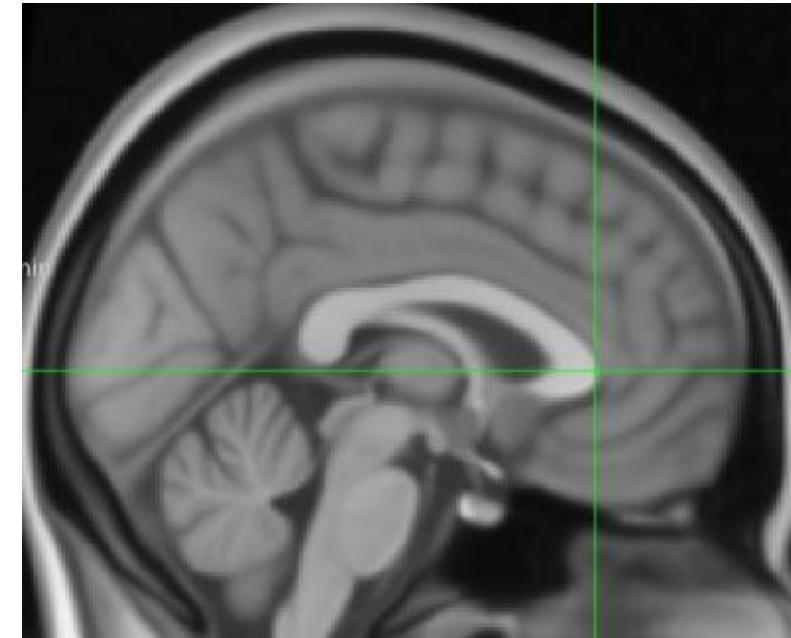
# Spaces

Individual vs Normalized space

My brain

MNI152

Location
Coordinates: Scanner anatomical
-2.573767
55.75864
33.5925
Volume

Location
Coordinates: MNI152
-0.742368
32.35208
4.126101
Volume
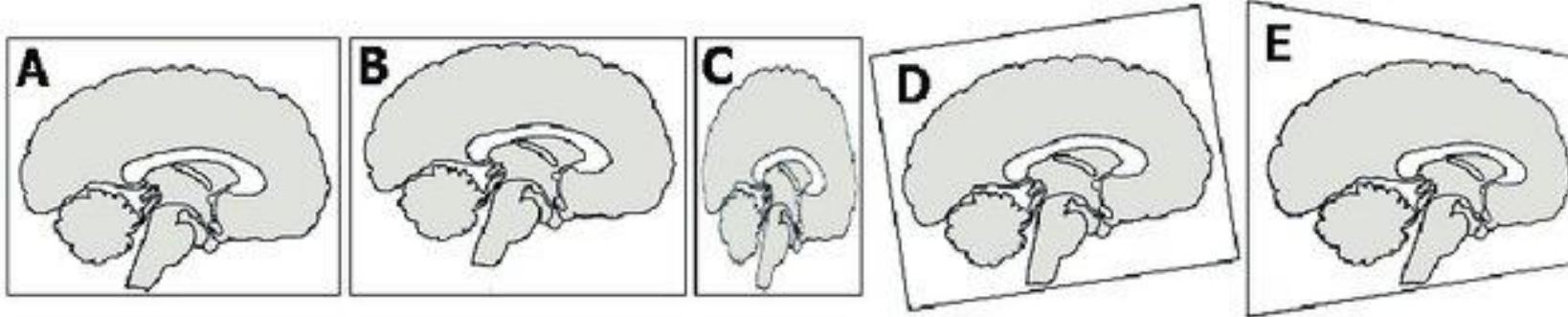
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Normalisation
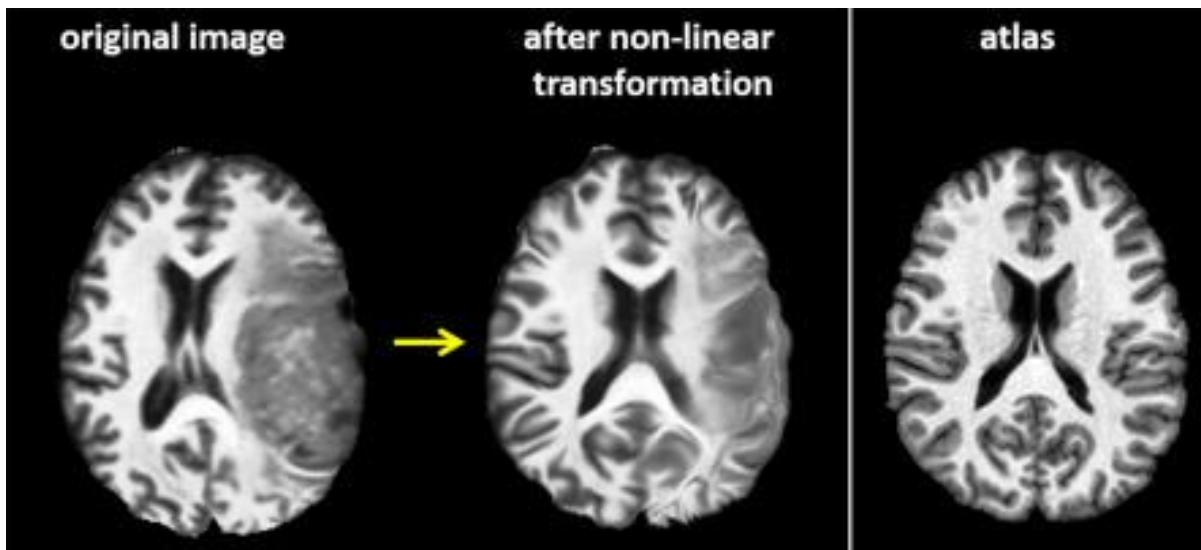
How can my brain fit an average brain?

Most importantly for us, **how can we make a lesion fit an average brain?**

Rorden & Brett, 2000; *Behav. Neurol.*

Linear transformation
- Affine (preserves straight lines and proportions)
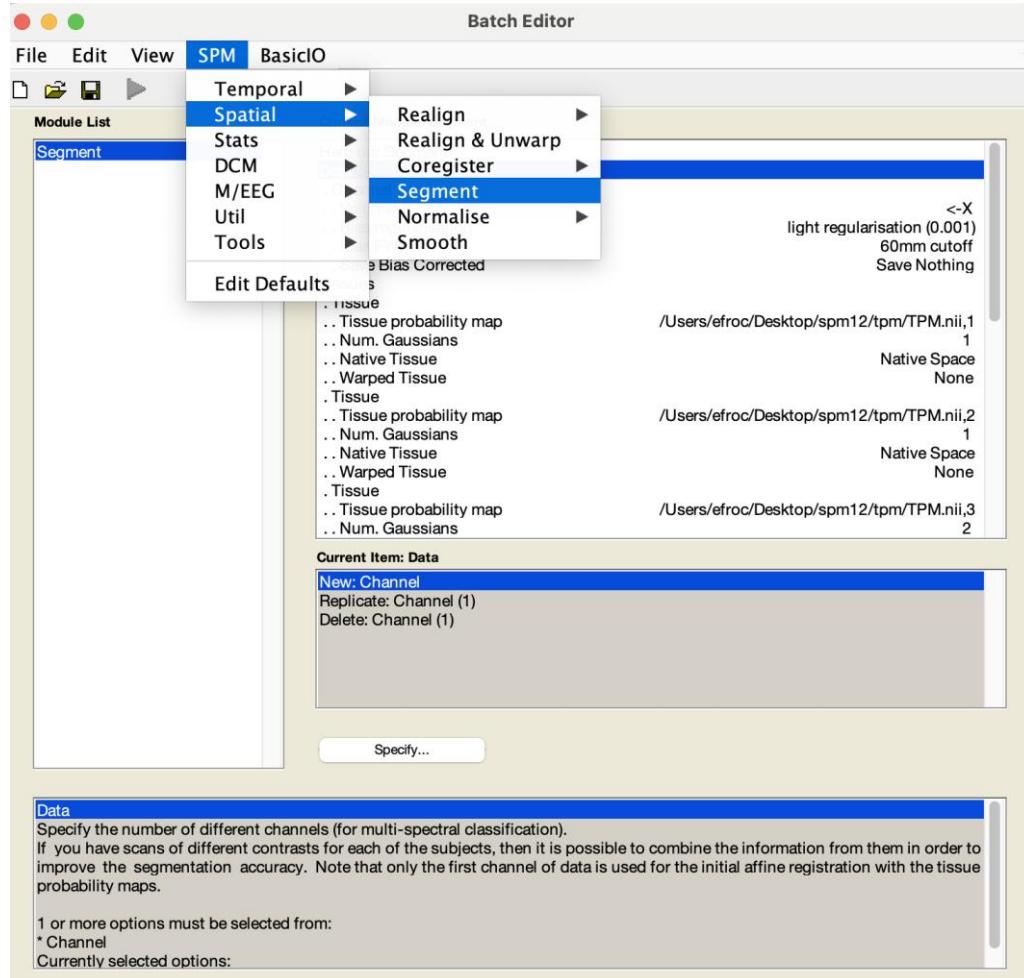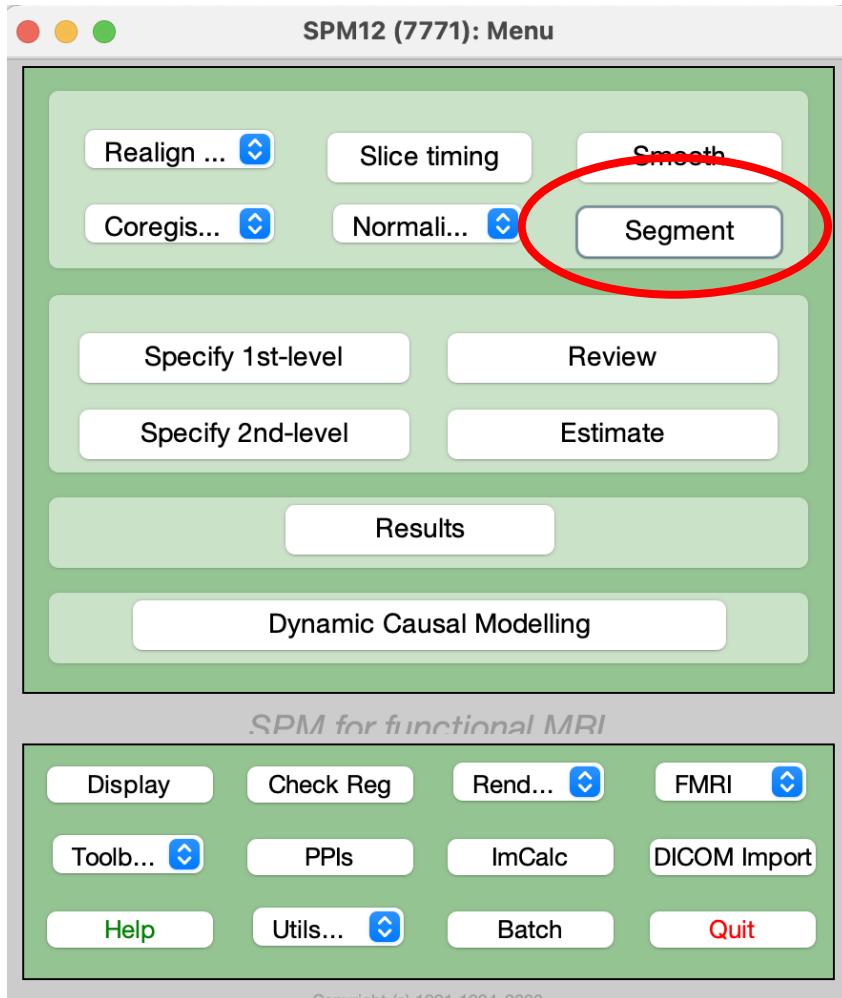
Non linear transformation
- Based on curvature (gyri/ sulci)

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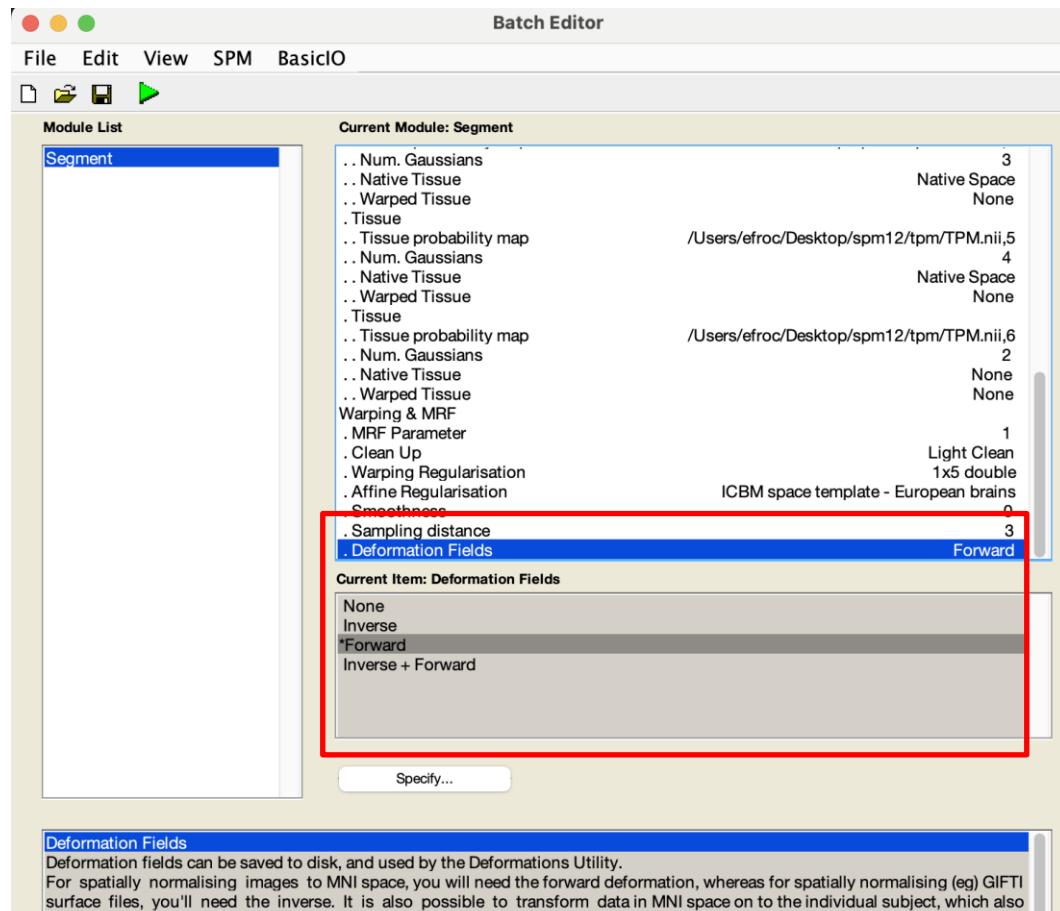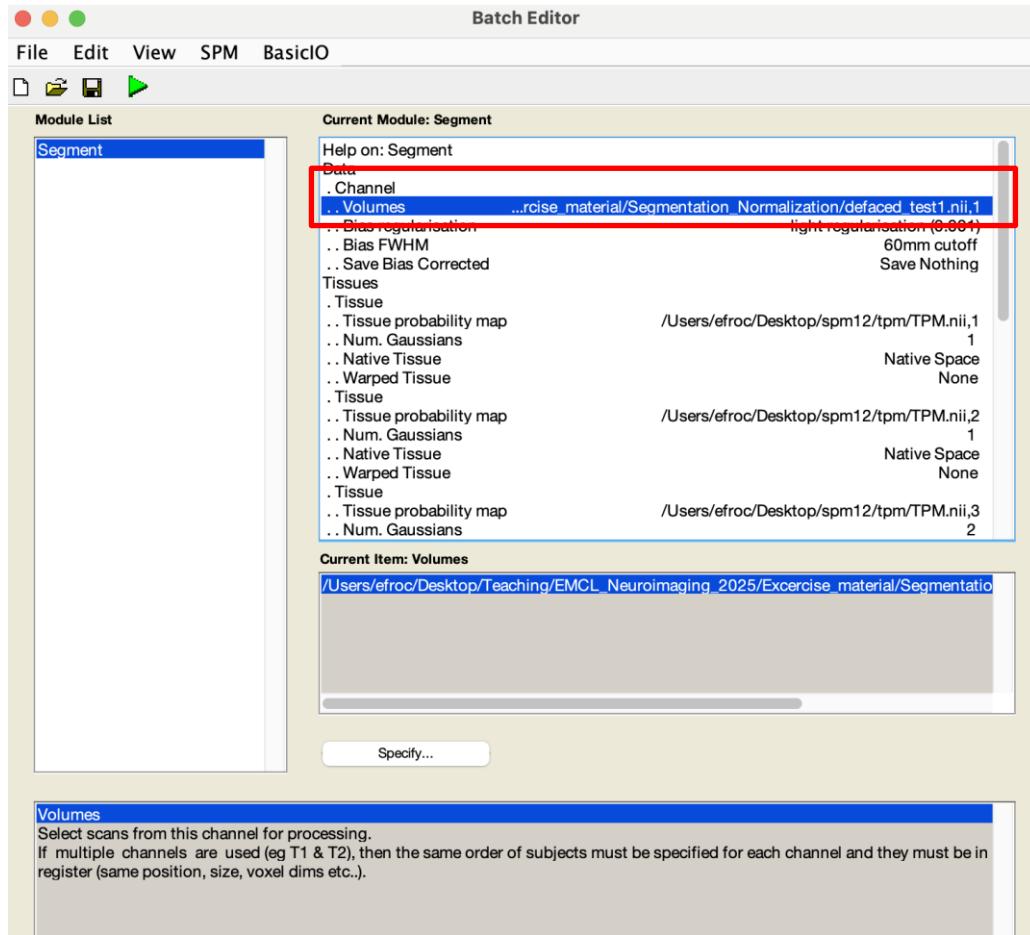
# Normalisation with SPM25

- You can minimize the graphic and processes windows
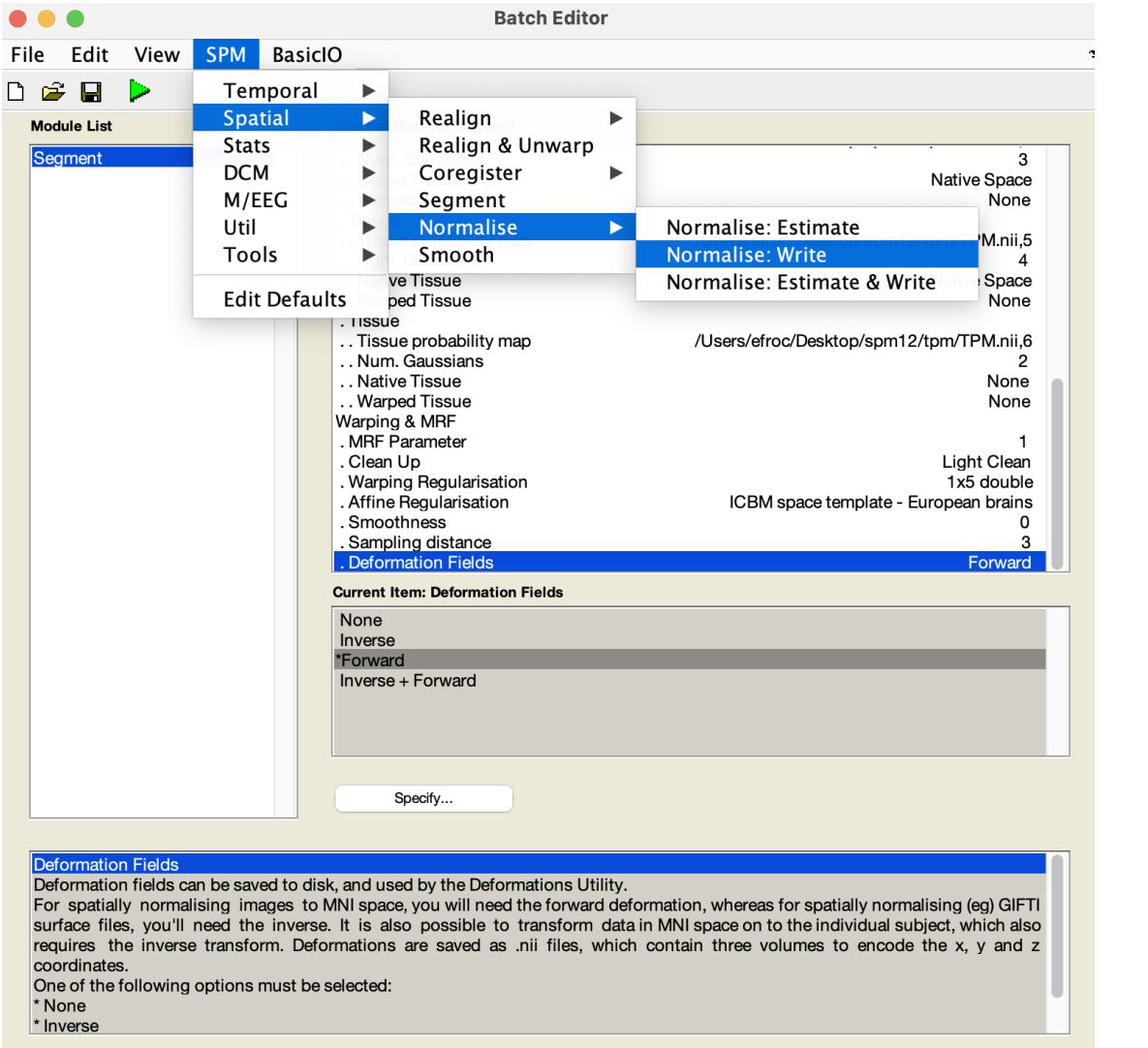
Normalisation with SPM25
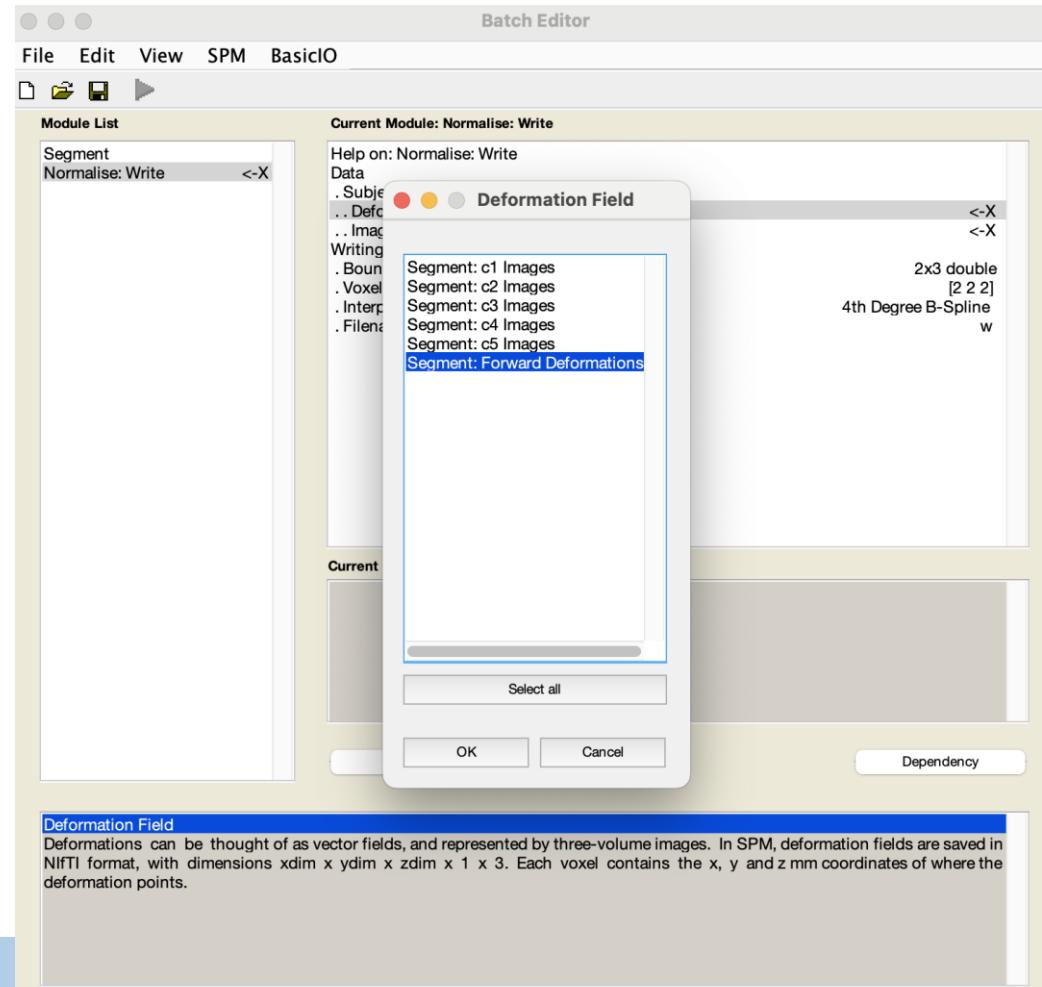
- Go where you downloaded the dummy data and double-click on "defaced_test1.nii.gz"
- You see a new file created with the name "defaced_test1.nii"

Normalisation with SPM25
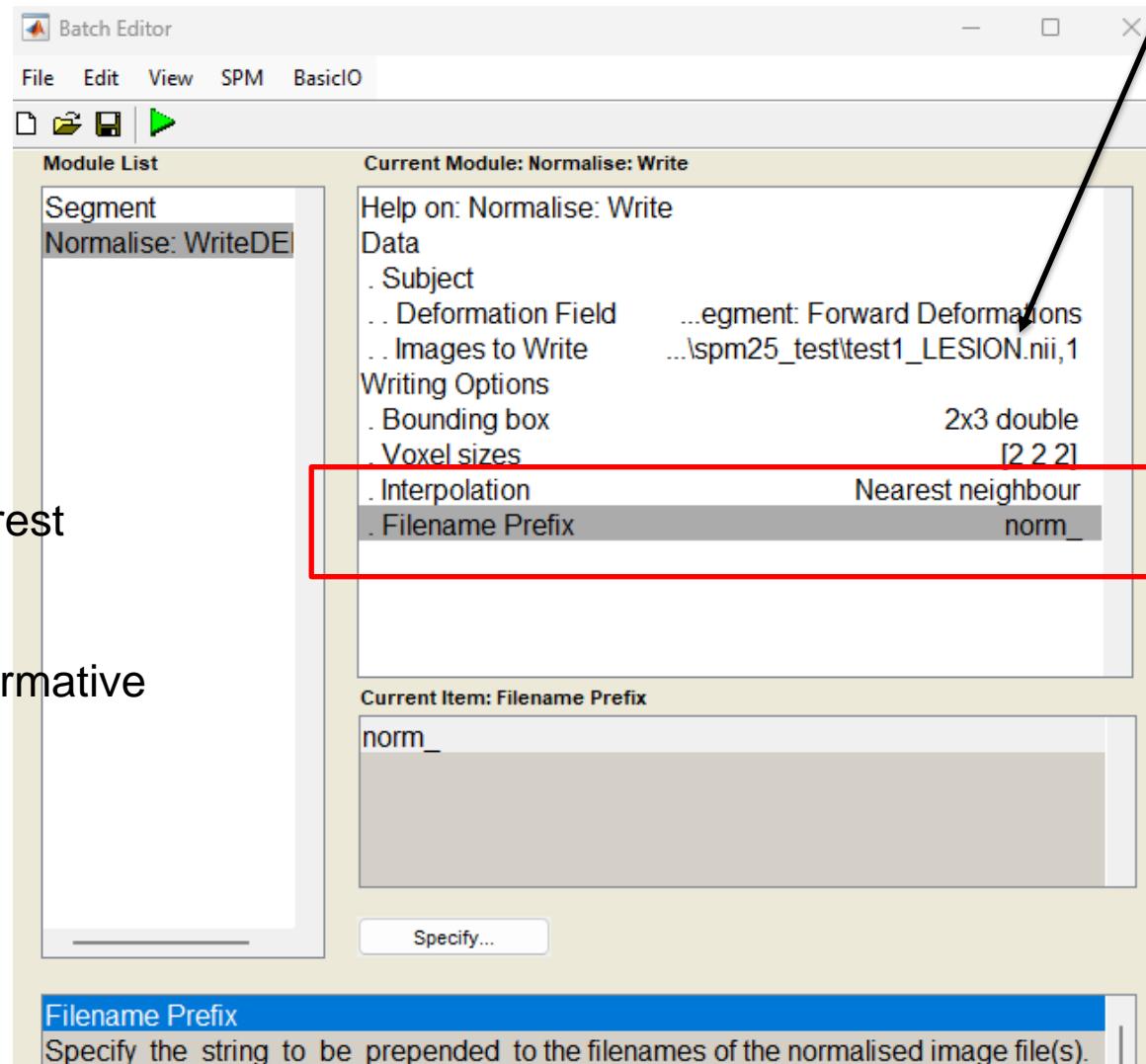
- Go to your second batch (i.e., Normalise: Write) on the "Module List"
- Double-click on "Data"

Normalisation with SPM25

For "Interpolation" choose „Nearest Neighbour".

Choose a filename prefix that is informative to you. I went with "norm_".

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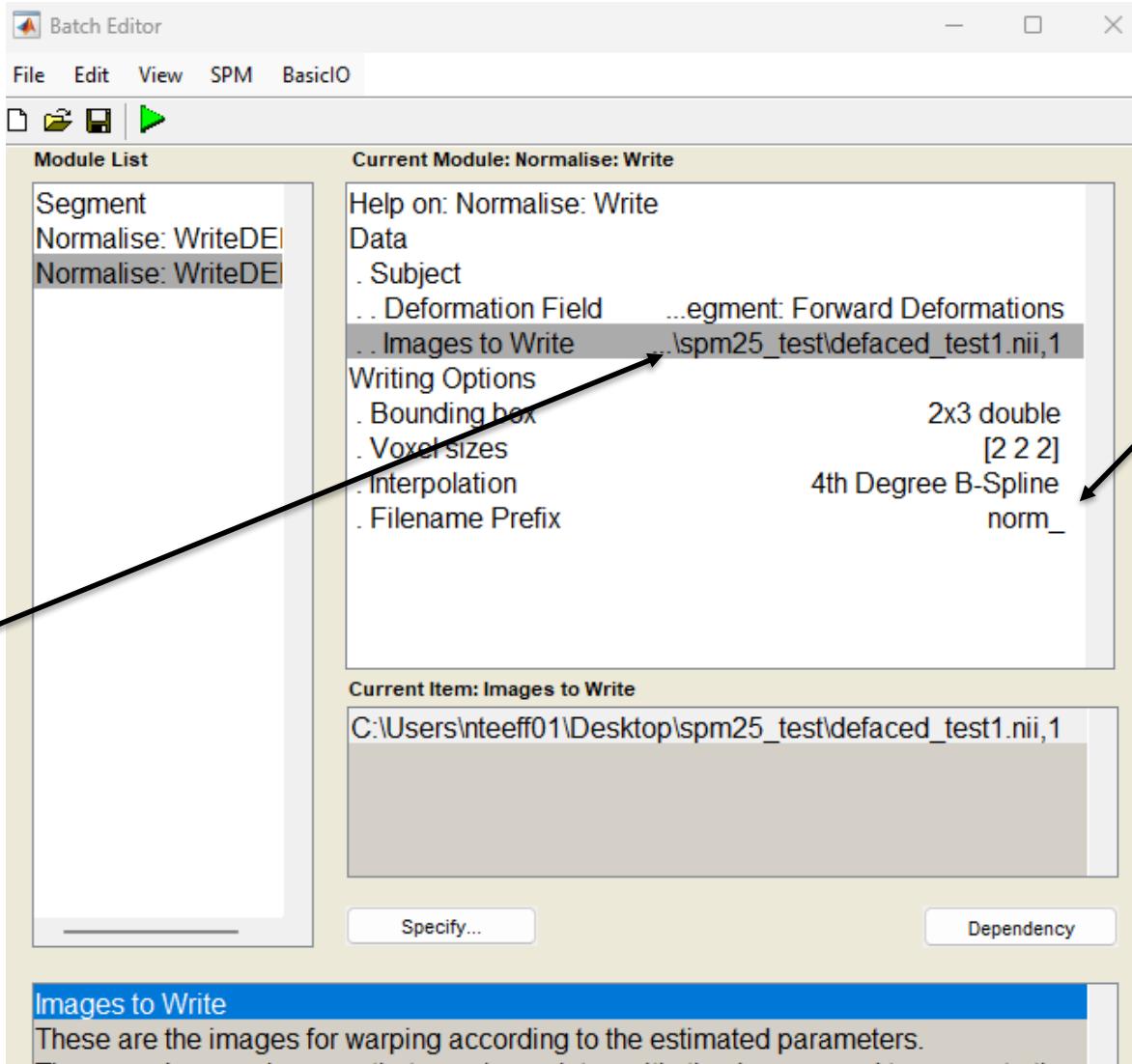
Normalisation with SPM25

Add another "Normalise: Write" module.

Last one, I promise.

For Images to Write under Data select "defaced_test1.nii"

Choose a file prefix that is informative to you. I went for "norm_".

If everything is ready, click on the little "Play" icon to run our Batch script!
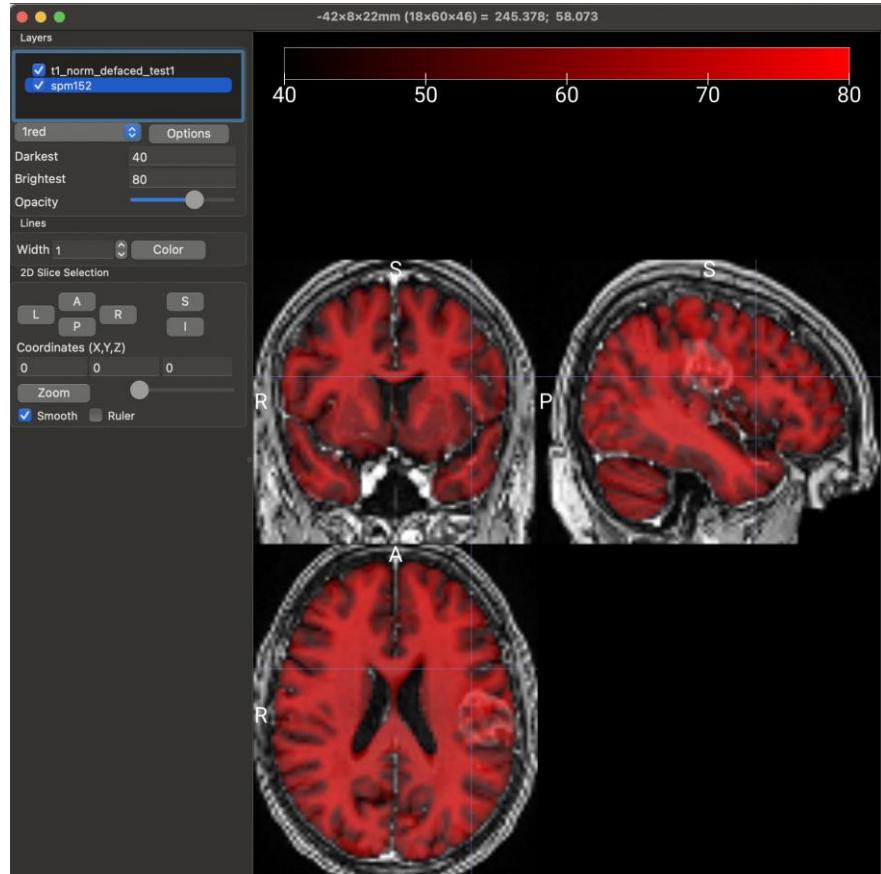
Be a bit patient…

Normalisation with SPM25
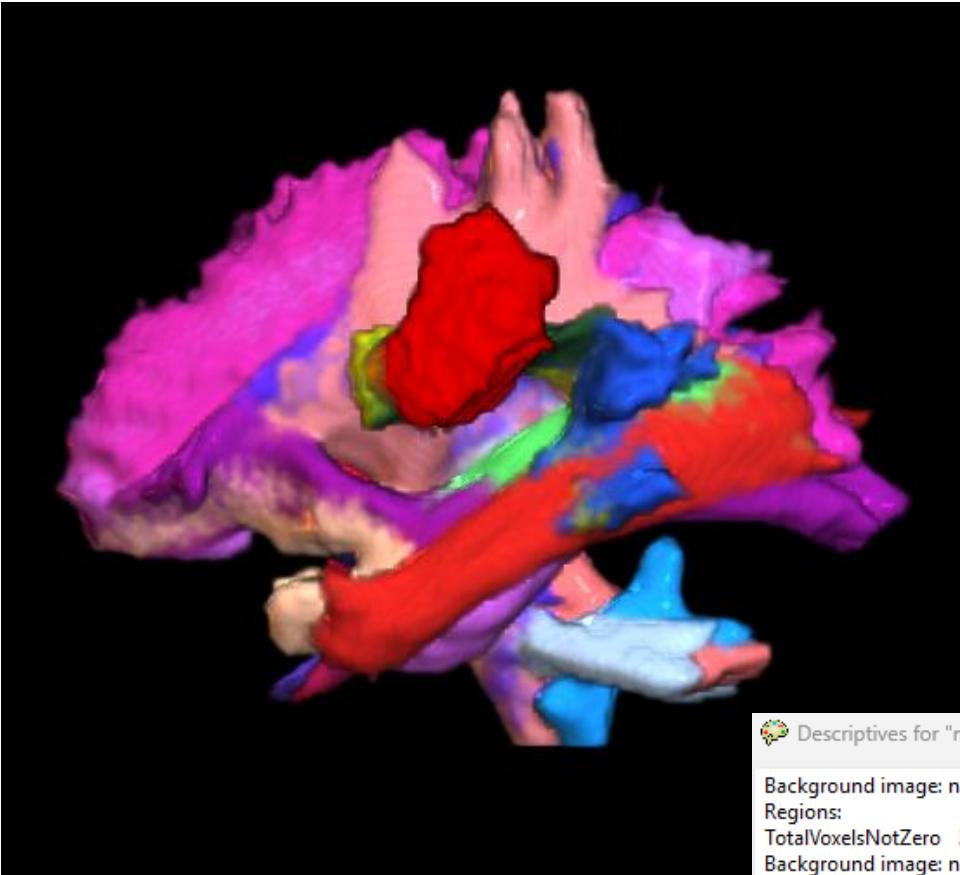
What was the output of the 3 modules we ran?

How can we check whether our normalization was successful?

Normalisation with SPM25

Which structrues are affected by the tumor?

Descriptives for "natbrainlab" (Copied to clip board)
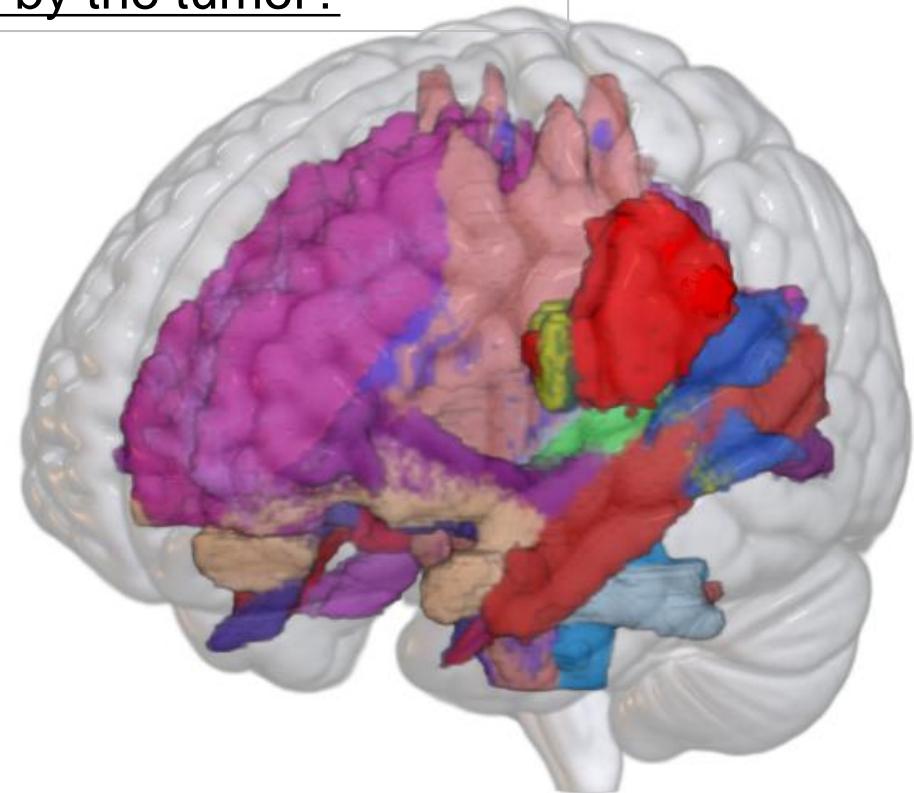
Background image: natbrainlab
Regions:
TotalVoxelsNotZero   3010
Background image: natbrainlab
Index   Name   numVox   numVoxNotZero   fracVoxNotZero
2   "Arcuate_Anterior_Segment_Left"   4095   2366   0.577777802944183
3   "Long_Segment_Left"   2984   644   0.21581768989563
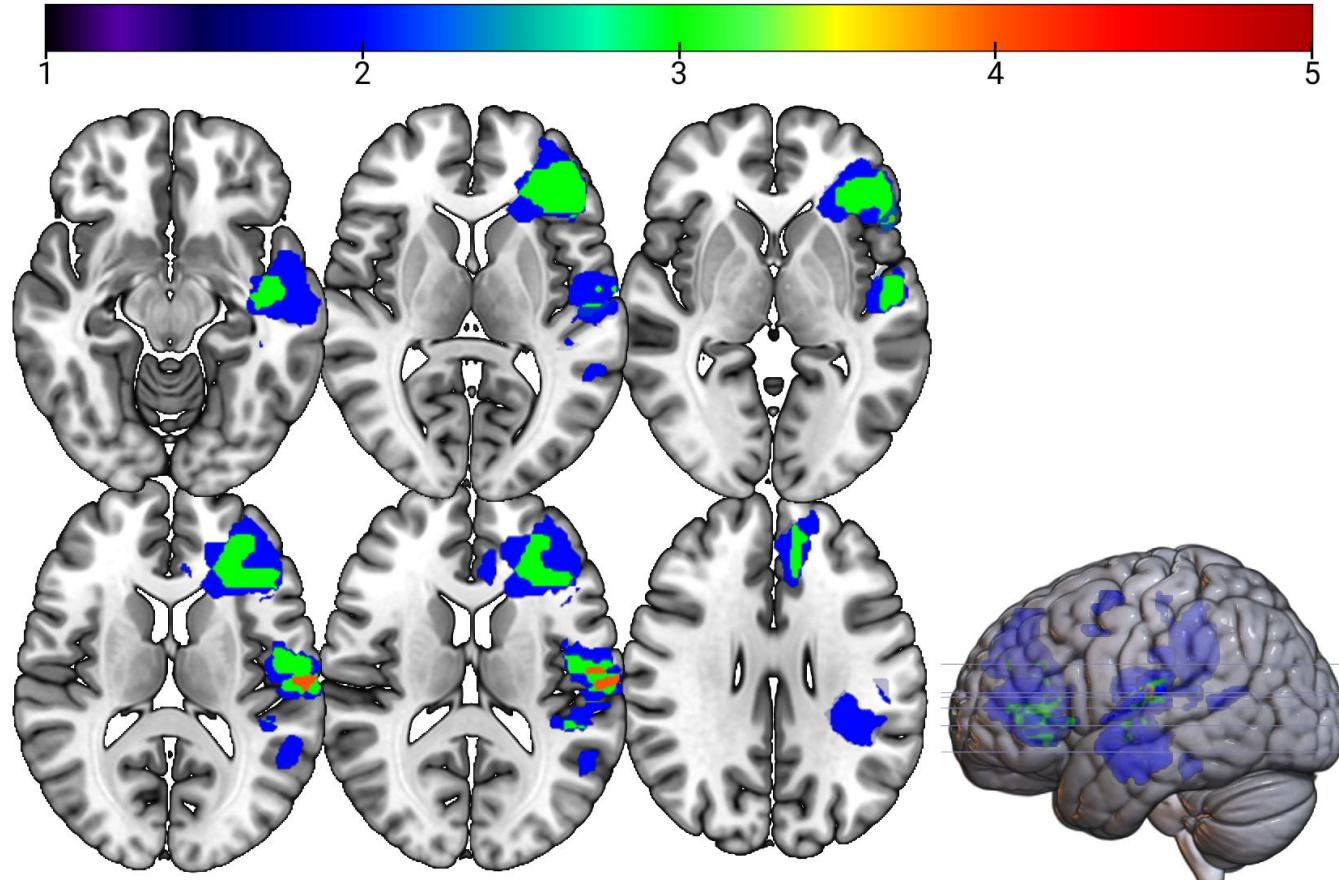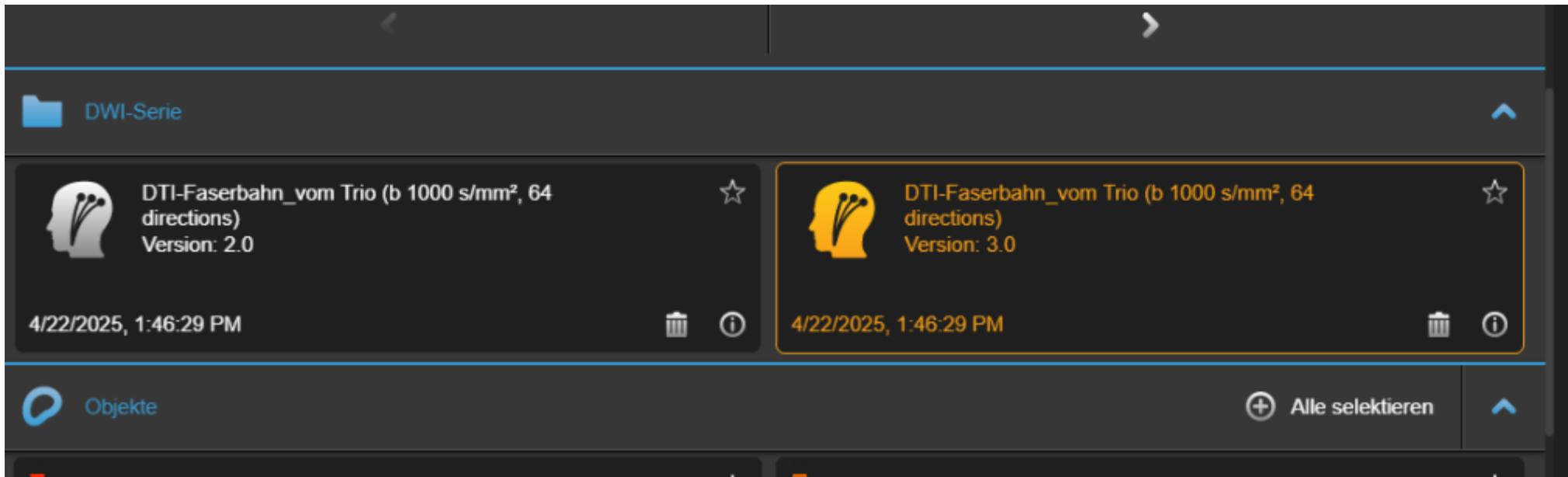
Lesion overlap figures

Let's say you have several normalised lesions and you would like to know where the maximum overlap is. How can you do that?
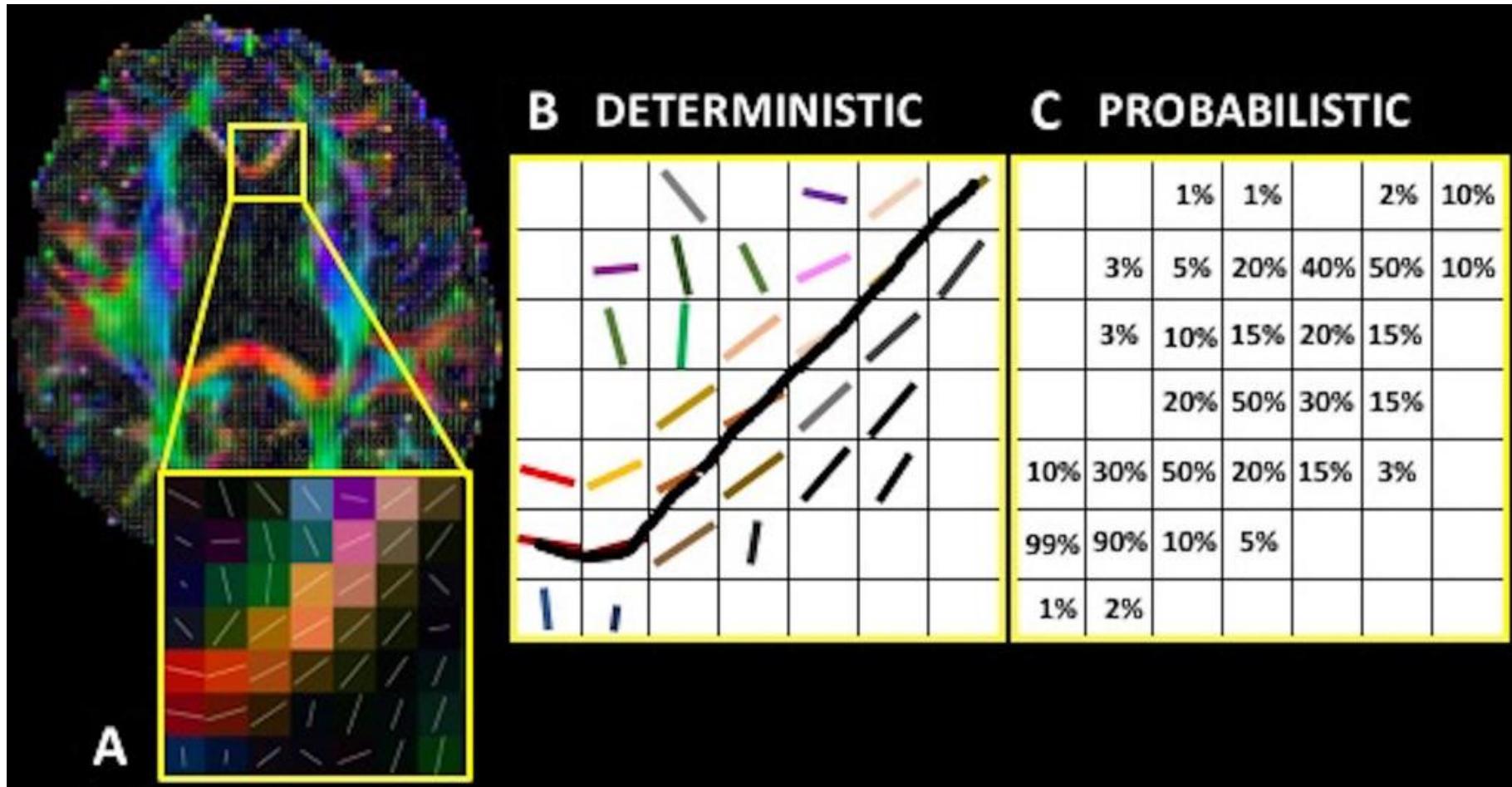
Brainlab & clinical tractography

Choose a patient and then → Cranial Planning

Brainlab & clinical tractography


Muller et al., 2018; *JNS*
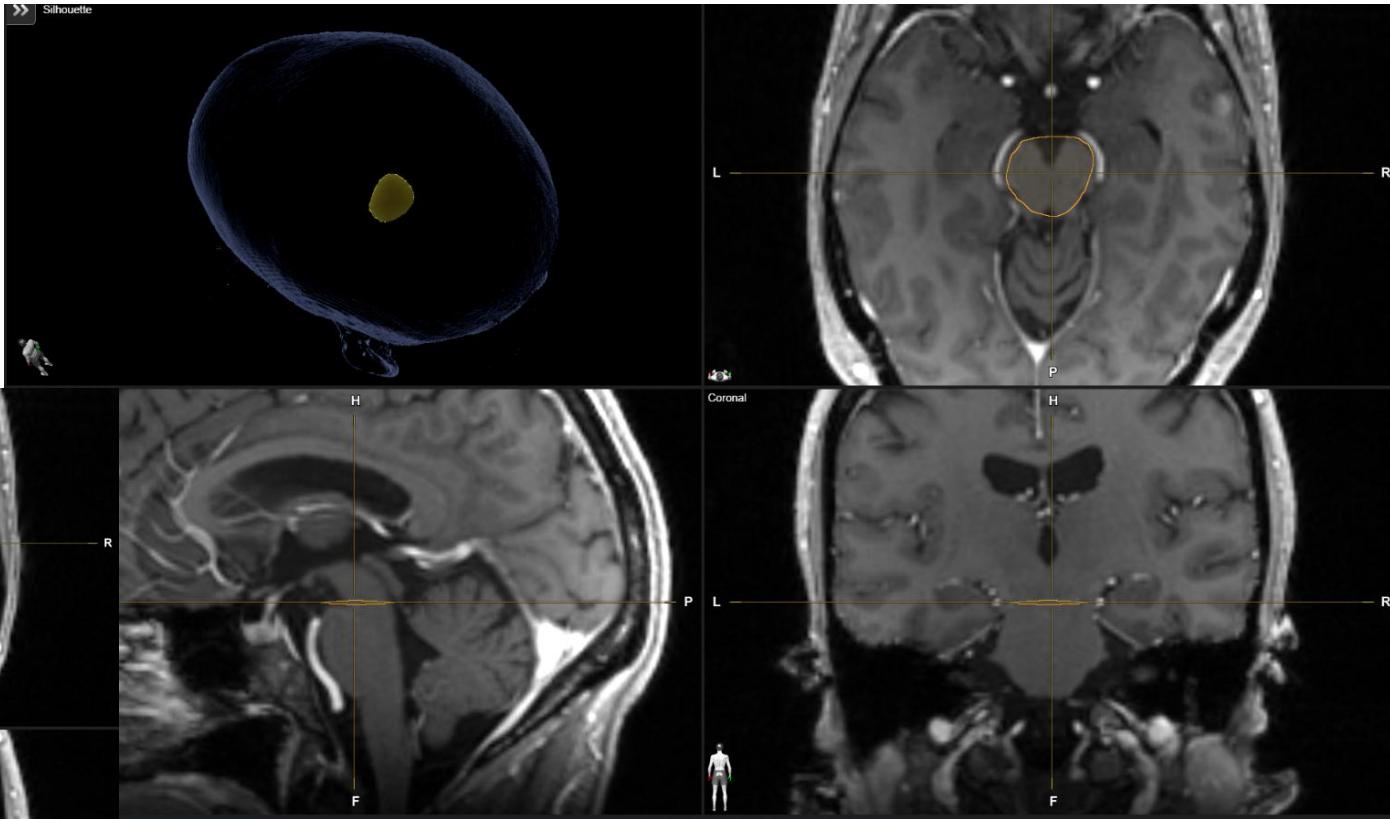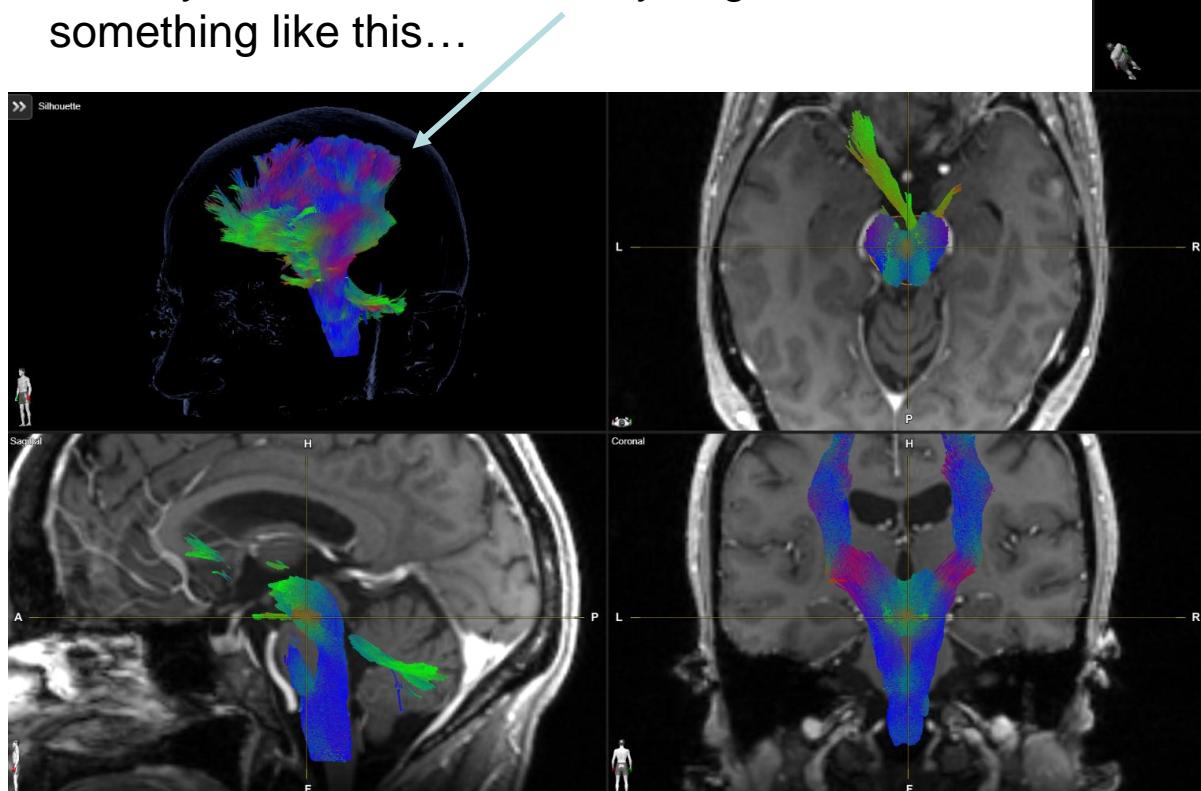
Brainlab & clinical tractography

2 ROI approach: 1 seeding + 1 refining

CST
Seed ROI: Brainstem

When you add the seed ROI you get something like this…
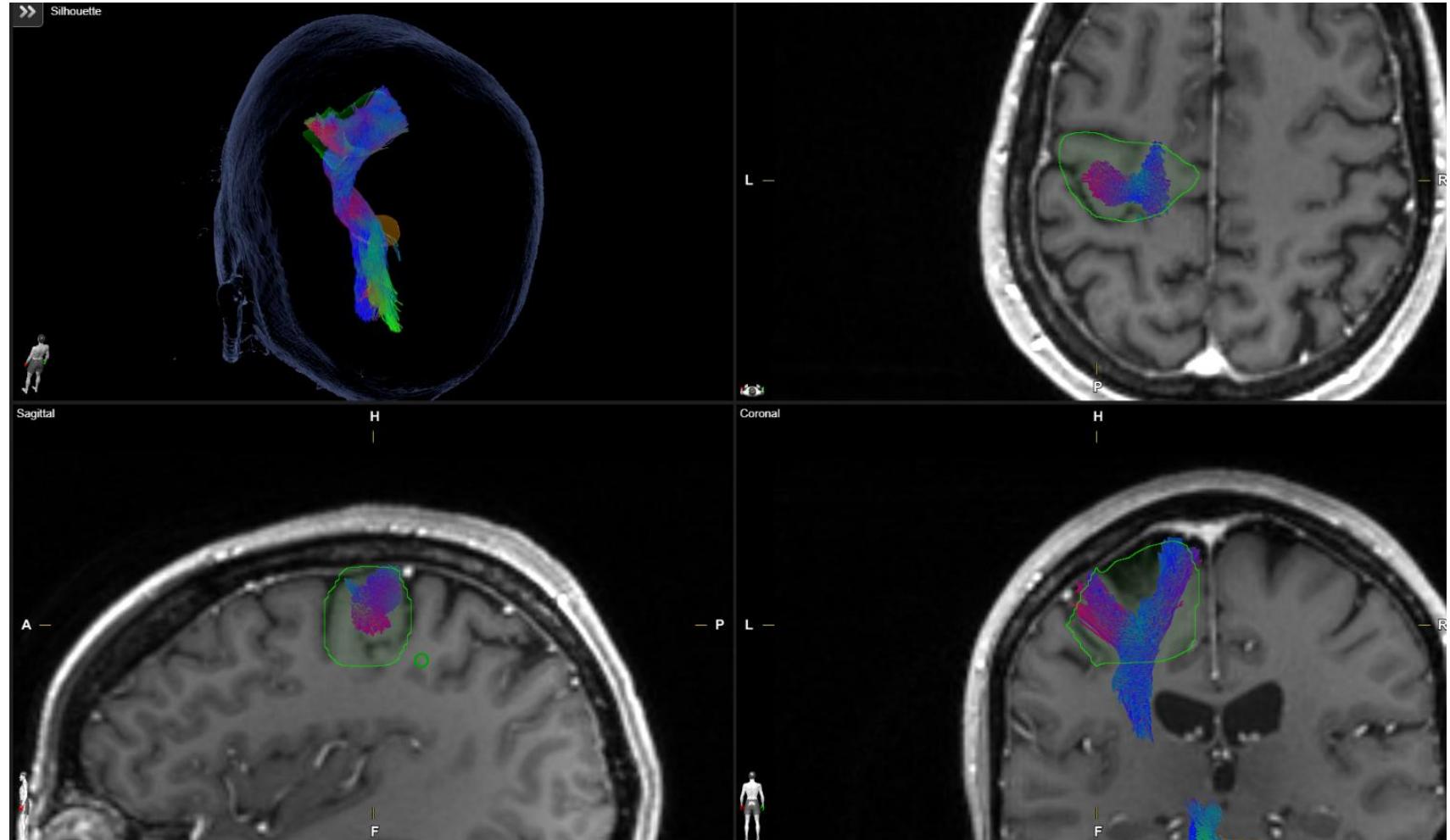
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CST

Refining: Precentral

You can split Leg from Hand CST.

The articulatory CST is trickier than leg and hand.
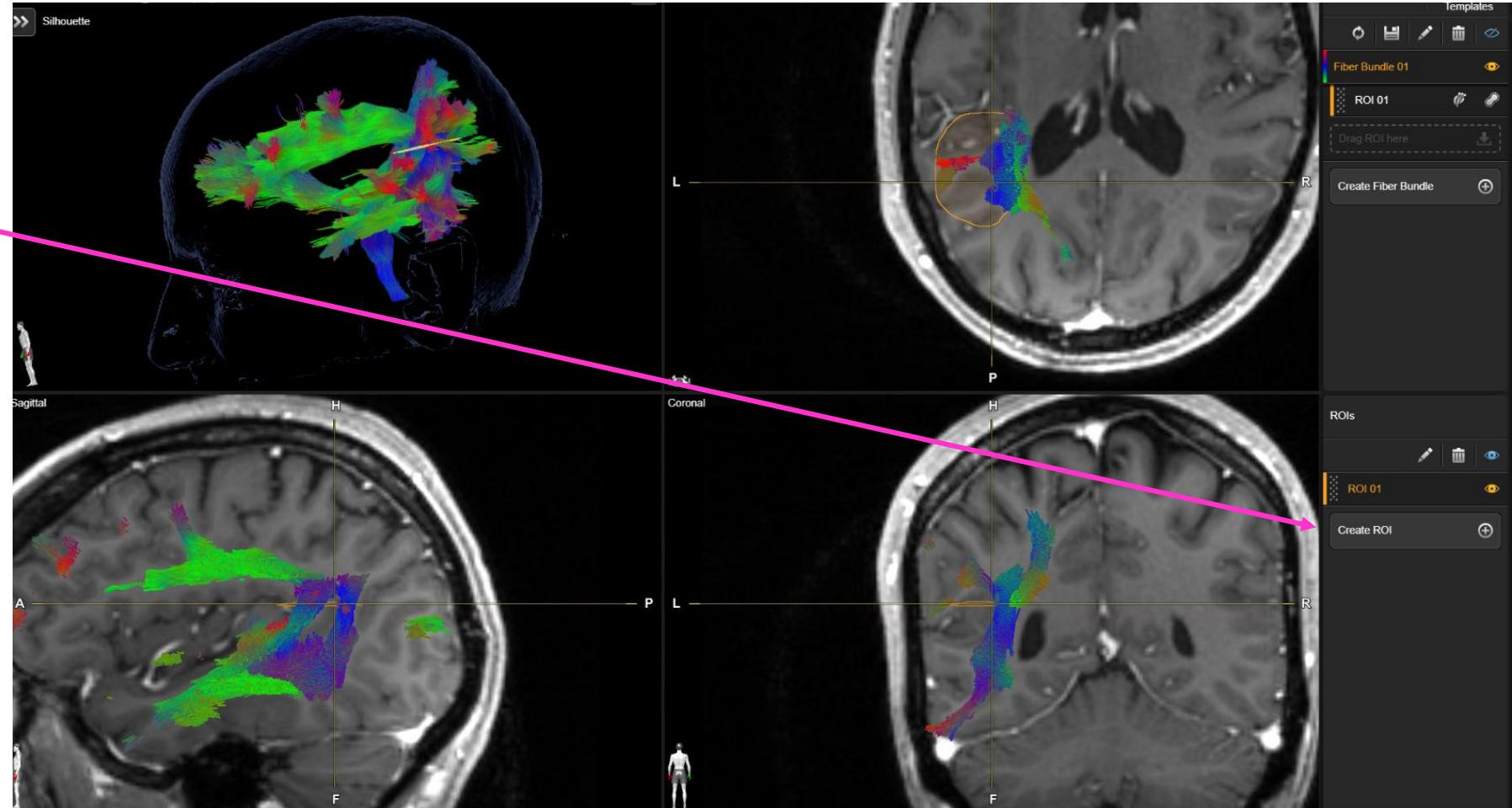
Brainlab & clinical tractography

Arcuate Fasciculus
Create a Fiber Bundle

Seeding ROI:
Create ROI

- On the sagittal plane set your crosshair as medial so that you see the beginning of the STS.
- Then go to the axial plane and create a circle with ca. 1.5 -3cm radius around the center of the crosshair.
- "Add" your seeding ROI to the Fiber Bundle.

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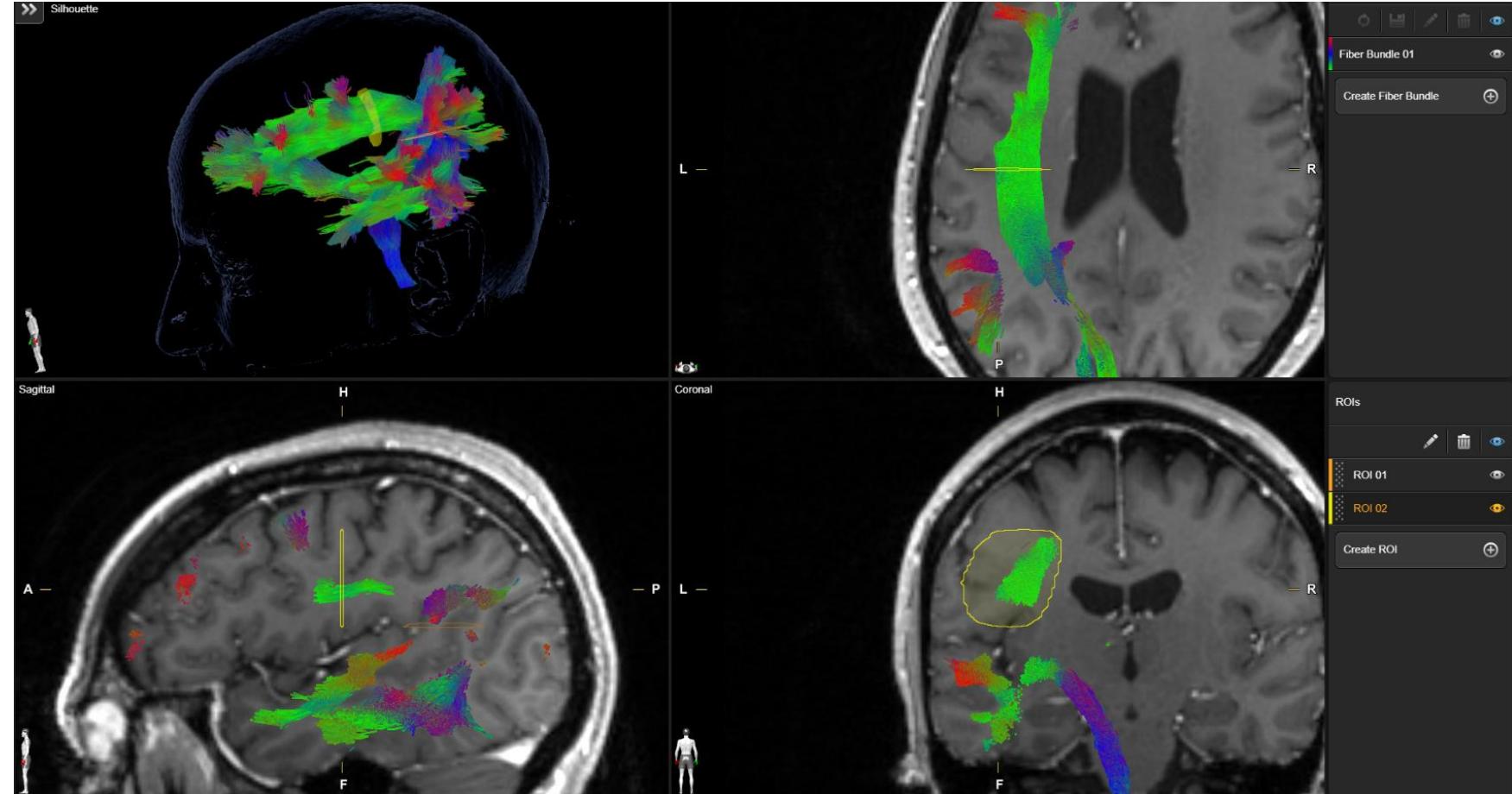
Brainlab & clinical tractography

Arcuate Fasciculus

Additional ROI:

- On the sagitall plane, find the deepest point of the post/central sulcus. Scroll to move the crosshair as medial so that you can see the beginning of the STS.
- Create a circular ROI with approx. 1.5 – 3cm radius around the crosshair.

Color: Blue
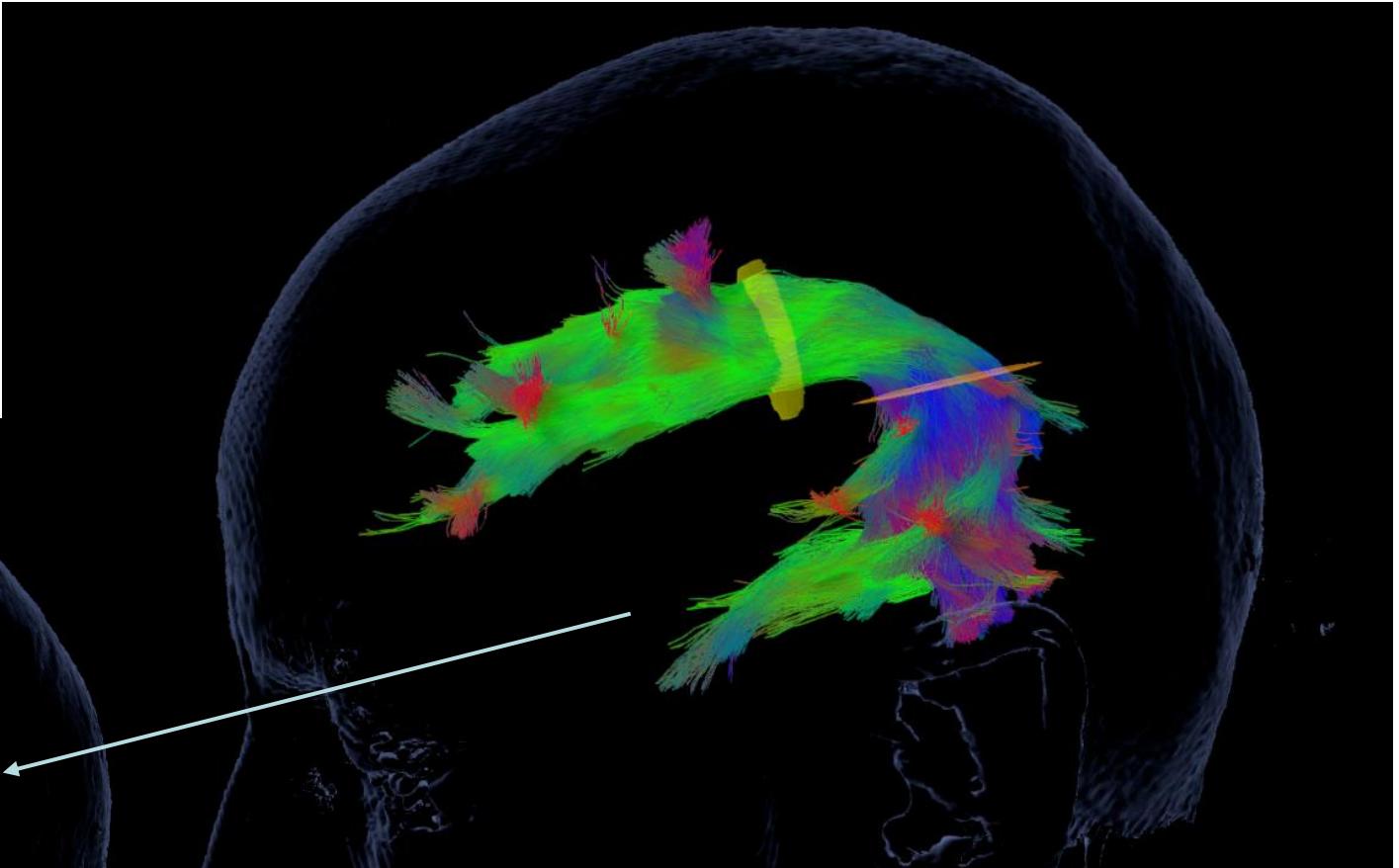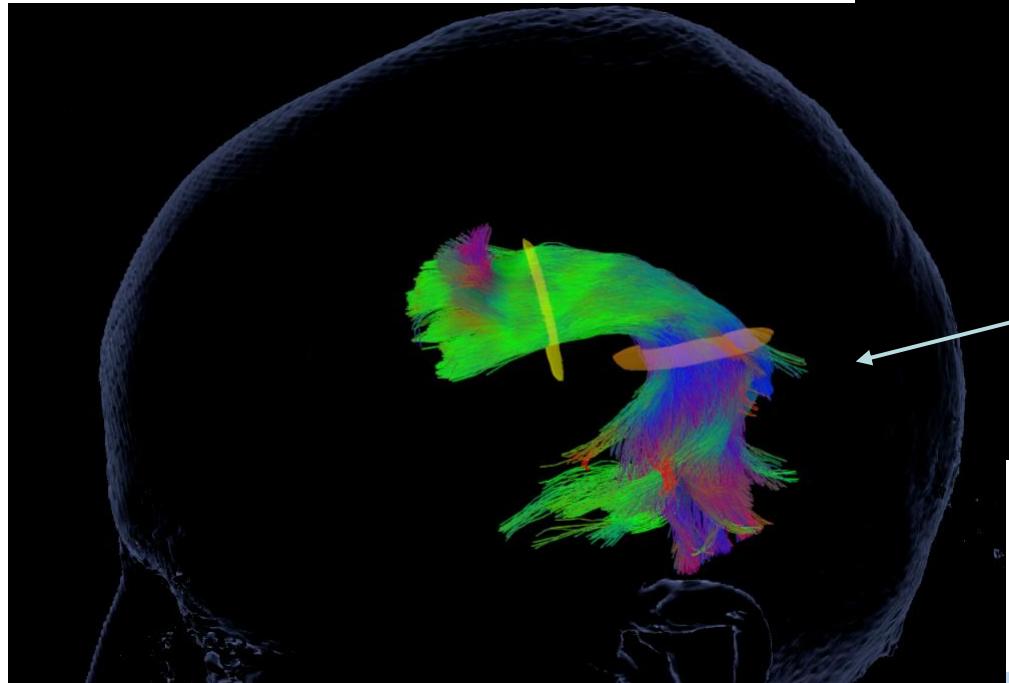
Brainlab & clinical tractography

Arcuate Fasciculus

Now add your refining ROI to the Fiber Bundle!

If you are not totally happy, you can edit the Fiber Bundle by clicking "Remove Fibers"!
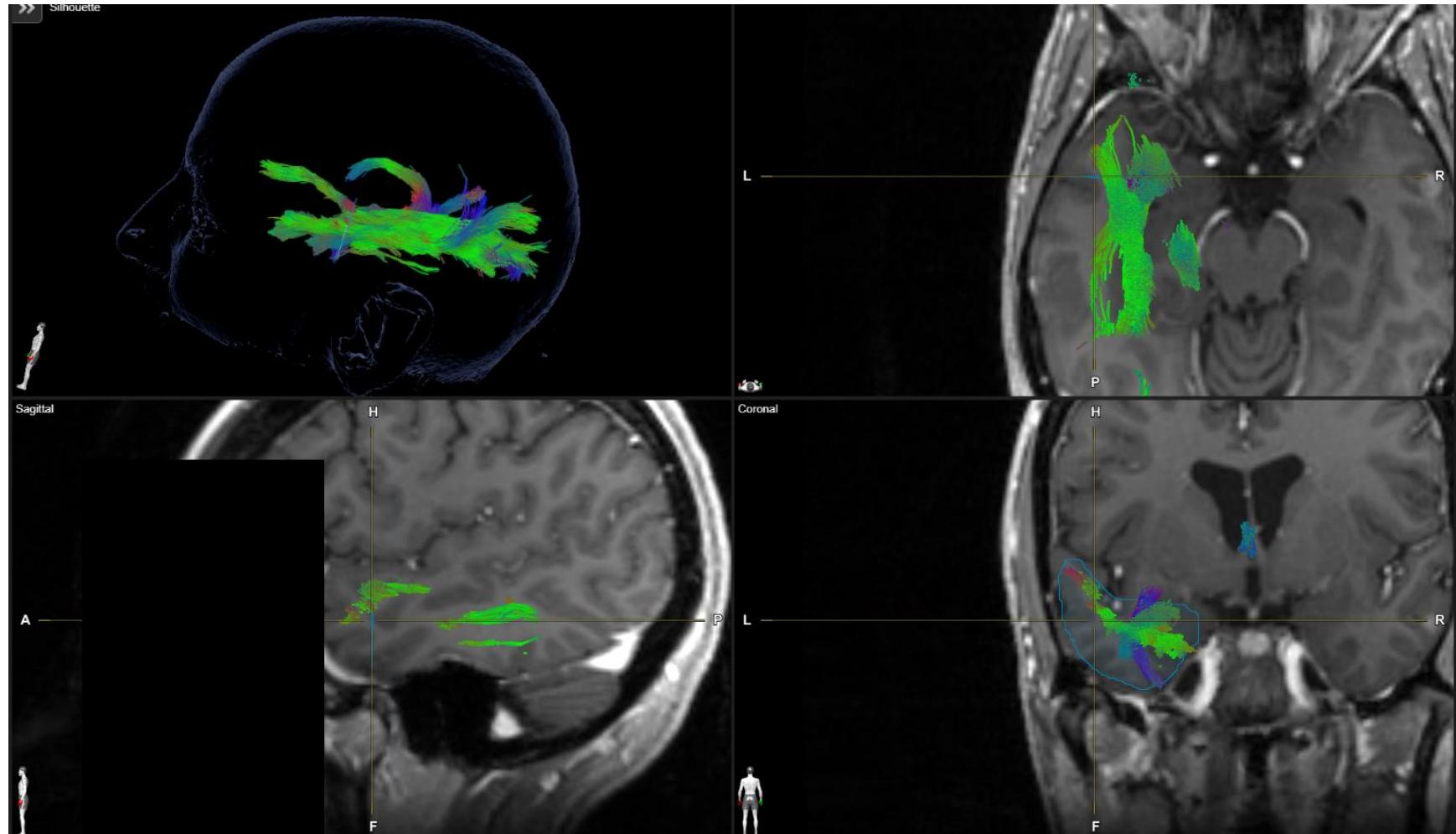
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Brainlab & clinical tractography

<u>Inferior Longitudinal Fasciculus (both ROIs on coronal)</u>

<u>Seed:</u> Anterior temporal lobe, coronal plane
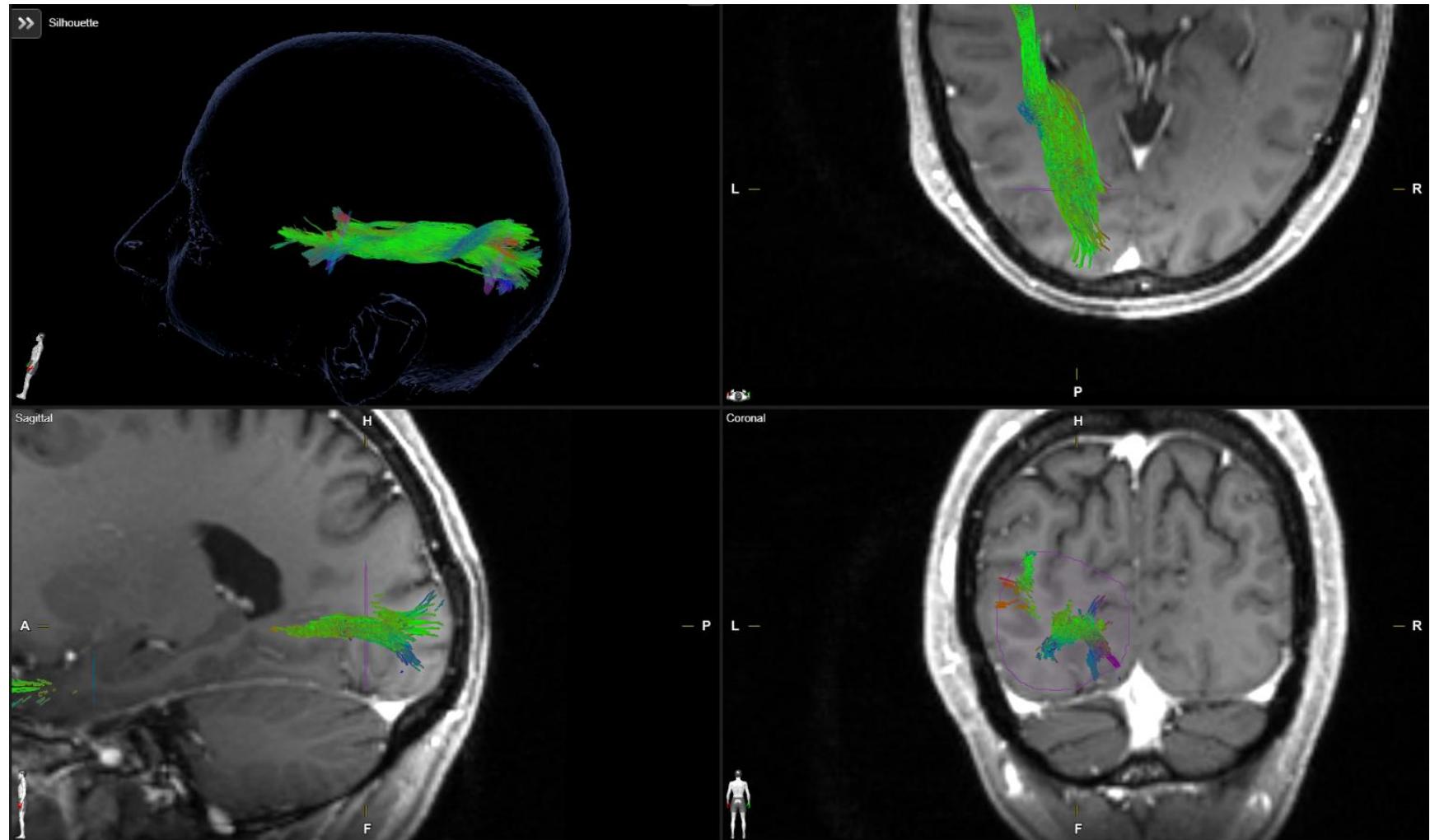
Brainlab & clinical tractography

Inferior Longitudinal Fasciculus

Refining: Occipital lobe, posterior right above the "end" of the cerebellum. Coronal plane.
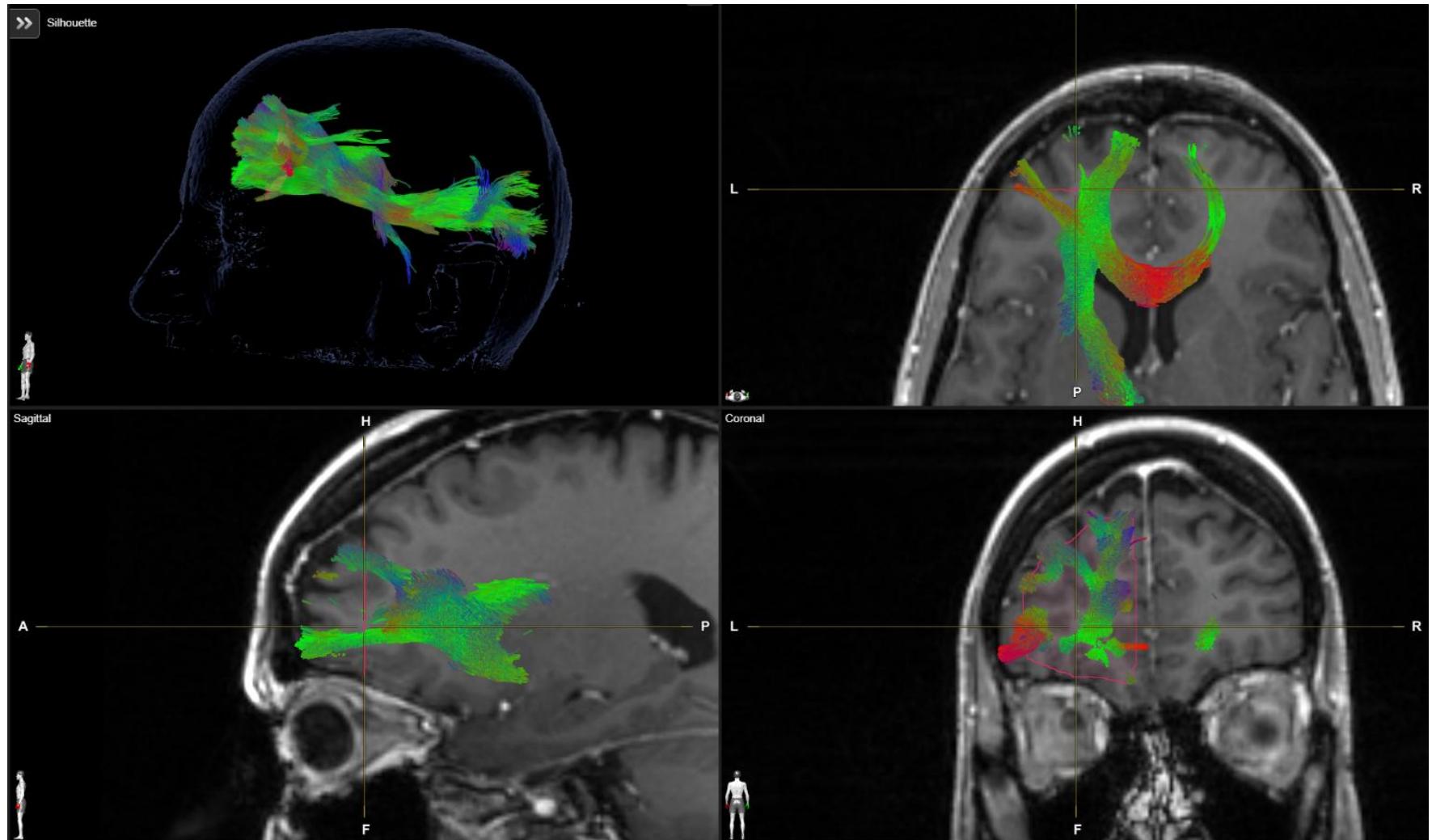
Color: Purple

Brainlab & clinical tractography

<u>Inferior Fronto-Occipital Fasciculus (both ROIs on coronal)</u>

<u>Seed:</u> Prefrontal cortex.
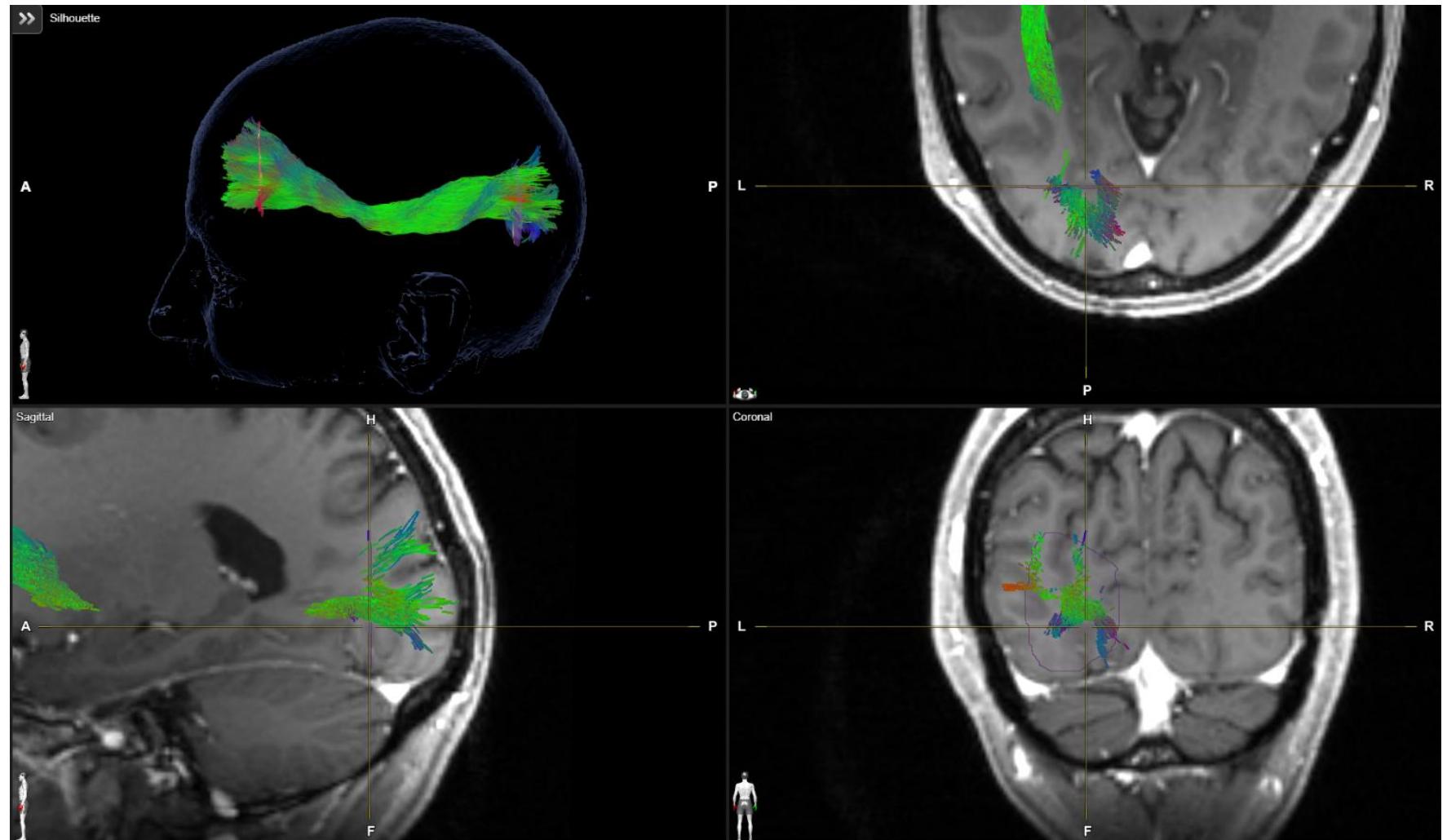
Brainlab & clinical tractography

<u>Inferior Fronto-Occipital Fasciculus (both ROIs on coronal)</u>

<u>Refining:</u> You can reuse the ILF refining ROI. These two tracts terminate in very similar occipital regions.

Color: Green
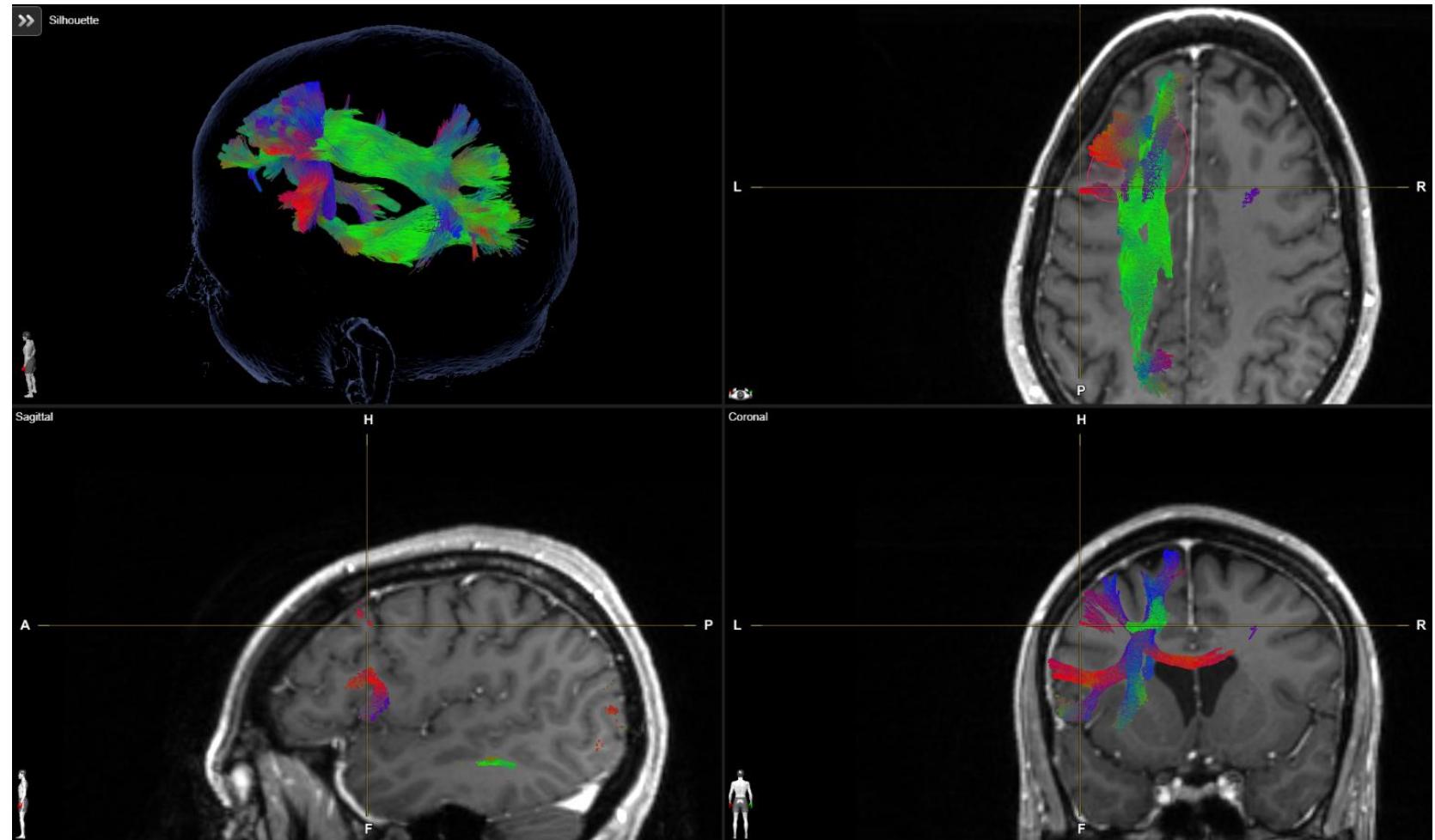
Brainlab & clinical tractography

<u>Frontal Aslant Tract (Axial + Sagittal)</u>

<u>Seed:</u> Place a circle with a 1.5-3cm radius approx. over the SMA using the coronal plane.
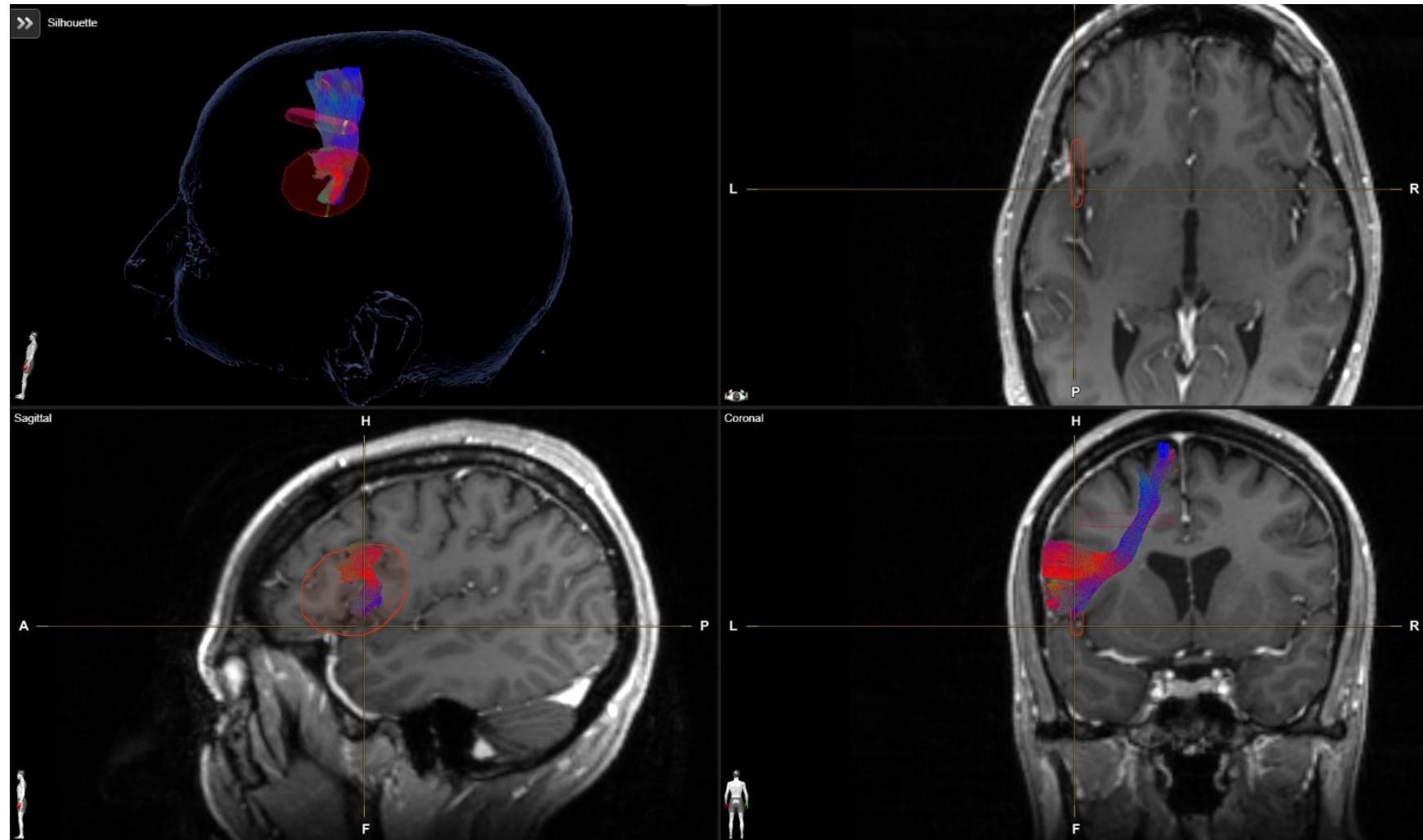
Brainlab & clinical tractography
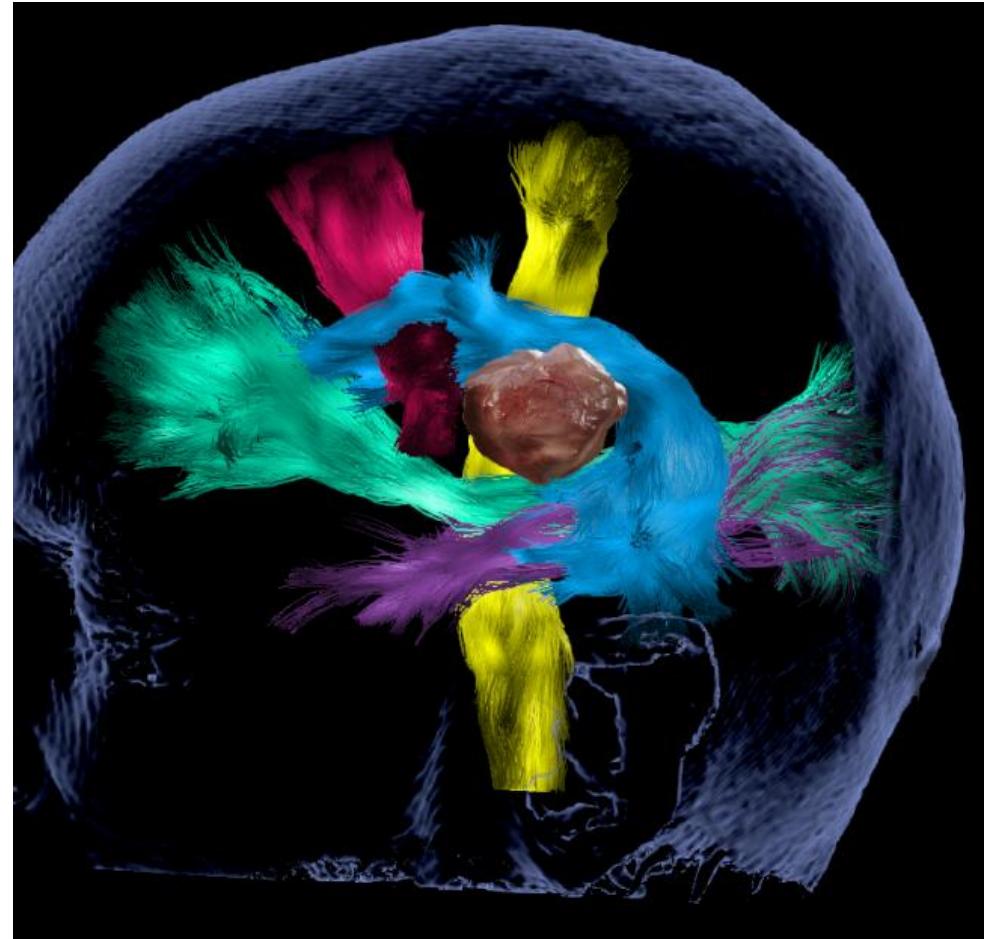
<u>Frontal Aslant Tract (Axial + Sagittal)</u>

<u>Refining:</u> Broca area ROI using the sagittal plane to capture IFG terminations.
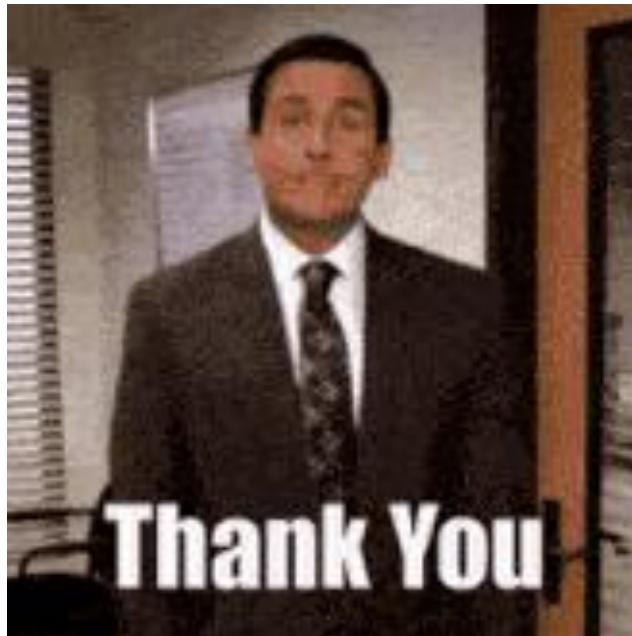
Color: Pink

Brainlab & clinical tractography

For questions/comments:
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