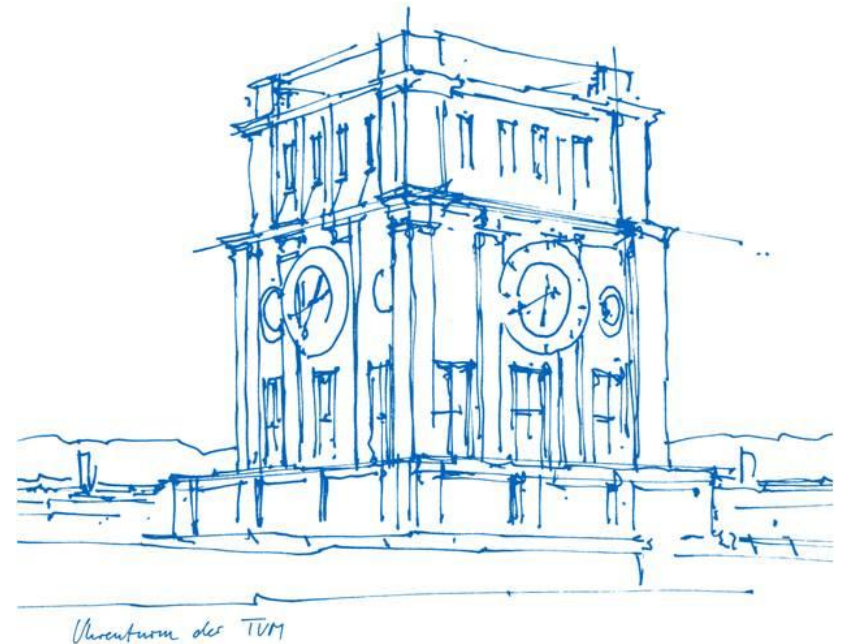


A data preprocessing pipeline for multimodal human connectomics

Student: Ding Zhou 03737422

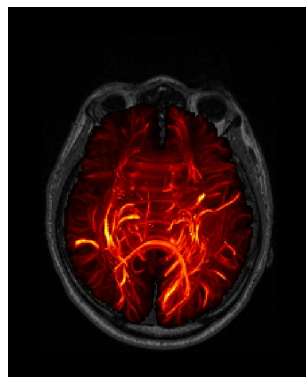
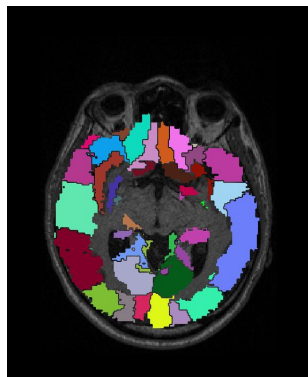
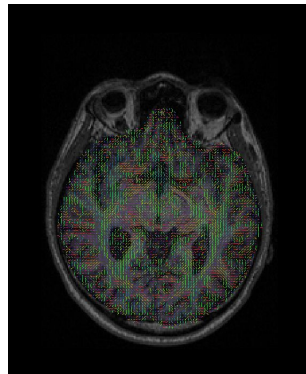
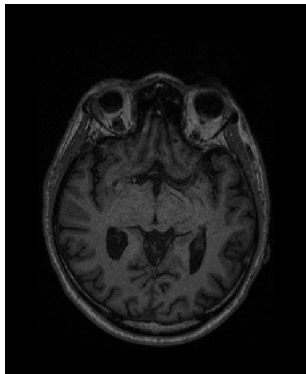
Supervisor: Yifan Mayr, Prof.Dr. Igor Yakushev

Technical University Munich



Introduction

- Human connectomics



Disease

Intelligence

Brain function

etc.

- Combining multiple modalities to acquire richer information

Multimodal Fusion



PET

DWI

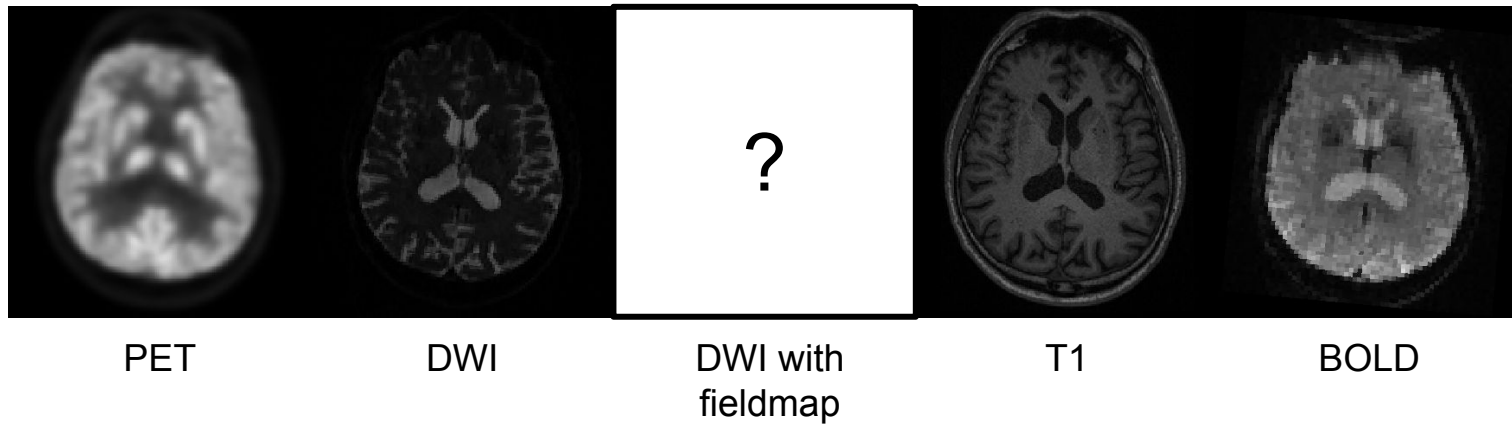
DWI with
fieldmap

T1

BOLD

- Potential challenges: Missing modality and scanner parameters

Multimodal Fusion



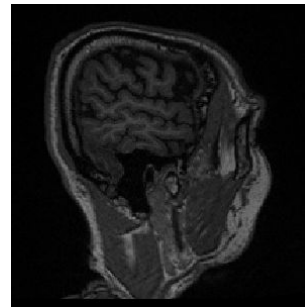
Experiment

- T1 Processing
- DWI Processing
- BOLD Processing
- PET processing
- Connectivity analysis
- Potential improvement

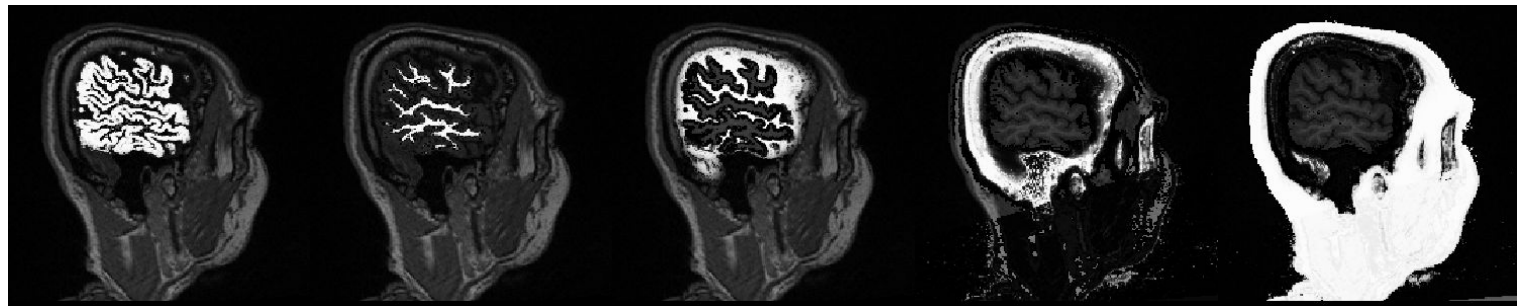


- Brain region segmentation
- Brain reconstruction
- Standard brain registration
- Standard brain region atlas

- **Brain region segmentation**
 - Segment the T1 image into GM, WM, CSF, Bone, Others
 - Tools: SPM Segmentation



T1



GM

WM

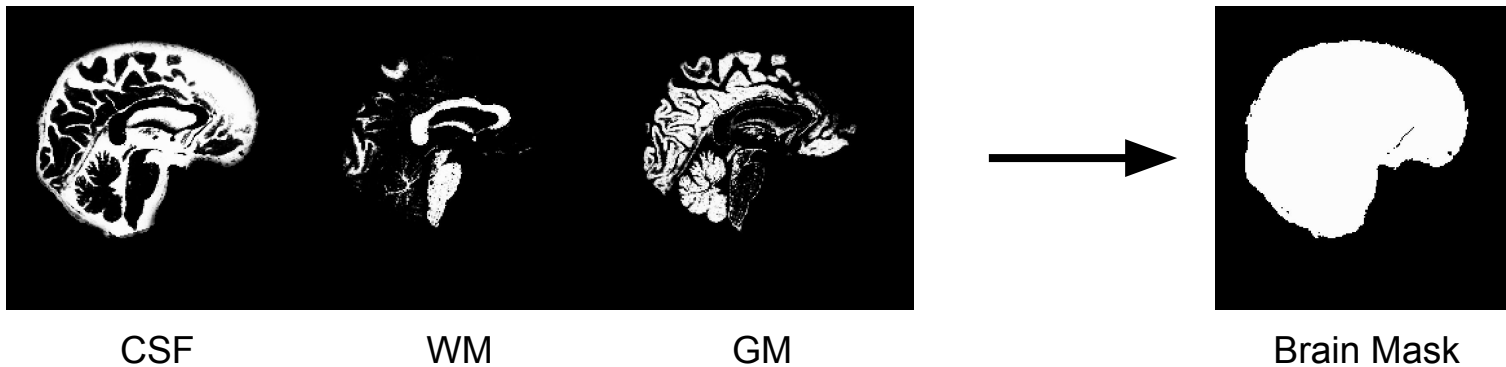
CSF

Bone

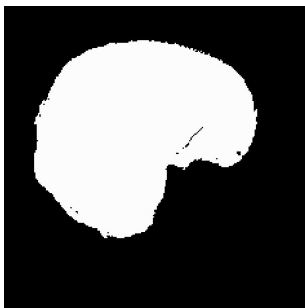
Others

- **Brain reconstruction**

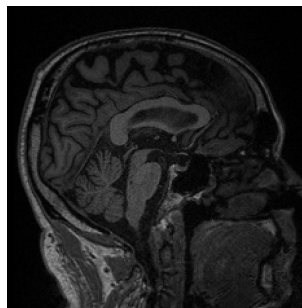
- Create the mask of brain by GM + WM + CSF
- Tools: FSL maths



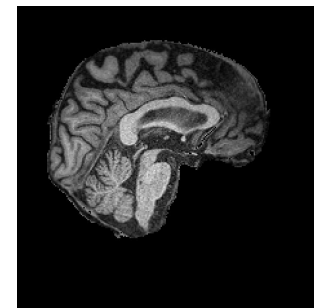
- **Brain reconstruction**
 - Reconstruct the brain by $T1 + \text{Brain Mask} = \text{Brain region}$
 - Tools: FSL maths



Brain Mask

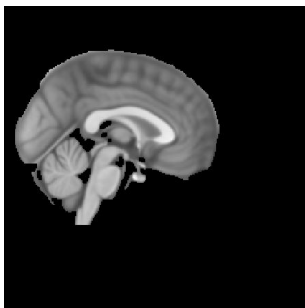


T1

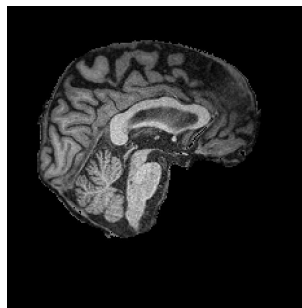


Reconstructed
Brain

- **Standard brain registration**
 - Register the standard brain into reconstructed brain (T1)
 - Get the transform function
 - Tools: antsRegistration



Standard
Brain

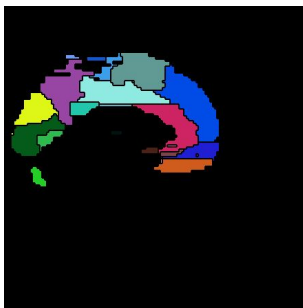


Reconstructed
Brain



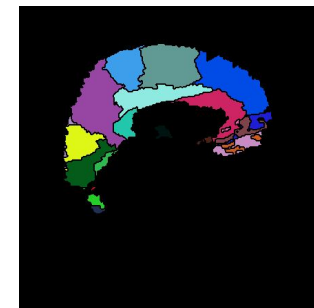
Registered
Standard
brain

- **Standard brain region atlas**
 - Atlas the standard brain region into our brain (T1 volume)
 - Use the transform function getted from registration
 - Tools: `antsApplyTransforms`



Standard
Brain Region

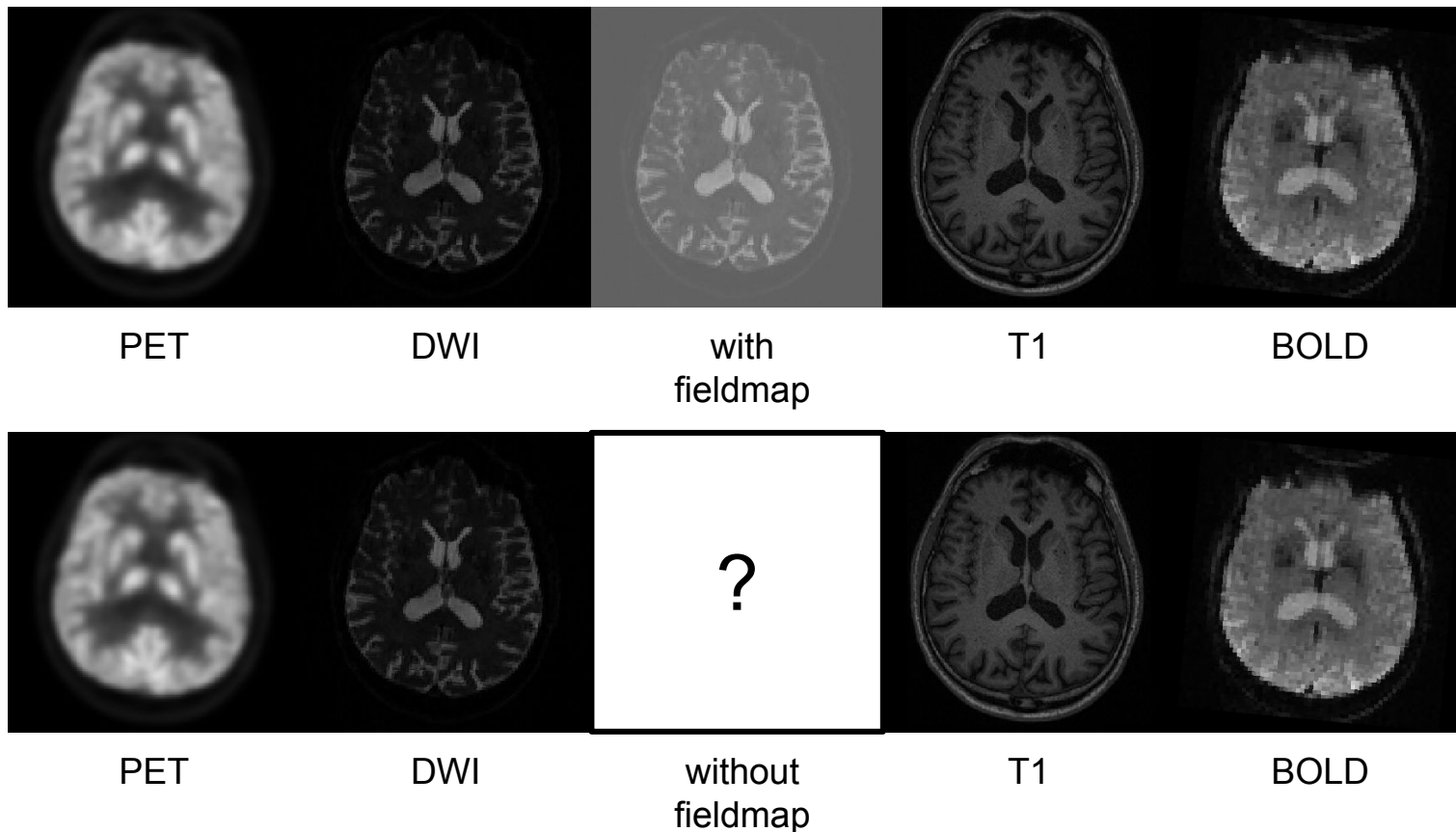
Transform function
getted from registration



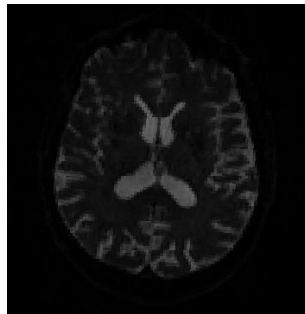
Atlased Brain
Region

- Field map processing
- Calculate the WM fiber orientation
- Track the fiber connection

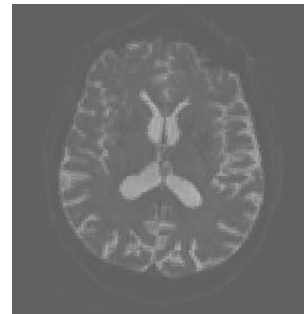
- Field map processing
 - We need acquire parameters of the scanner to correct distortion like eddy current eg.



- **Field map processing**
 - Sometimes the acquire parameters of the scanner are missing
 - Then use the image without correction

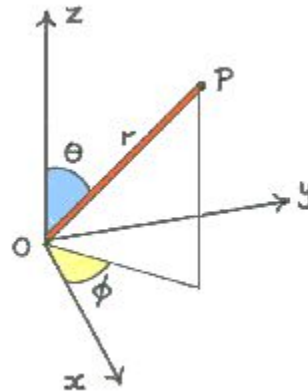


DWI
without
fieldmap



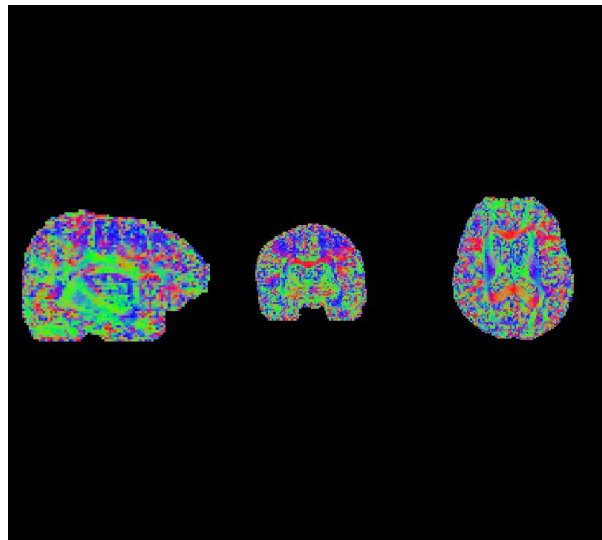
DWI
with
fieldmap

- Calculate the WM fiber orientation
 - Use theta and phi to describe the fiber orientation
 - Tools: FSL BedpostX

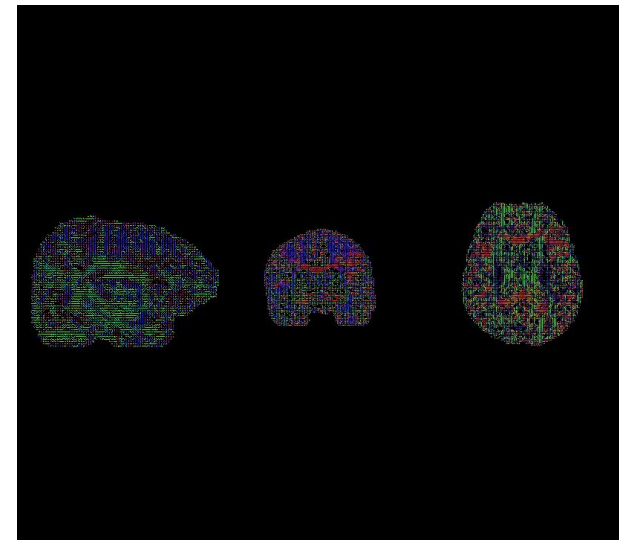


- **Calculate the WM fiber orientation**
 - Visualize the theta and phi by colors
 - Tools: FSL BedpostX

- X
- Y
- Z

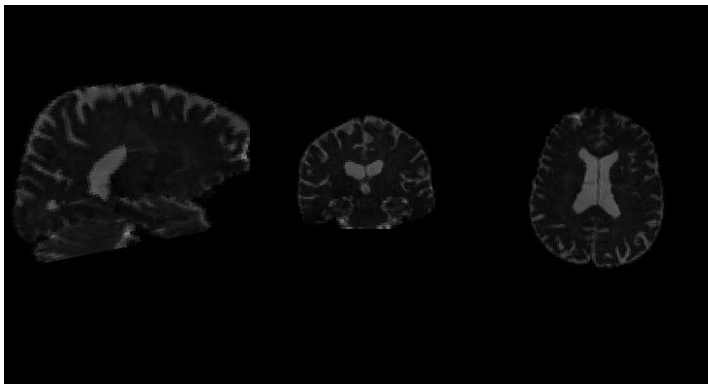


color dot image (RBG)

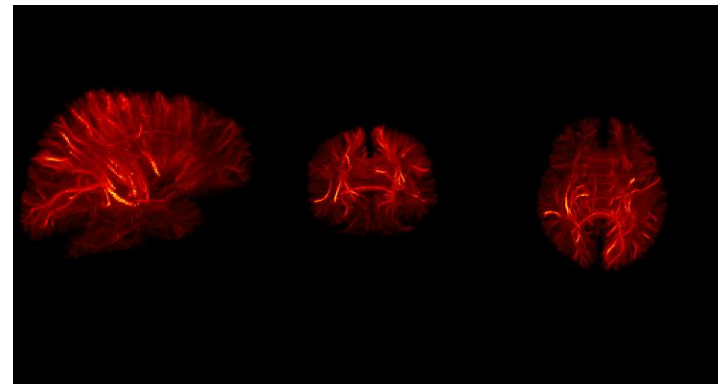


streamline image (RBG)

- **Track the fiber connection**
 - Connect the neighbour voxels with the most similar orientation
 - Tools: FSL probtrackX

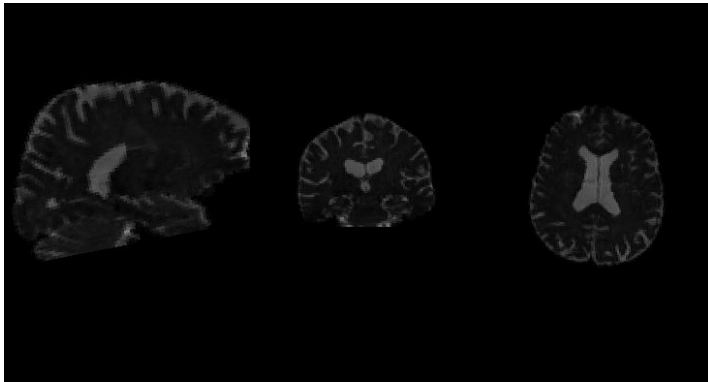


DWI image

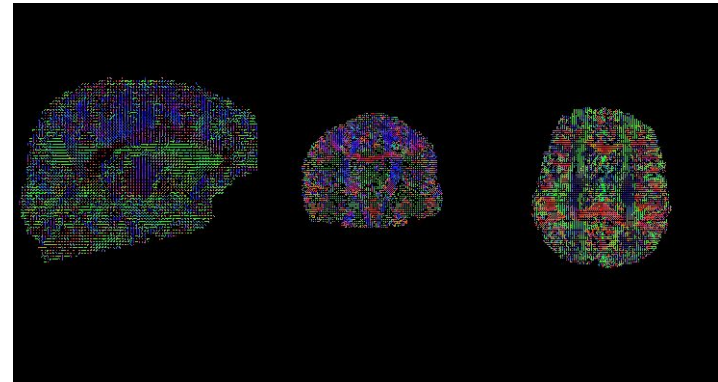


Fiber connection

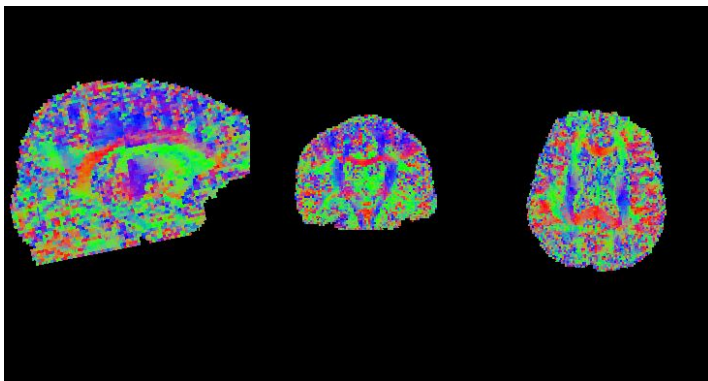
- Track the fiber connection
 - Comparison of the DWI, Fiber orientation and connection



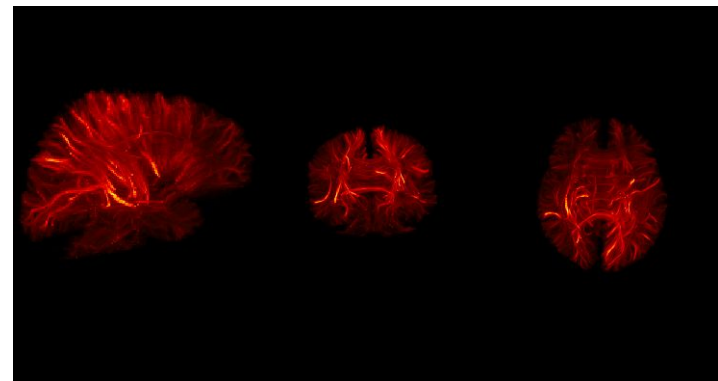
DWI image



color line image (RGB)



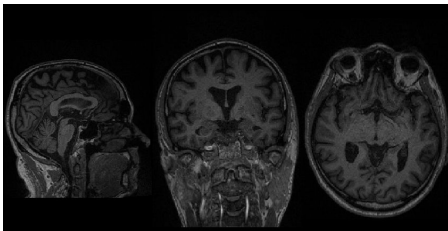
color dot image (RGB)



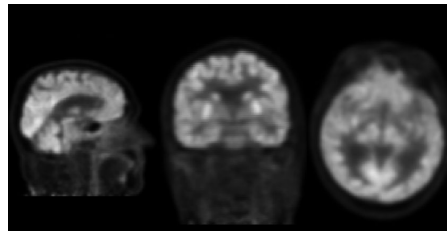
Fiber connection

- Registration from T1 to PET
- Split standard brain into regions
- FDG uptake extraction

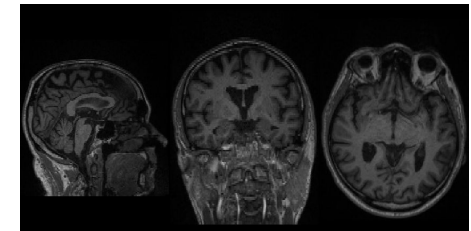
- **Registration from T1 to PET**
 - Register the T1 image into the PET format
 - Tools: FSL flirt



T1

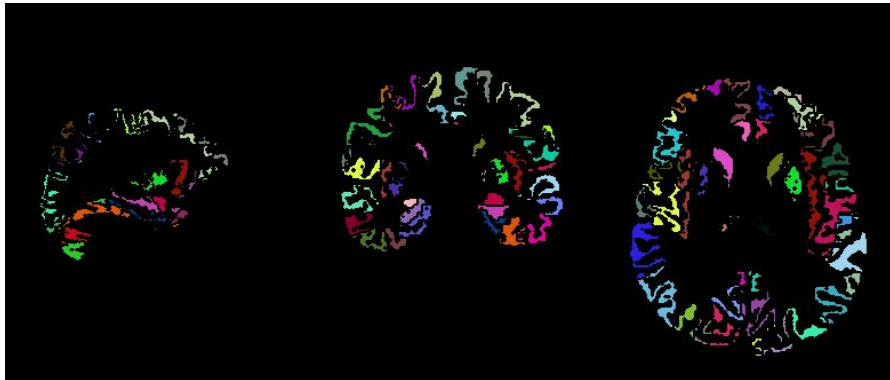


PET

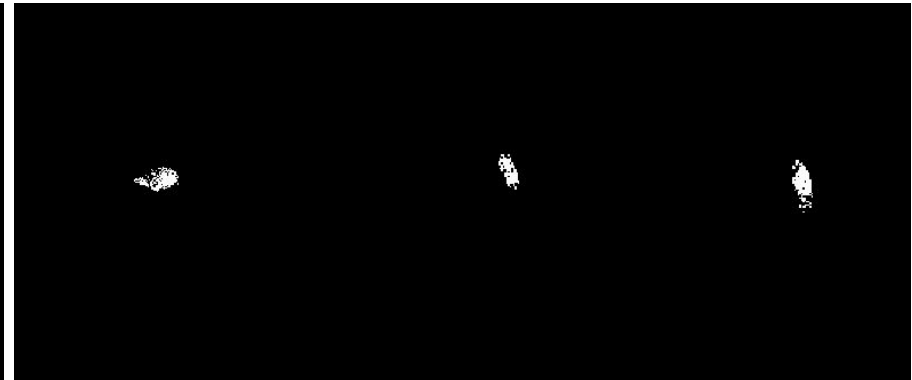


T1 in PET space

- **Split standard brain into regions**
 - Split standard brain in T1 space
 - Tools: FSL maths

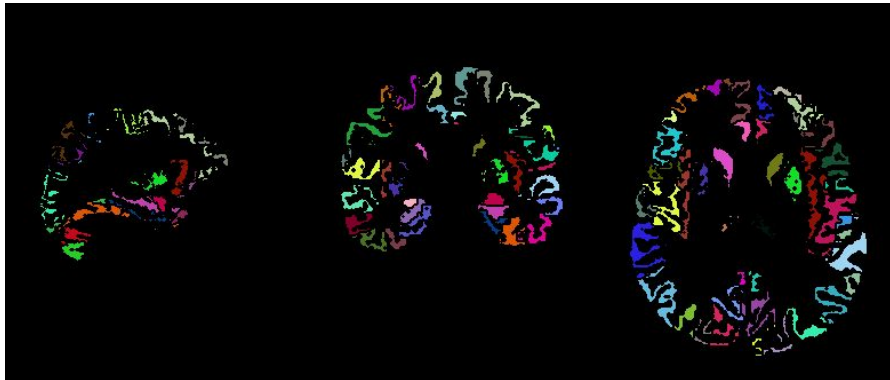


Standard brain in T1 space



ROI 77

- **Split standard brain into regions**
 - Split standard brain in T1 space
 - Tools: FSL maths



Standard brain in T1 space

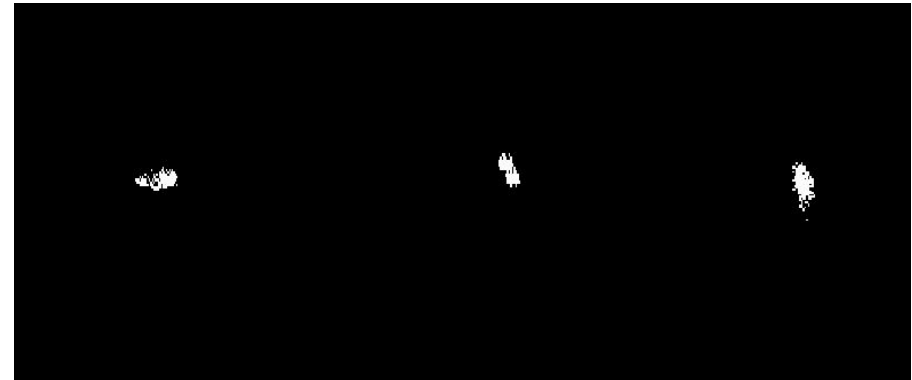


Overlay

- **Split standard brain into regions**
 - Split standard brain in PET space
 - Tools: FSL maths

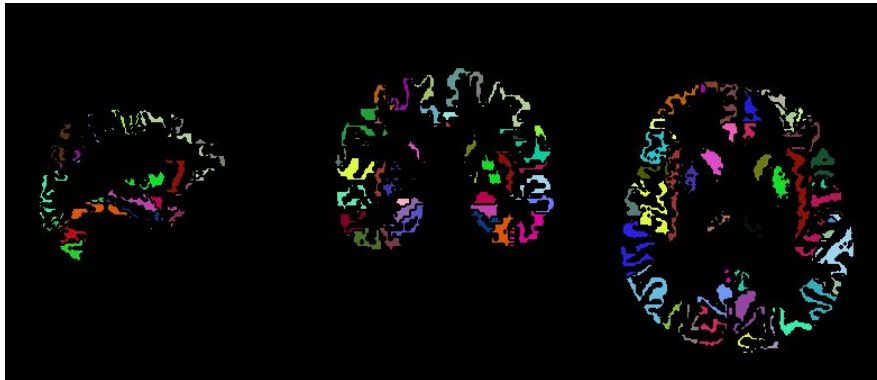


Standard brain in PET space

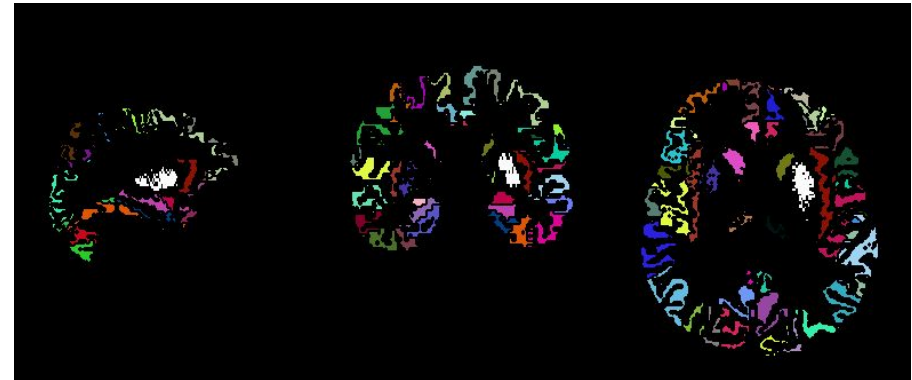


ROI 77

- **Split standard brain into regions**
 - Split standard brain in PET space
 - Tools: FSL maths

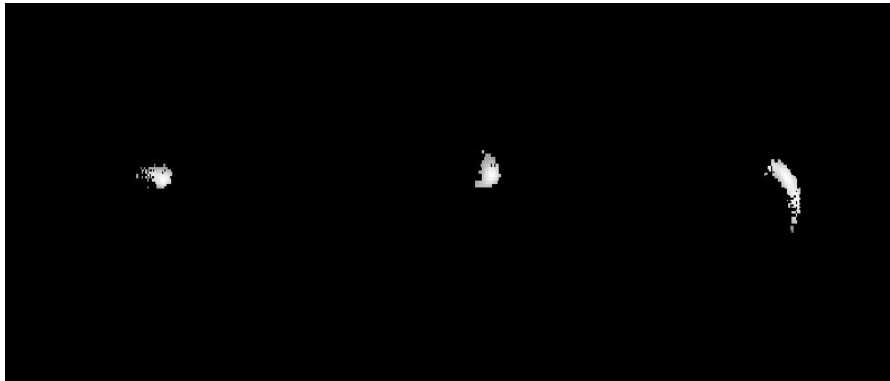


Standard brain in PET space



Overlay

- **FDG uptake extraction**
 - Extract the FDG uptake for each brain regions
 - Tools: FSL stats -M (Output mean intensity for nonzero voxels)



ROI 77 in PET space

11475.828974



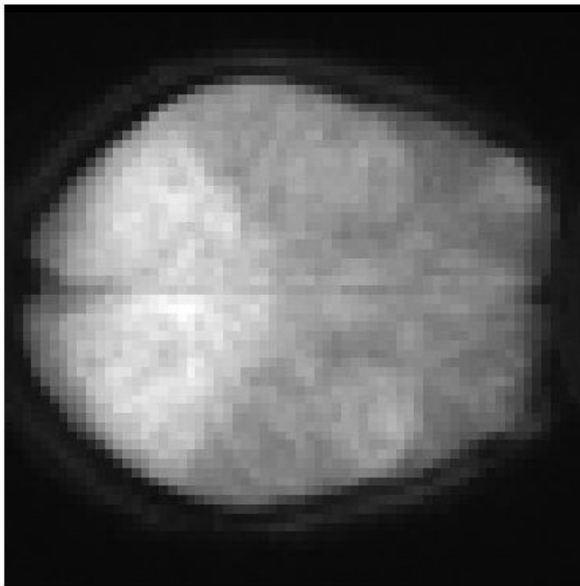
- **FDG uptake extraction**

- Extract the FDG uptake for each brain regions
- Tools: FSL stats -M (Output mean intensity for nonzero voxels)

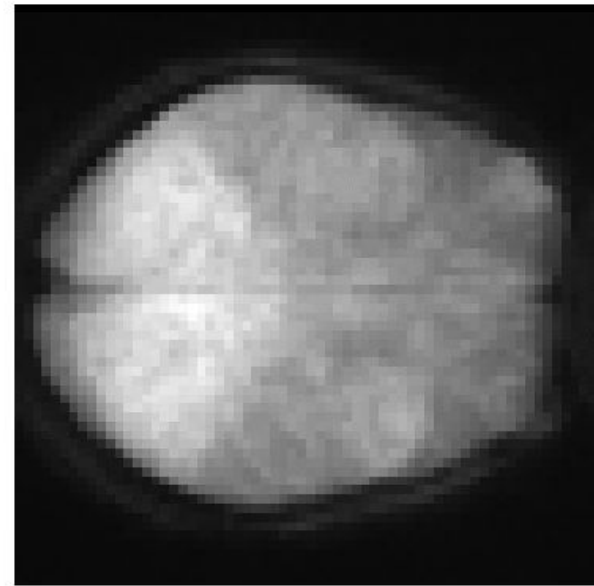
ROI	Mean Intensity
1	9378.304431
2	9267.954202
3	9030.360747
4	9369.651360
.....	
120	8609.852758

- Volume time correction
- Denoise
- Registration from T1 to BOLD
- Split standard brain into regions

- **Volume time correction**
 - Rearrange the acquire time of the volume (4D)
 - Tools: Matlab SPM

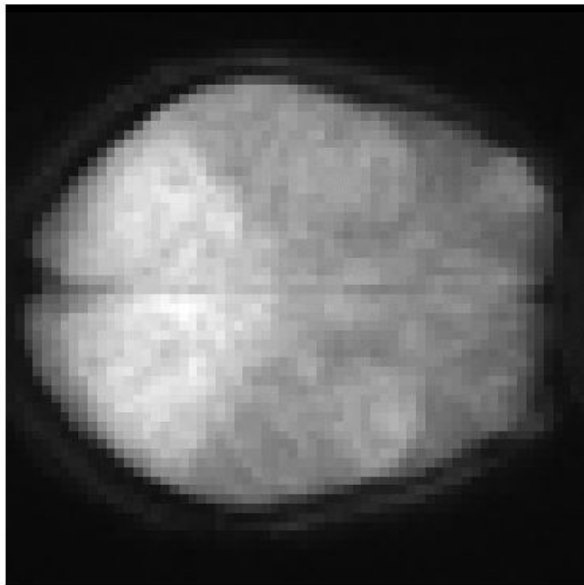


Before time correction

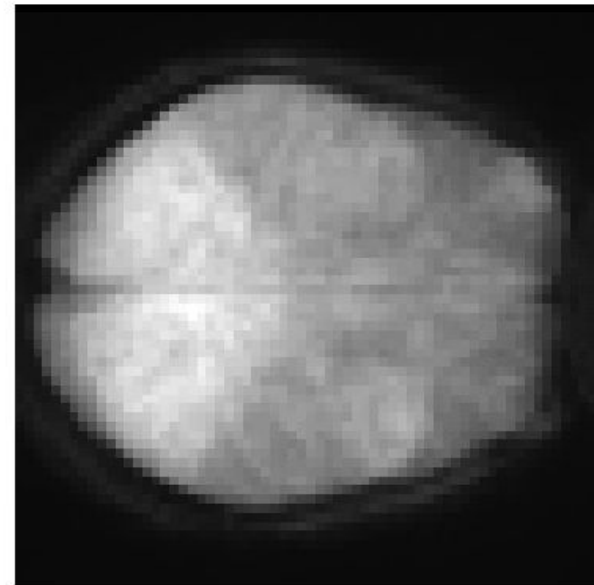


After time correction

- Denoise
 - Apply filters to denoise
 - High pass filter: eliminate low frequency noise
 - Low pass filter: eliminate high frequency noise



After time correction

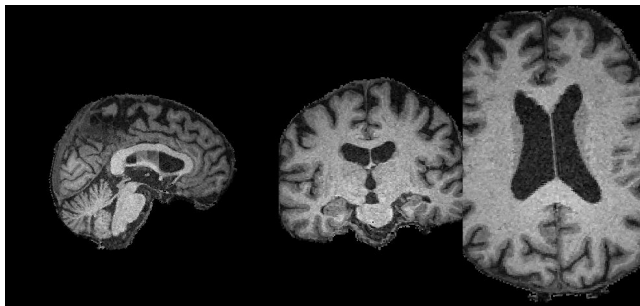


After filters

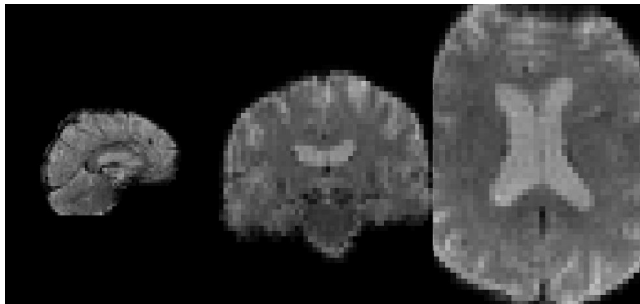
BOLD Processing



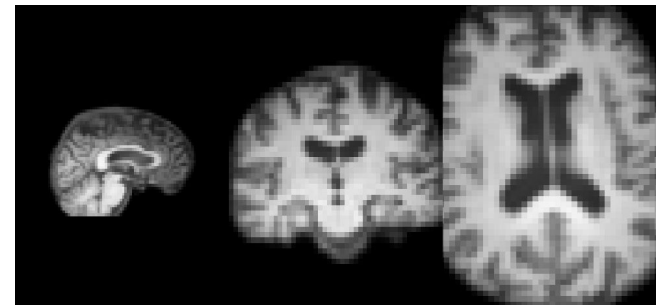
- **Registration from T1 to BOLD**
 - Register the T1 image into the BOLD format
 - Tools: FSL flirt



T1

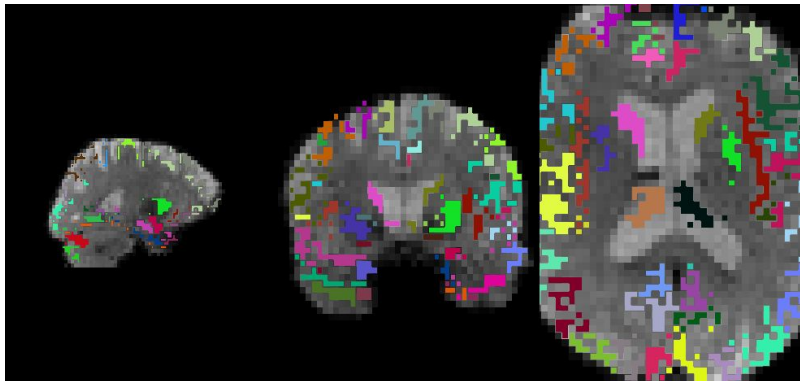


BOLD

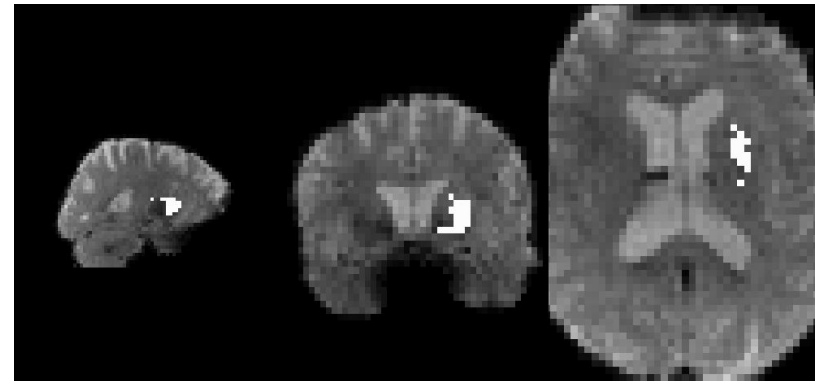


Register T1 to BOLD

- **Split standard brain into regions**
 - Split standard brain in BOLD space
 - Tools: FSL maths

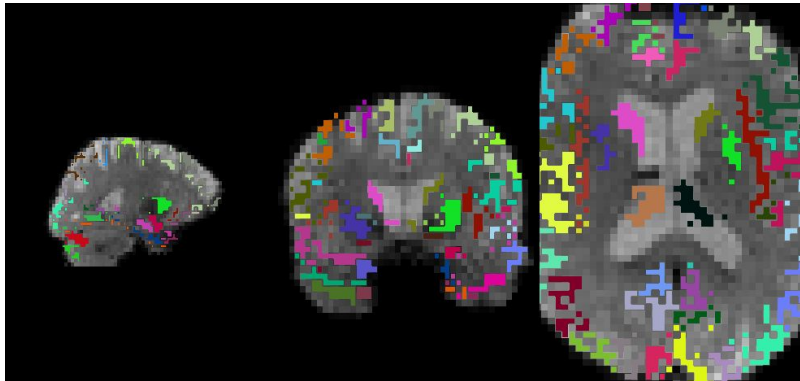


Standard brain in BOLD space

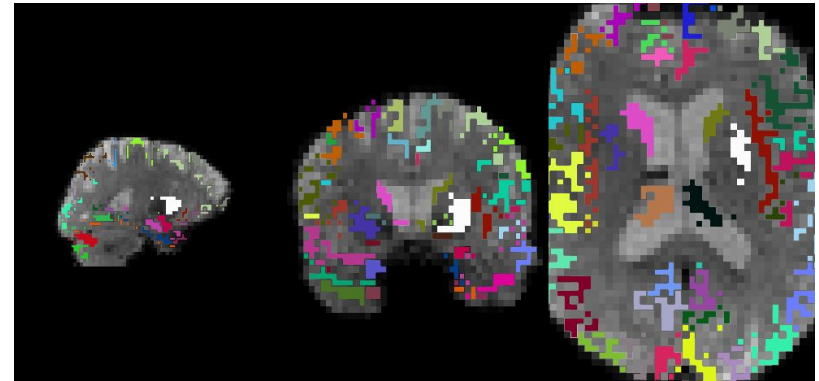


ROI 77

- **Split standard brain into regions**
 - Split standard brain in BOLD space
 - Tools: FSL maths



Standard brain in BOLD space



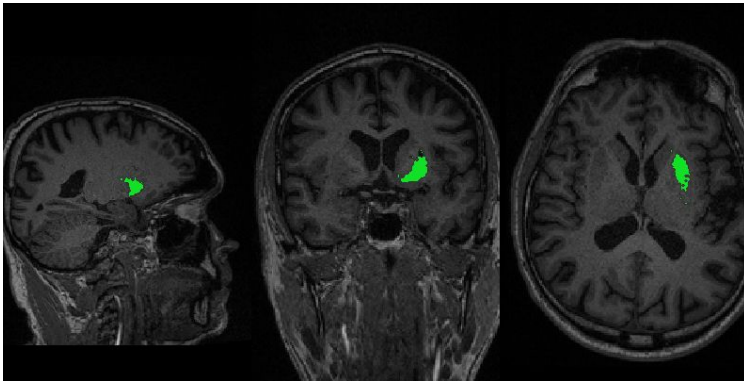
Overlay

- Brain volume reshape
- Grey Matter density statistic
- Grey Matter volume statistic

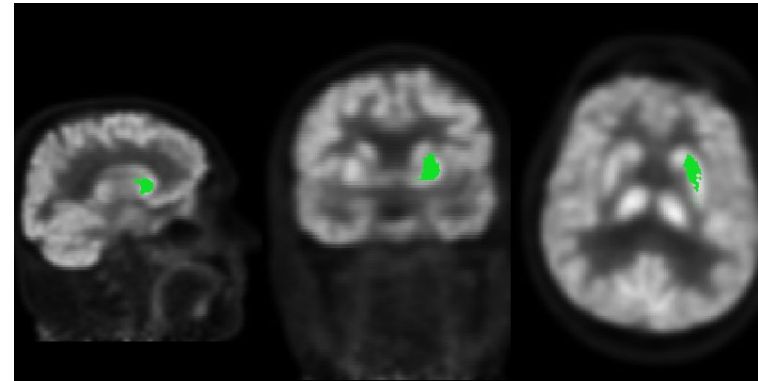
Connectivity analysis

- **Brain volume reshape**

- We already split the brain into brain regions in different imaging space
- But some regions have bias

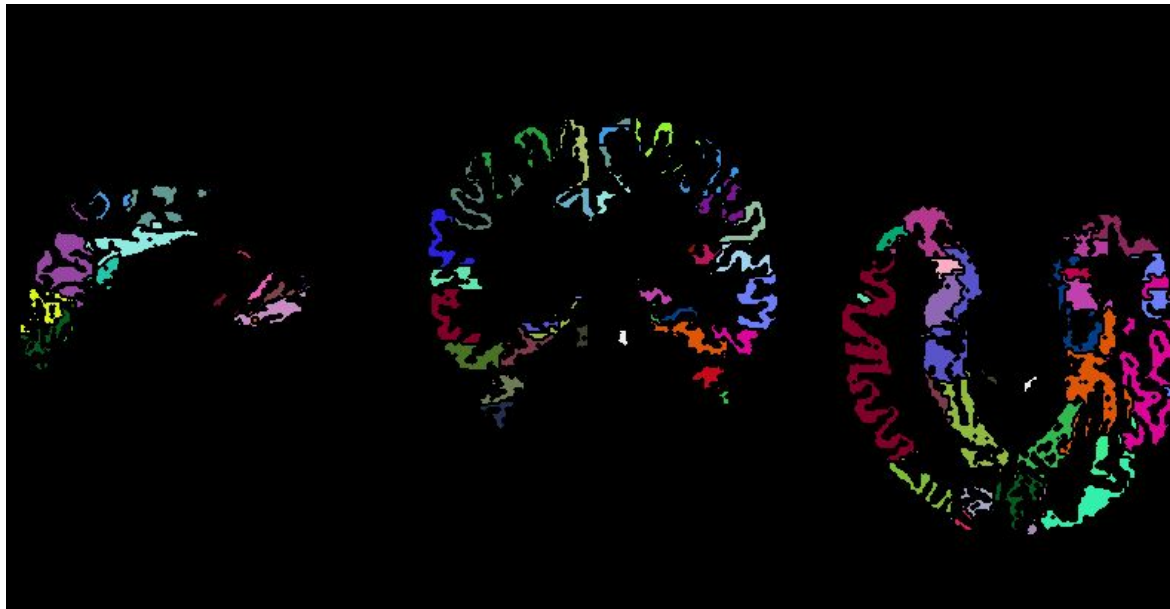


ROI 77 in T1 space



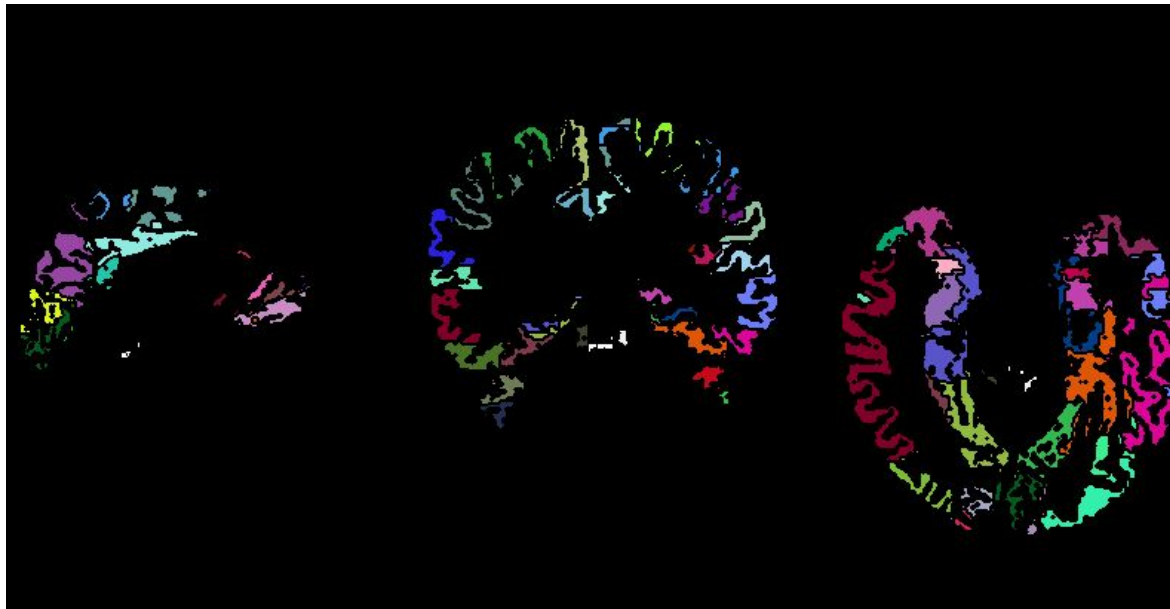
ROI 77 in PET space

- **Brain volume reshape**
 - For example: ROI 113 and ROI 114 both belong to Cerebellar vermis
 - Solution: Merge them together



ROI in T1 space

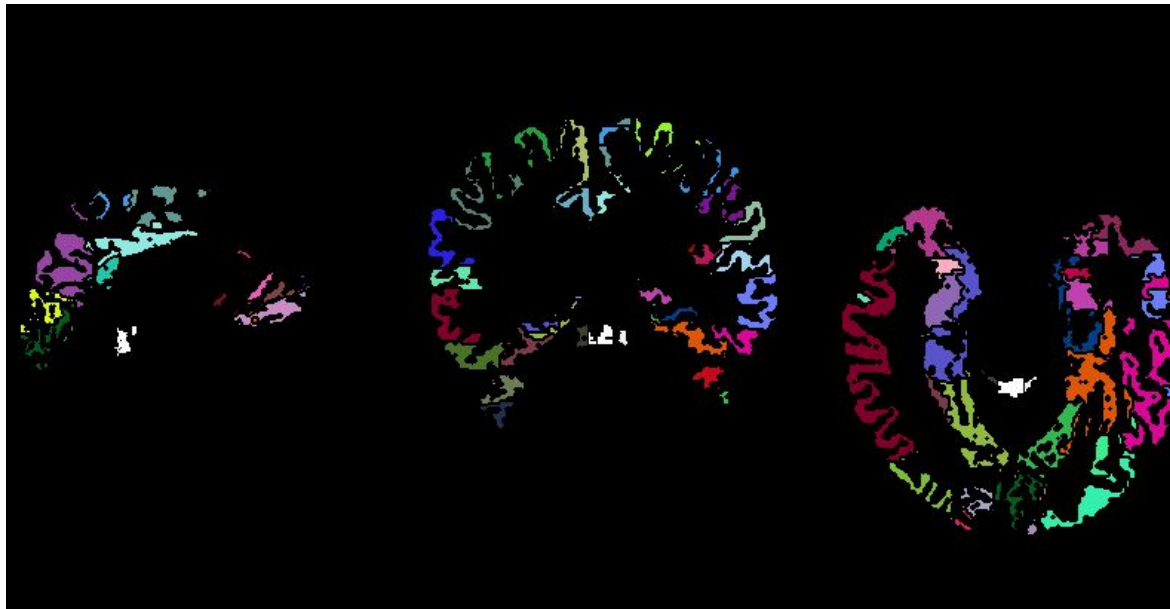
- **Brain volume reshape**
 - For example: ROI 113 and ROI 114 both belong to Cerebellar vermis
 - Solution: Merge them together



ROI 113 in T1 space

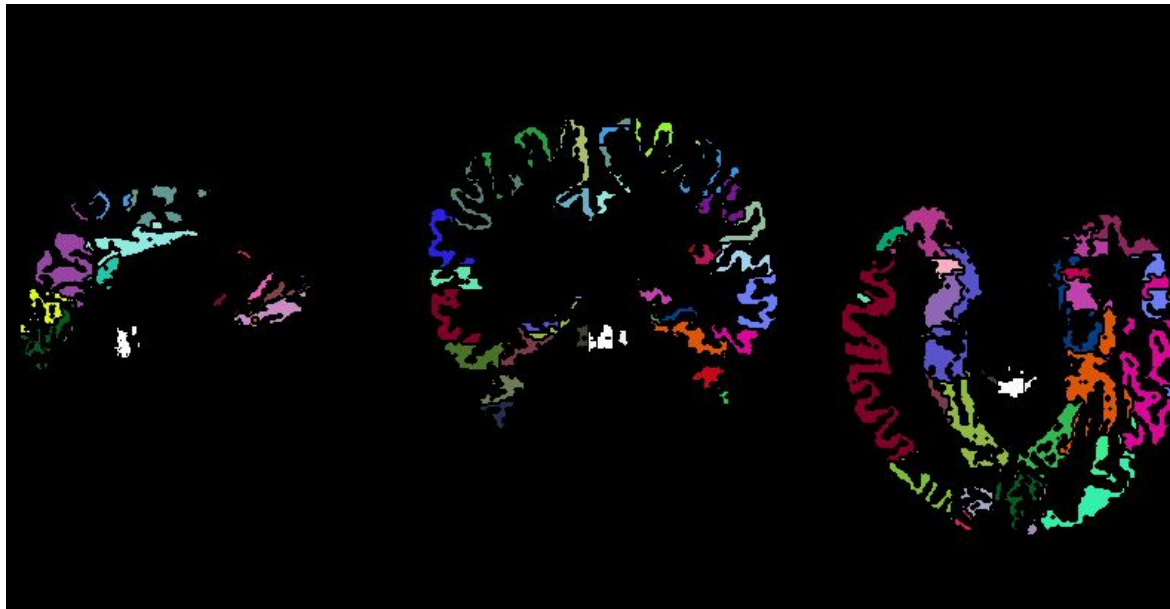
- **Brain volume reshape**

- For example: ROI 113 and ROI 114 both belong to Cerebellar vermis
- Solution: Merge them together



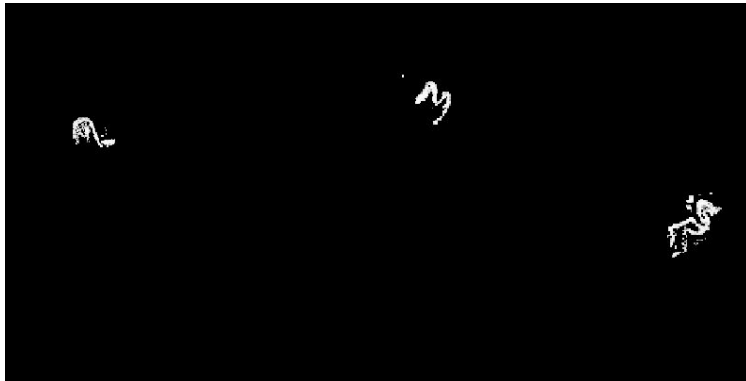
ROI 114 in T1 space

- **Brain volume reshape**
 - For example: ROI 113 and ROI 114 both belong to Cerebellar vermis
 - Solution: Merge them together



Merge 113 and 114 in T1 space

- **Grey Matter density statistic**
 - Calculate the density of each ROI
 - Tools: FSL stats -M (Output mean intensity for nonzero voxels)



ROI 1 in T1 space

0.885876

Connectivity analysis



- **Grey Matter density statistic**
 - Calculate the density of each ROI
 - Tools: FSL stats -M (Output mean intensity for nonzero voxels)

ROI	Mean Intensity
1	0.885876
2	0.870191
3	0.886363
4	0.887498
.....	
106	0.917121

Connectivity analysis

- **Grey Matter volume statistic**
 - Calculate the volume of each ROI
 - Tools: FSL stats -V (Number of nonzero voxels)



ROI 1 in T1 space

10135

Connectivity analysis



- **Grey Matter volume statistic**
 - Calculate the volume of each ROI
 - Tools: FSL stats -V (Number of nonzero voxels)

ROI	Mean Intensity
1	10135
2	10050
3	14303
4	14407
.....	
106	1118

Potential improvement

- Multimodal registration
- Regression our brain data with standard brain data

Potential improvement

- **Multimodal registration**
 - Registerate the PET, BOLD, DWI and T1
 - The script has shown this idea
 - But the methods it uses is wrong in Maths!

- **Multimodal registration**
 - Register the PET, BOLD, DWI and T1

The wrong method of the script:

1. Register standard brain in T1
2. Register T1 to another space like PET, DWI
3. Apply the second registration function on standard brain in T1

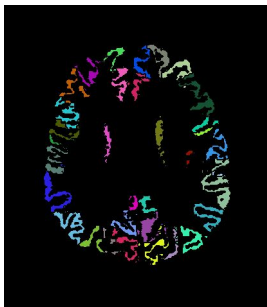
Definitely, this way will decrease the resolution!

Potential improvement

- **Multimodal registration**
 - Register the PET, BOLD, DWI and T1

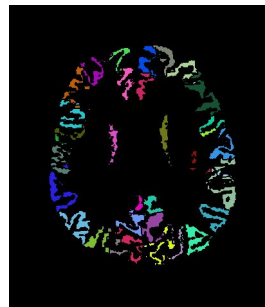
The result of this wrong methods:

T1



PixDim1	PixDim2	PixDim3	Size
1mm	1mm	1mm	X:176, Y:240, Z:256 (mm)

PET



PixDim1	PixDim2	PixDim3	Size
1.043mm	1.043mm	1.043mm	X:359, Y:359, Z:258 (mm)

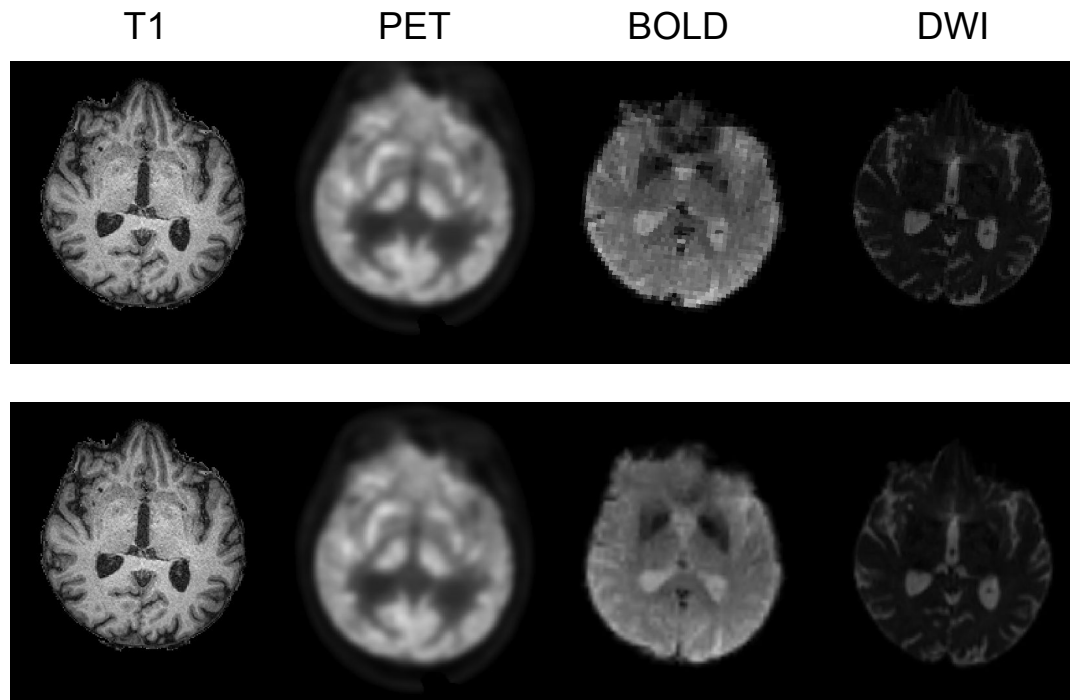
BOLD



PixDim1	PixDim2	PixDim3	Size
3mm	3mm	3.6mm	X:209, Y:233, Z:182 (mm)

Potential improvement

- **Multimodal registration**
 - Right way:
 - Register the PET, BOLD, DWI into T1 space at first
 - Then atlas the standard brain into different space

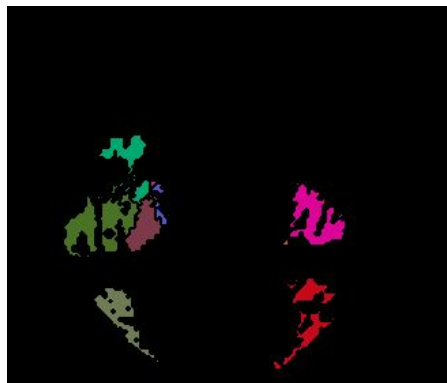


After registration to T1

Potential improvement

- **Multimodal registration**
 - Right way:
 - Registrare the PET, BOLD, DWI into T1 space at first
 - Then atlas the standard brain into different space

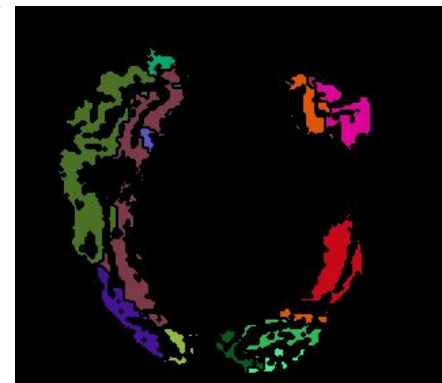
T1 Space



Dimensions

Number of dimensions	3D
dim1	176
dim2	240
dim3	256
pixdim1	1 mm
pixdim2	1 mm
pixdim3	1 mm
Size	X=176 mm Y=240 mm Z=256 mm

PET Space



Dimensions

Number of dimensions	3D
dim1	176
dim2	240
dim3	256
pixdim1	1 mm
pixdim2	1 mm
pixdim3	1 mm
Size	X=176 mm Y=240 mm Z=256 mm

Obviously, my method works, they are in the same unit and size :D

- **Regression our brain data with standard brain data**
-
1. Assume we have already coregistered all modalities
 2. Assume we have then atlases the standard brain in all modalities.
 3. Now, we can split the standard brain into ROI, only when all the modalities are coregistrated.
 4. Further steps