

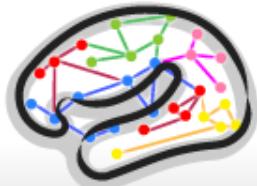


Structural Brain Connectivity Analysis on HCP Dataset

Zhengwu Zhang

Feb. 2 , 2016

Joint work with Hongtu Zhu, Anuj Srivastava and Maxime Descoteaux



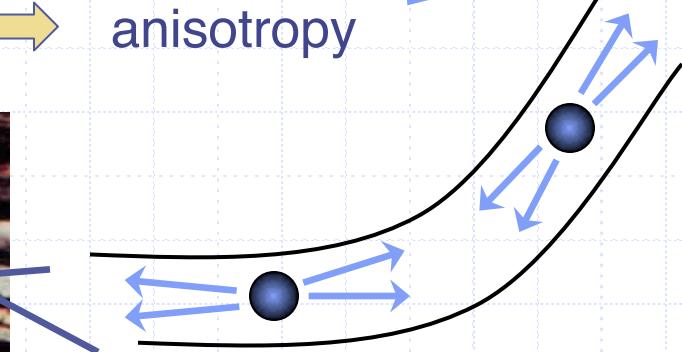
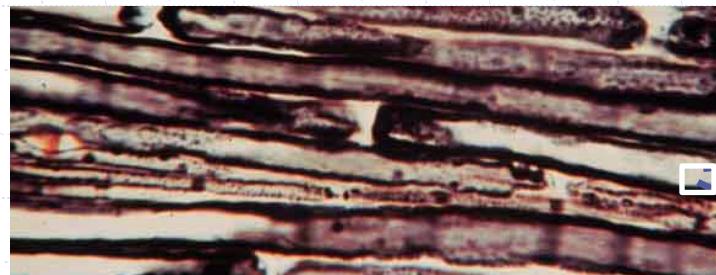
Diffusion in Brain Tissue

- Water molecules in different brain tissues have different diffusion properties.

- **Gray matter:** Diffusion is unrestricted ↔ isotropy

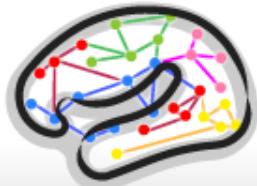


- **White matter:** Diffusion is restricted ↔ anisotropy



- More diffusion along axon fibers

- Diffusion MRI measures the water diffusion movement inside brain



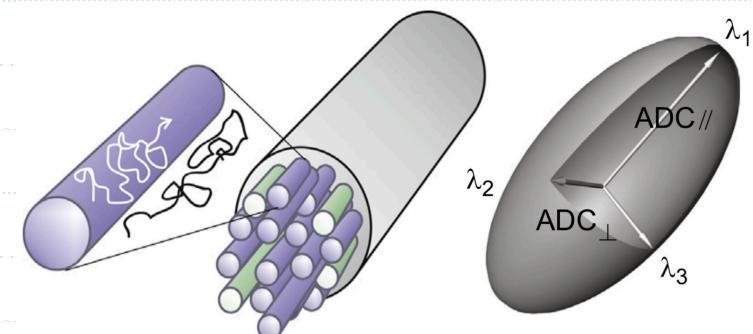
Representation of the Diffusion Directions

- At each voxel, we want to know:
 - What is the orientation of the diffusion?
 - What is the magnitude of diffusion?

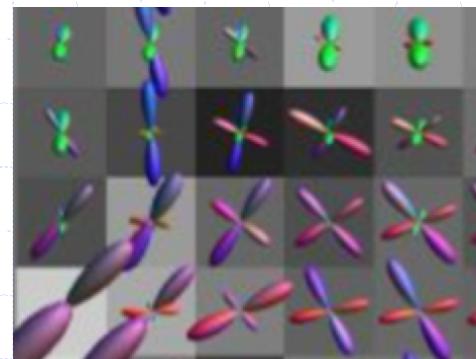
- Two popular representations:

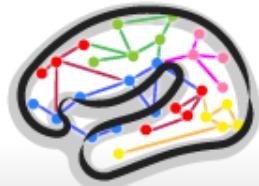
- Diffusion tensor image (DTI)

$$D = \begin{pmatrix} d_{1,1} & d_{2,1} & d_{3,1} \\ d_{2,1} & d_{2,2} & d_{3,2} \\ d_{3,1} & d_{3,2} & d_{3,3} \end{pmatrix}$$



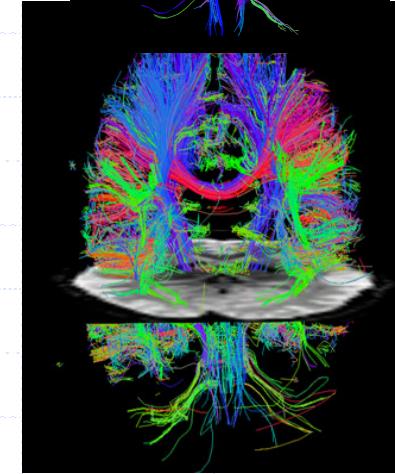
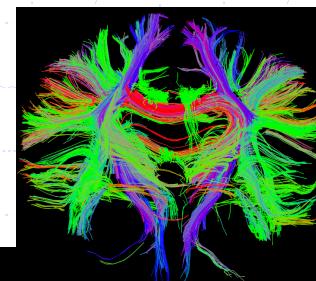
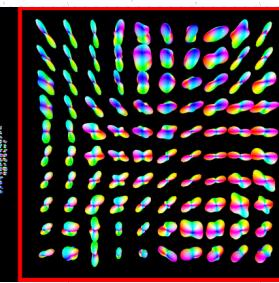
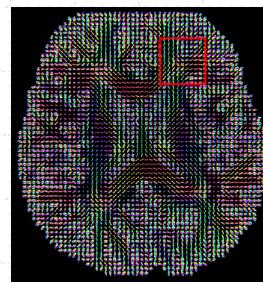
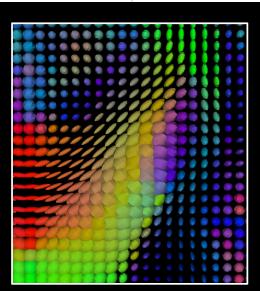
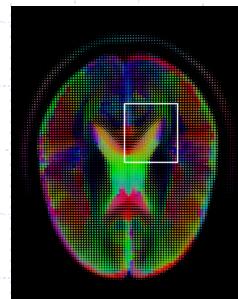
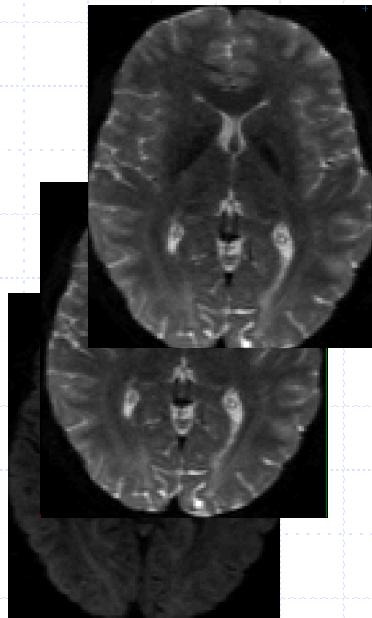
- High angular resolution diffusion imaging (HARDI)
 - Orientation distribution function [Tuch' 04]
 - Diffusion spectrum [Wedgeon' 05]
 - Ball-and-stick [Behren's 03]
 - ...



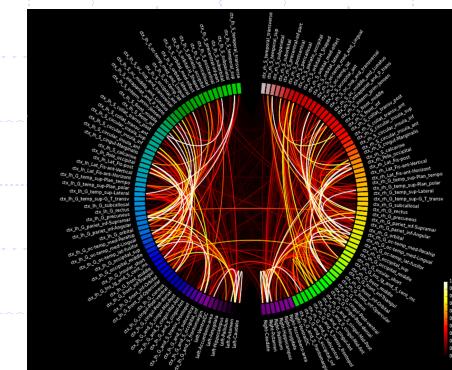
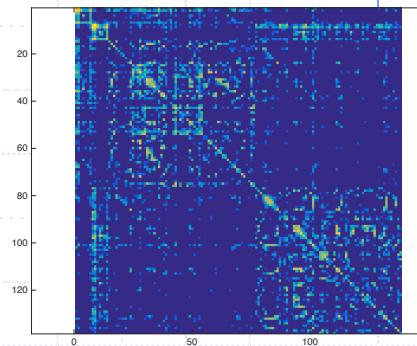


Diffusion MRI to Connectome

- From dMRI to structural connectomics



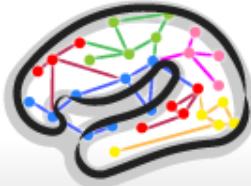
streamlines



dMRI

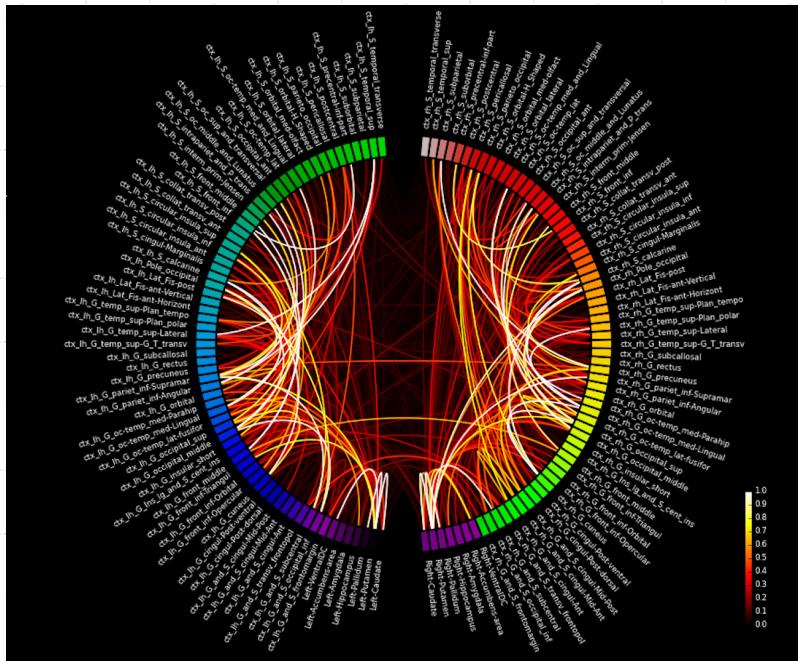
diffusion directions

connectivity matrix

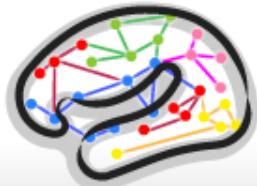


Diffusion MRI to Connectome

- From raw data to structural connectomics
 - From connectomics to brain network analysis

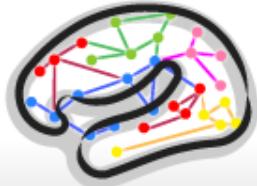


- Inheritance analysis
 - Brain network analysis
 - Prediction of phenotypes



Introduction of Human Connectome Project

- May, 2009 : Request for Applications from NIH Blueprint
- Sept. 2010 : NIH awarded HCP grants to two consortia
 - Washington U, U of Minn, Oxford U,...
 - MGH and UCLA,...
- Goal of HCP: Characterize human brain connectivity and function
 - Scan ~1,200 healthy adults , ages 22-35, including
 - Twins and their non-twin siblings: MZ twins and DZ twins
- Dec. 2015: 900 subjects dataset release (**Latest release**)



Data Acquisition

(1) Imaging Data:

- 4 modalities, 1200 subjects, 1 customized 3T scanner (WashU)
 - Structural MRI (T1-weighted, T2-weighted)
 - Resting-state fMRI (rfMRI)
 - Task fMRI (tfMRI)
 - Diffusion MRI (dMRI)
- Improved scanners, pulse sequences: **producing high quality data**



Data Acquisition

(1) Imaging Data:

(2) MEG/EEG Data:



Data Acquisition

(1) Imaging Data:

(2) MEG/EEG Data:

(3) Behavioral Data:

➤ Measures that have the potential to covary with brain connectivity and function:

- NIH Toolbox ; Penn Neuropsychological Battery

➤ Diverse phenotypes

Cognition; Emotional health; Motor skills; Sensory; Personality; Fluid intelligence; Family environmental factors

➤ Demographic, physical data

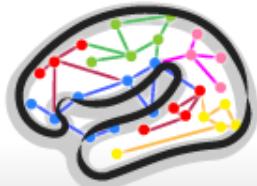
➤ Psychiatric status, substance use





Data Acquisition

- (1) Imaging Data:
- (2) MEG/EEG Data:
- (3) Behavioral Data:
- (4) Genetic Data:

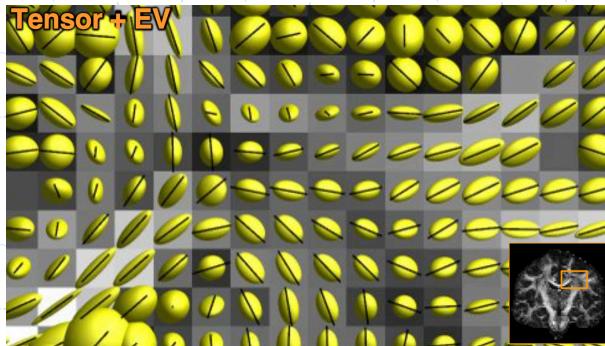


Connectome Extraction

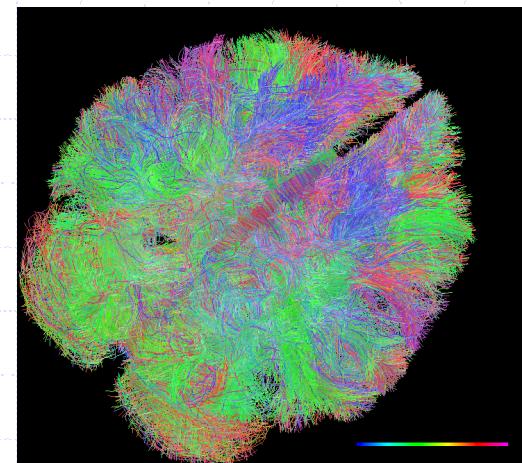
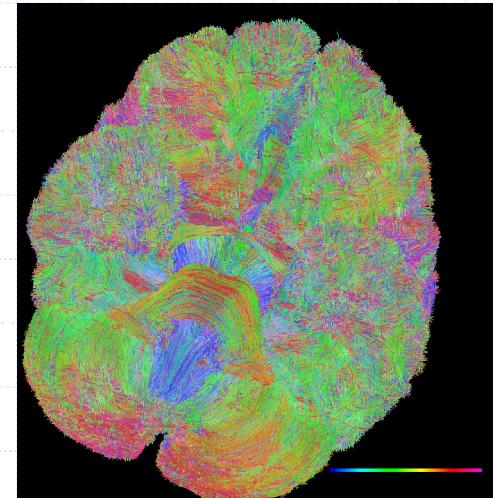
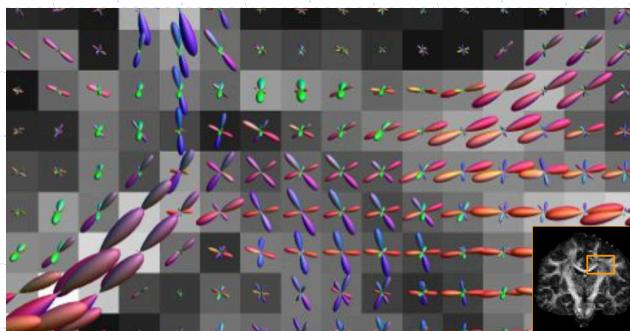
- We are interested in extracting the connectome from dMRI in HCP dataset.

- Step1. Construct HARDI:
better than DTI, can handle fiber crossing

DTI:



HARDI:

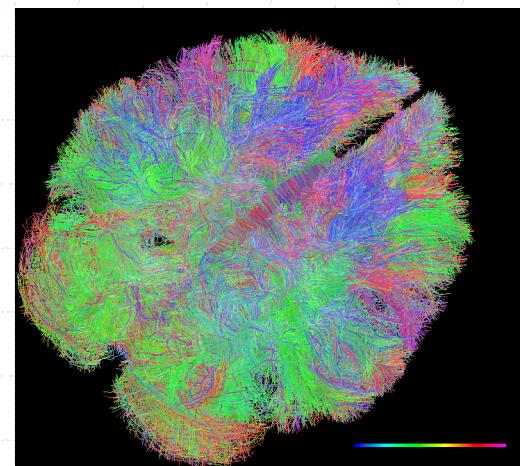
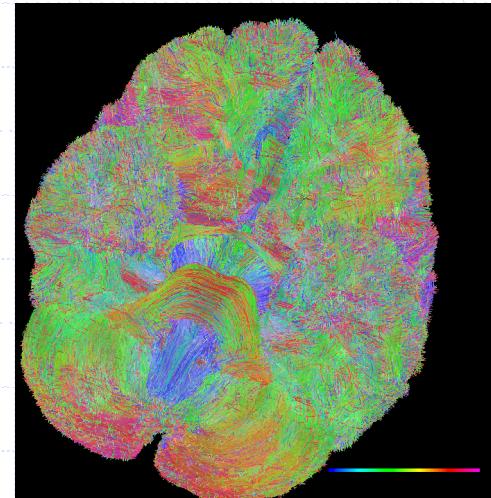




Connectome Extraction

- We are interested in extracting the connectome from dMRI in HCP dataset.

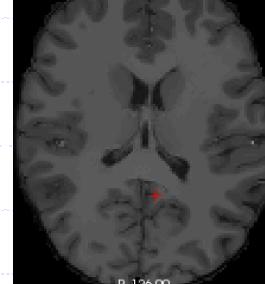
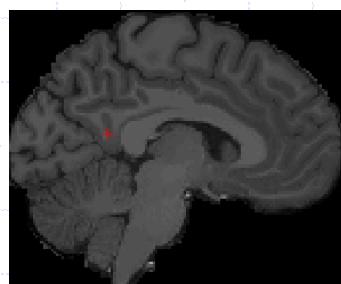
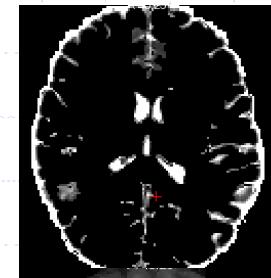
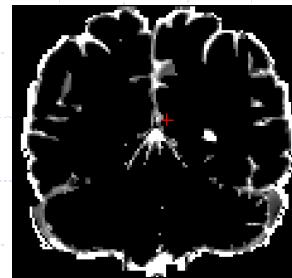
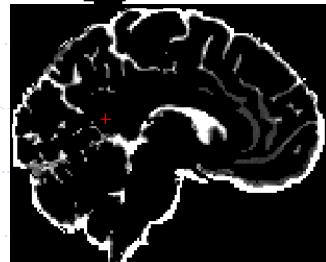
- Step 1. Construct HARDI:
better than DTI, can handle fiber crossing
- Step 2. Fiber tracking:
 - Masking
 - Seeding
 - Streamline growing

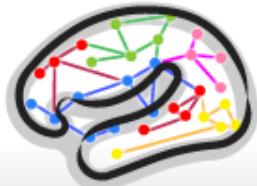




Masking and Seeding

- Masking is used to
 - decide the propagation of a streamline
 - include the stopped streamlines

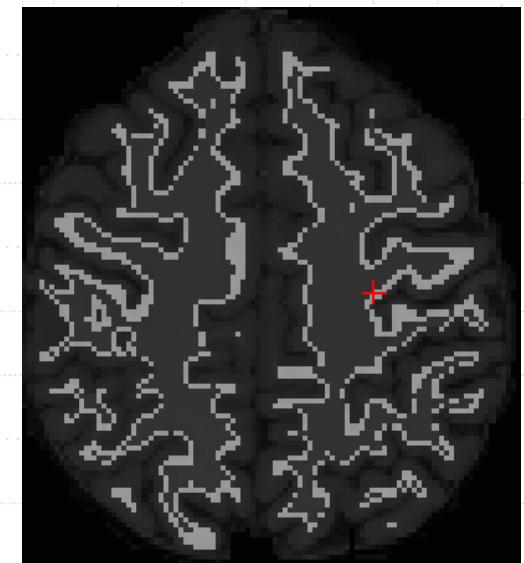
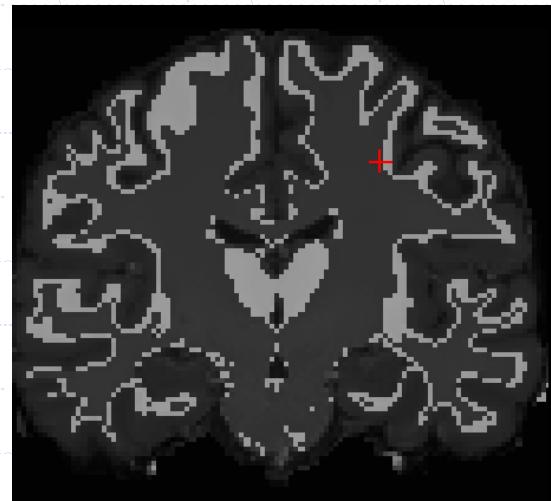
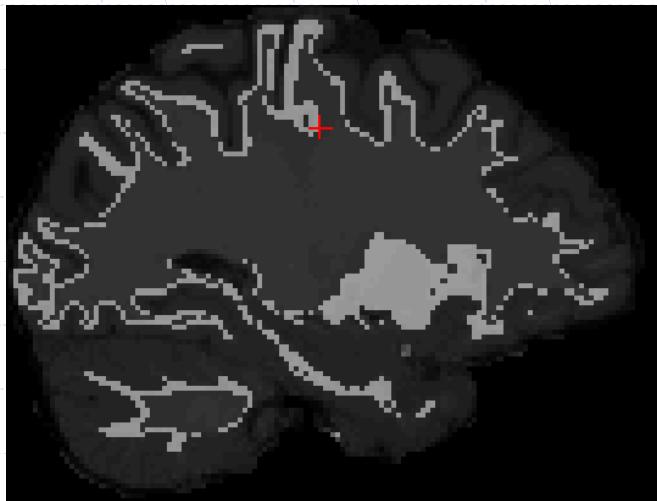


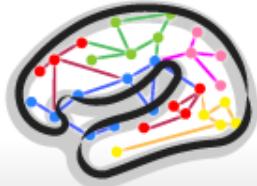


Masking and Seeding

- Seeding is used to
 - reduce the bias of streamlines

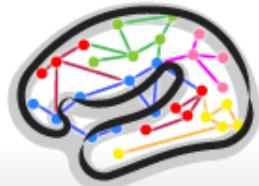
Seeding mask (the interface between GM and WM):





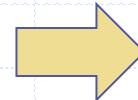
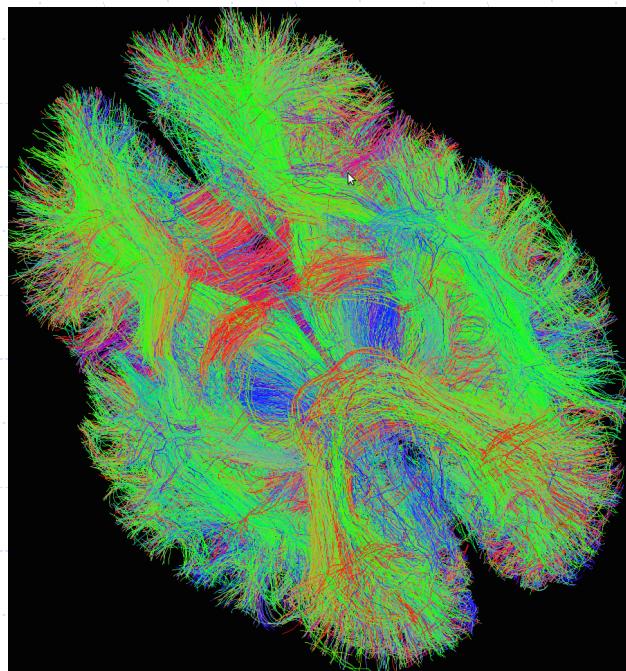
Streamline Growing

- Streamlines growing
 - (1) probabilistic
 - (2) deterministic
 - (3)

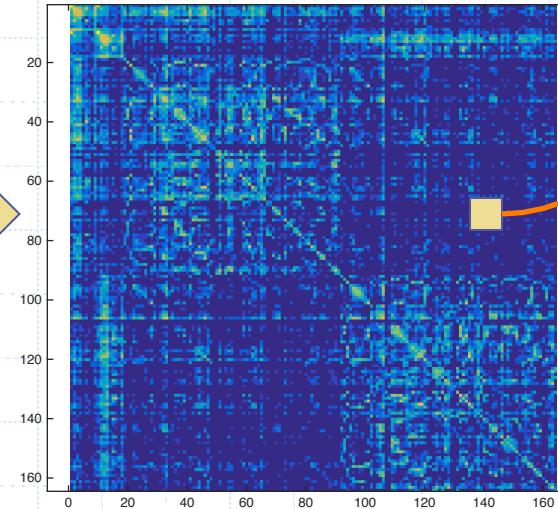


Low Dimensional Representations

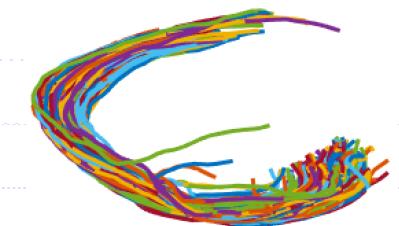
- Whole brain tractography is complicated
- A low dimensional representation is necessary for statistical inference

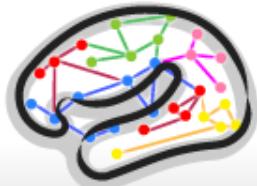


Connectivity Matrix



???



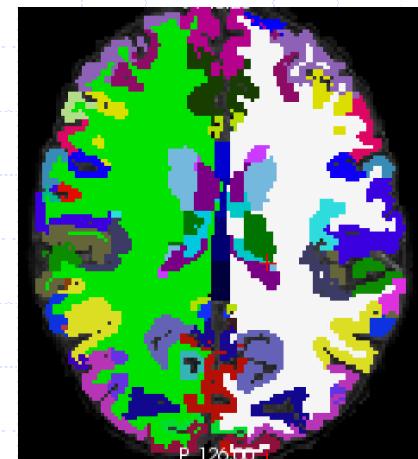
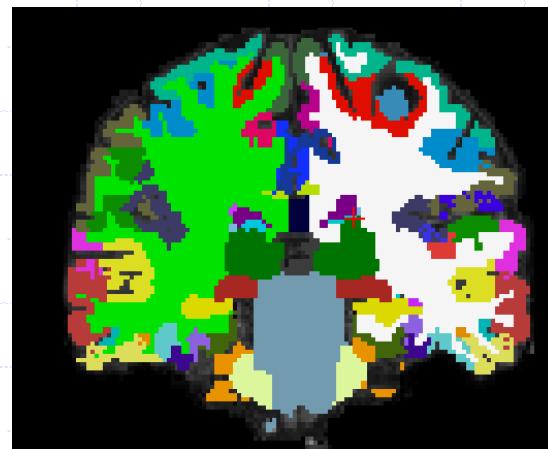
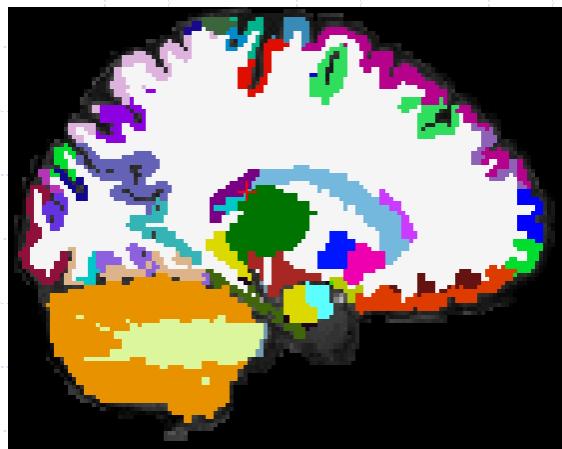


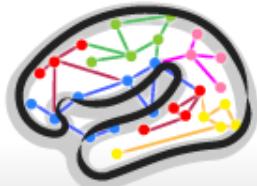
Connectivity Matrix

- Connectivity matrix is a summarization of the brain connections
- Given streamlines:

Step 1. Brain parcellation – *freesurfer / other software*

- Use Destrieux atlas in FreeSurfer: ~ 170 ROIs





Connectivity Matrix

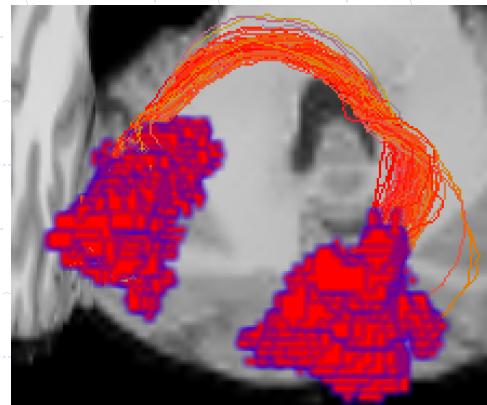
➤ Connectivity matrix is a summarization of the brain connections

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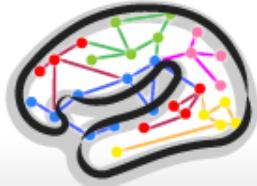
Step 2. Find the fibers connecting each pair of regions

$CM(41,160) =$



In order to include more streamlines:

- ROI dilation
- Streamline ending points expansion



Problems with the Connectivity Matrix

- The connectivity matrix contains millions of fibers
 - saving, loading, and analyzing are difficult
 - Compression is needed
- Summarize the connectivity matrix
 - Extract robust measure(s) of connectivity strength



Compression of Connectivity Matrix

- Examples of fibers in $CM(1,160)$ for different subjects

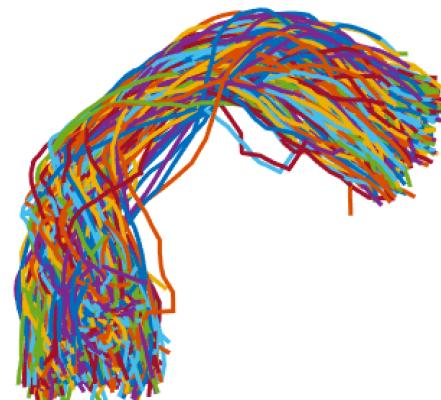
1 - left-lateral-ventricle

160 - ctx-rh-S-parieto-occipital



- Observations:

- They have similar **shapes** after removing the translation, rotation, scaling and re-paramterization.



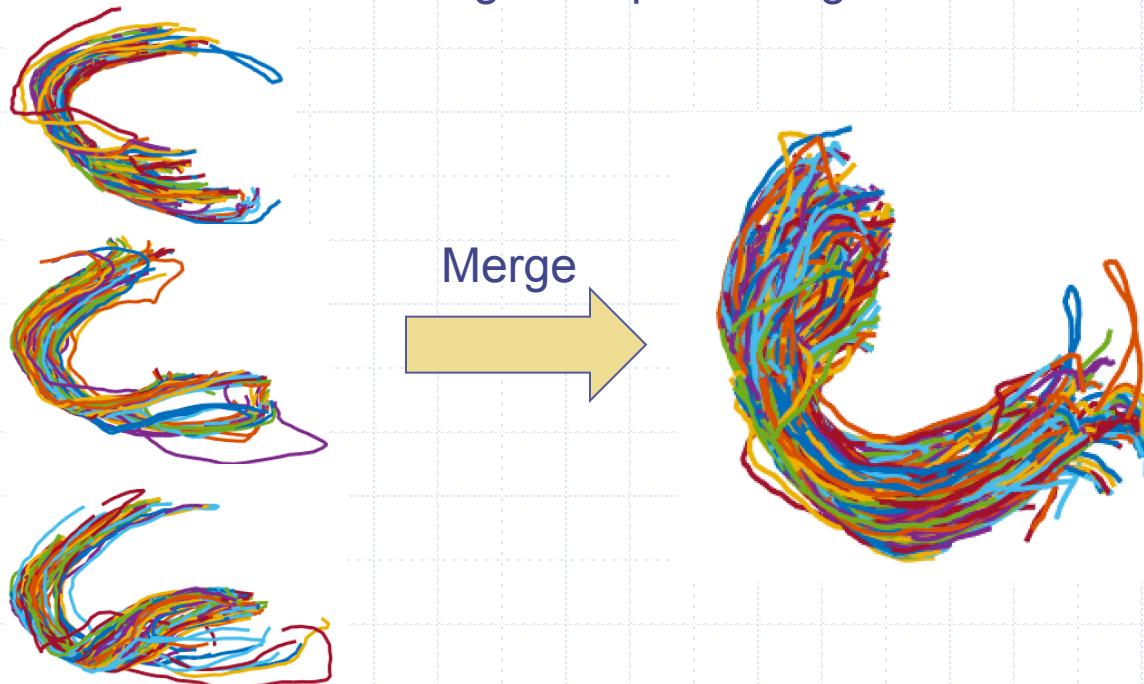


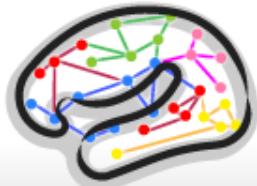
Compression of Connectivity Matrix

- Compression happens at efficiently representing the **shapes** of fibers
- Learn basis functions to represent the fibers connecting a pair of regions

Step 1. Generate **atlas** for fibers connecting each pair of regions

Randomly select healthy subjects:





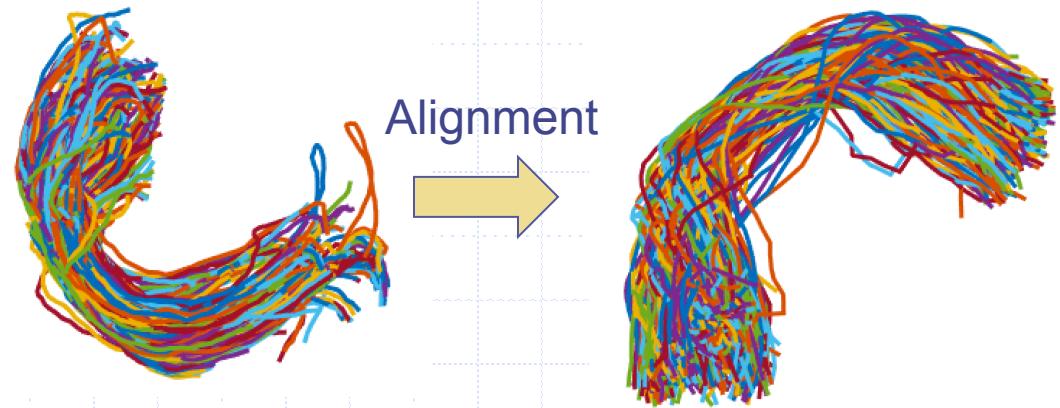
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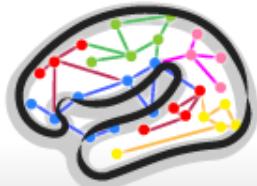
- Compression happens at efficiently representing the **shapes of fibers**
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Step 1. Generate **atlas** for fibers connecting each pair of regions

Step 2. Alignment using the **Elastic Shapes Analysis** framework (Srivastava et al. 2012)

- rotation
- translation
- scaling
- re-parameterization





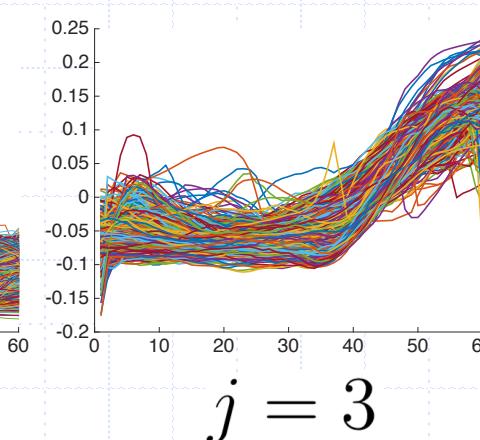
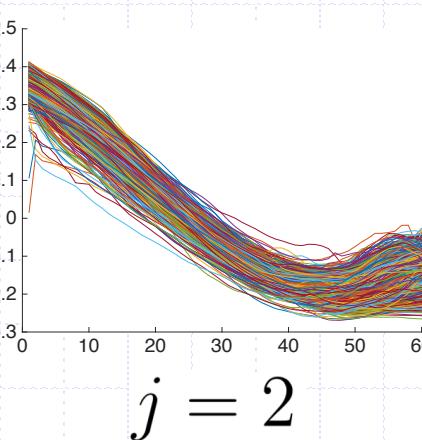
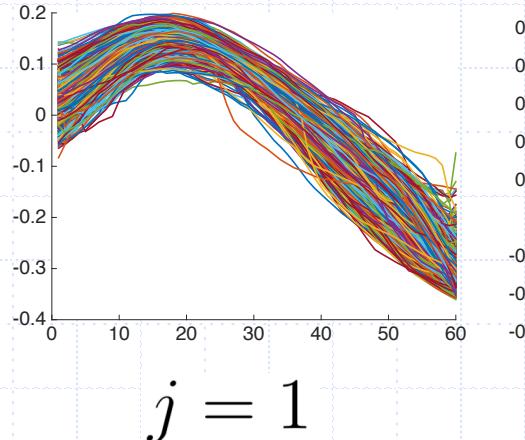
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- Learn basis functions to represent the fibers connecting a pair of regions

Step 1. Generate **atlas** for fibers connecting each pair of regions

Step 2. Alignment using the **Elastic Shapes Analysis** framework (Srivastava et al. 2012)

Step 3. Use **fPCA** to learn basis functions for each component



$$\begin{array}{c} \mu_j \\ \{\phi_{i,j}\} \end{array}$$



Compression of Connectivity Matrix

- Compression happens at efficiently representing the **shapes of fibers**
- Learn basis functions to represent the fibers connecting a pair of regions
- Encoding: given a new fiber f

Step 1. Align f to the mean fiber in the atlas

$$\underset{O \in SO(3), C \in \mathbb{R}^3}{\operatorname{argmin}} \|O * (f - C) - \mu\|$$

$$g = O * (f - C)$$

Step 2. Represent the aligned fiber using basis functions

$$\hat{g}_j = \mu_j + \sum_{i=1}^M c_{j,i} \phi_{j,i}$$



Parameters to save



Compression of Connectivity Matrix

- Compression happens at efficiently representing the **shapes of fibers**
- Learn basis functions to represent the fibers connecting a pair of regions
- Encoding
- Decoding: reconstruct f

$$\hat{f} = O' * \hat{g} + C$$



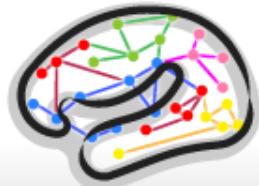
Compression of Connectivity Matrix

- Compression happens at efficiently representing the **shapes of fibers**
- Learn basis functions to represent the fibers connecting a pair of regions
- Encoding
- Decoding
- Compression Ratio: ~ 90-98%

$$\rho = 100 * \left(1 - \frac{N_c}{N_r}\right)$$

N_c # parameters after compression

N_r # parameters before compression



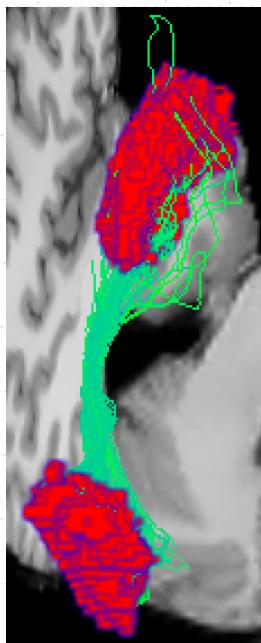
Robust Coupling Strength Measures

1. What is a good measure of the connectivity strength between two ROIs?

Right-Putamen (16)

ID: 104820

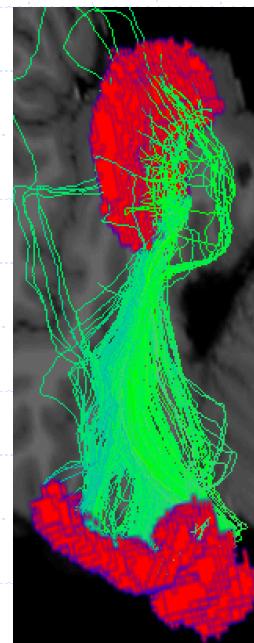
$|CM(16, 115)| = 483$



ctx_rh_G_occipital_sup(115)

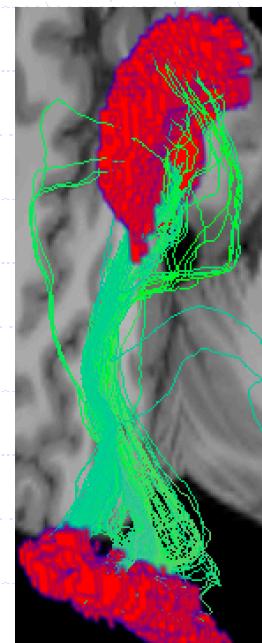
ID: 102311

$|CM(16, 115)| = 614$



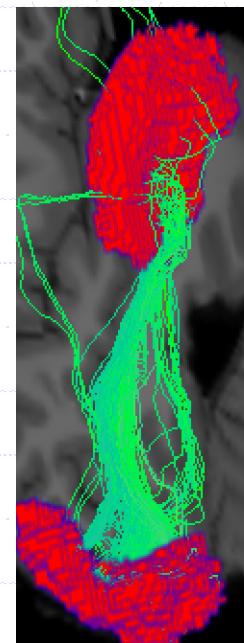
ID: 101006

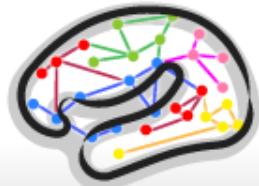
$|CM(16, 115)| = 758$



ID: 145836

$|CM(16, 115)| = 429$





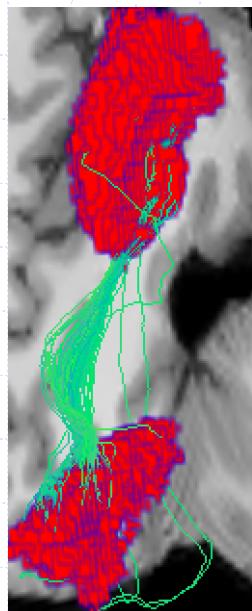
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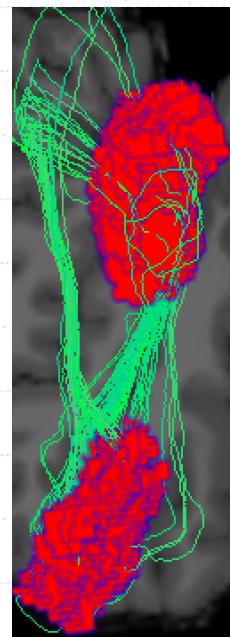
$|CM(16, 115)| = 89$



ctx_rh_S_parieto_occipital(160)

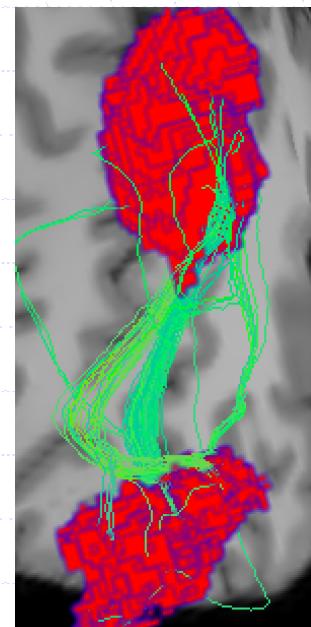
ID: 102311

$|CM(16, 160)| = 76$



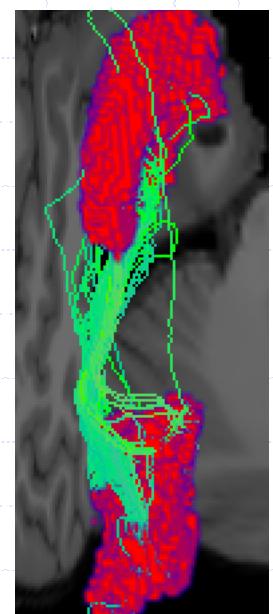
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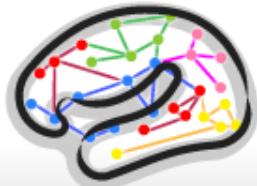
$|CM(16, 115)| = 226$



ID: 145836

$|CM(16, 160)| = 249$

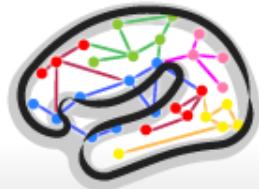




Robust Coupling Strength Measures

1. What is a good measure of the connectivity strength between two ROIs?

- Current people use only counts
- Should include:
 - Diffusion properties: FA values, AFD values along fibers
 - Geometry properties: Shapes, Loops, Clusters
 - Nodes information: Volume of nodes, Connected surface areas
- ...
- Working on extracting them now.
- Question: how to verify the measures?



HUMAN
Connectome
PROJECT

Mapping structural and functional connections in the human brain

Thank You