Machine learning for tract segmentation in dMRI data

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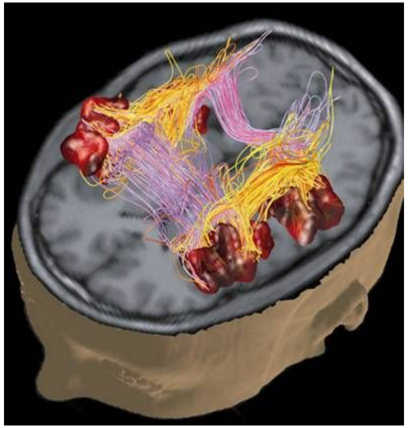
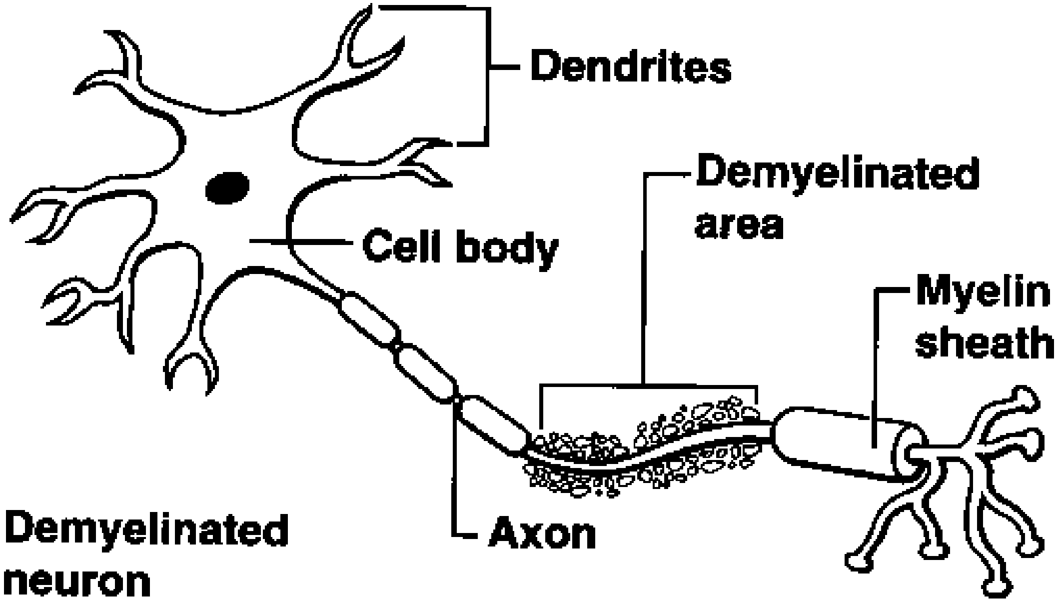
Contents

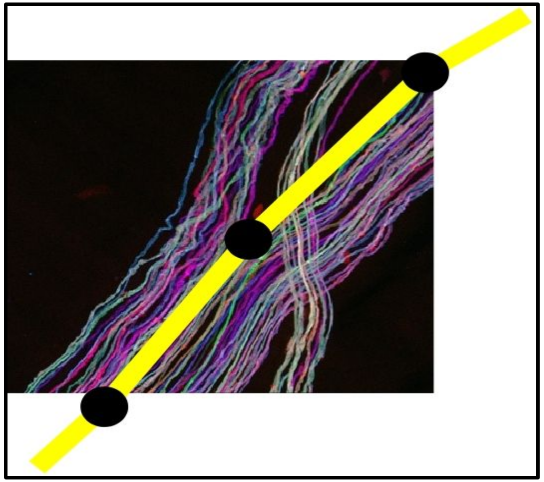
Axons





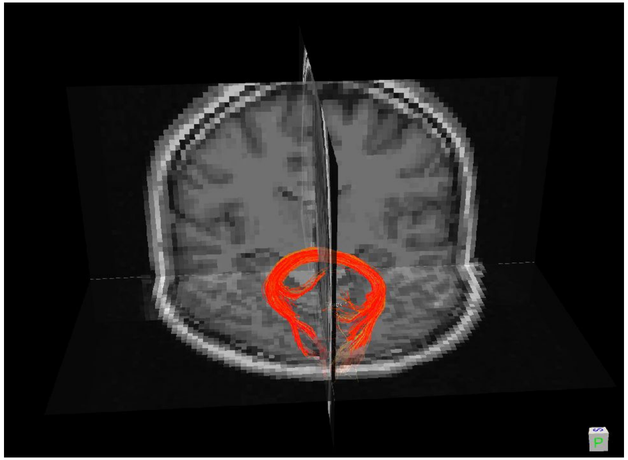
- Number: ~ 10^{12} axons
- Size: ~ 2-20µm

Streamline & Tractography

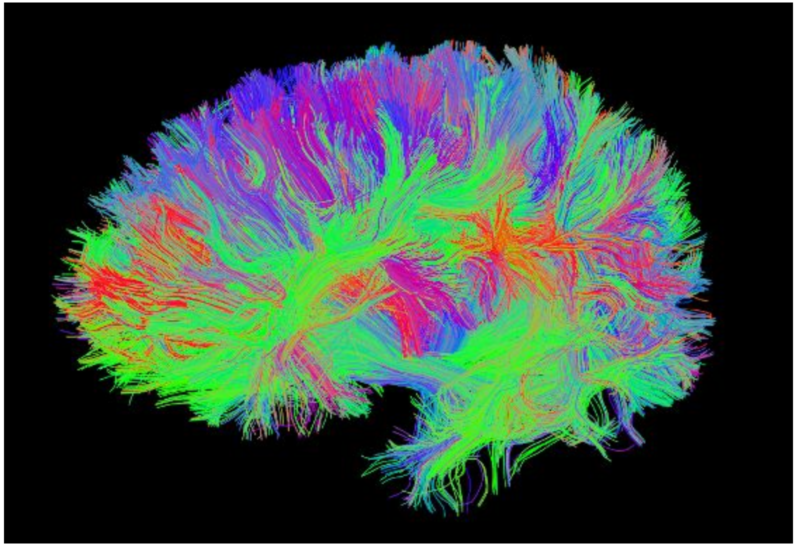


Streamline: a polyline representating thousands of axons. (fiber, track)

Bundle: a group of *'close'* streamlines



Tractography: presentation of whole brain by streamlines.

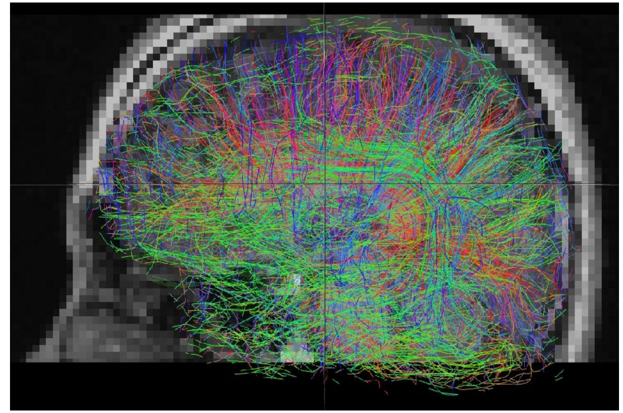


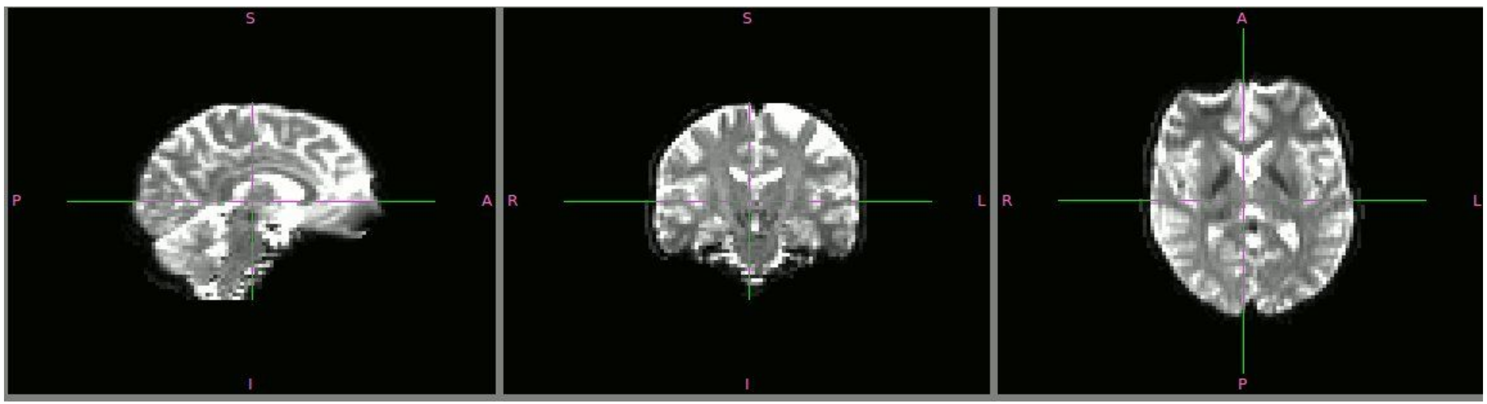
Tract: the real anatomical group of axons.

dMRI technique

(diffusion Magnetic Resonance Imaging)
in vivo (not invasive)
Denis Le Bihan, 1984

Tractography in 3D



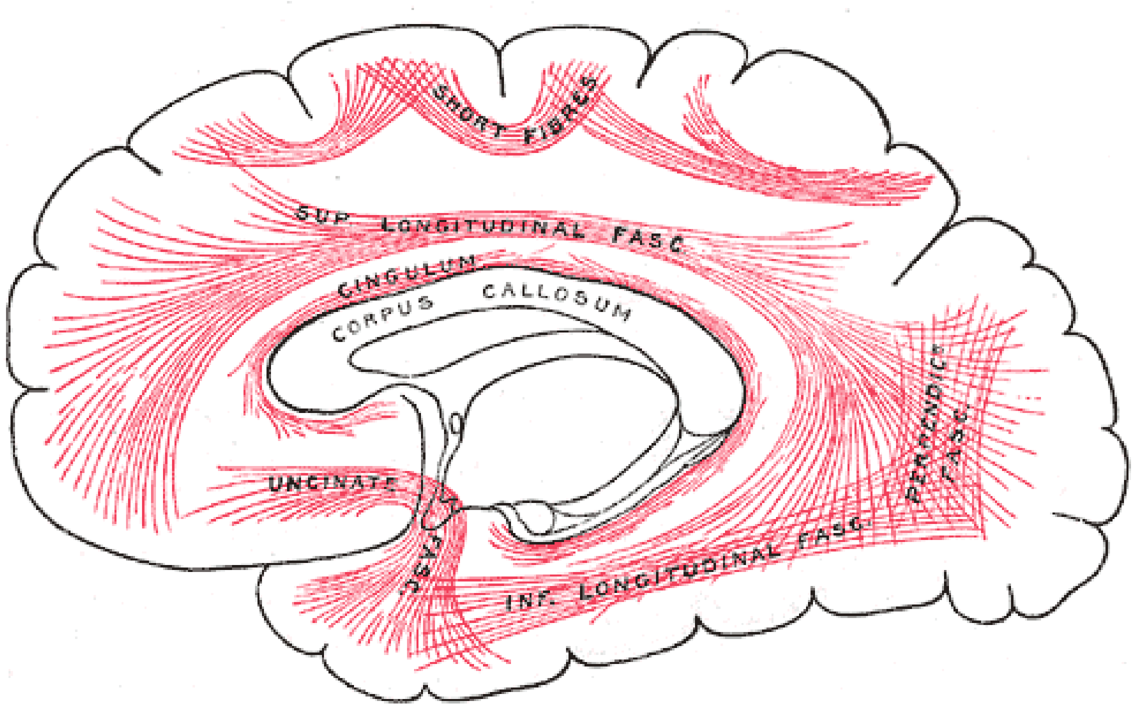


MRI images in 3D

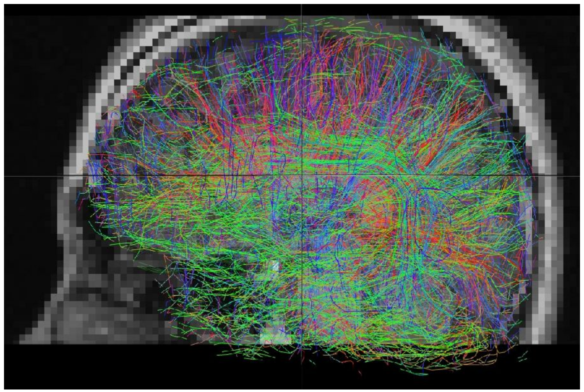
(*)

Garyfallidis et. al. 2012
(Towards an accurate brain tractography)

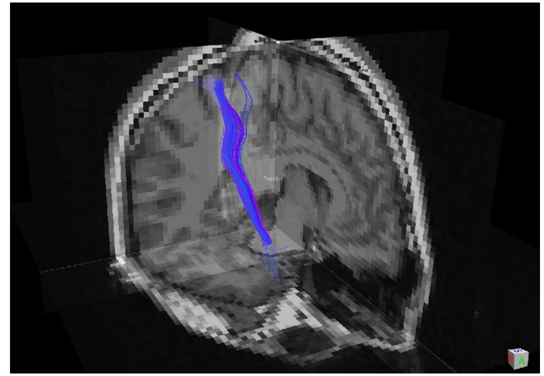
Tractography Segmentation



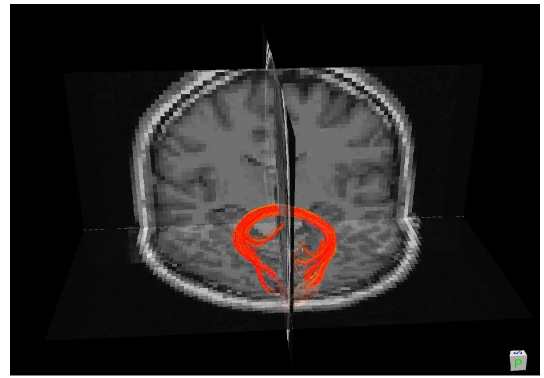
To group streamlines belonging to a common anatomical area into one segmentation



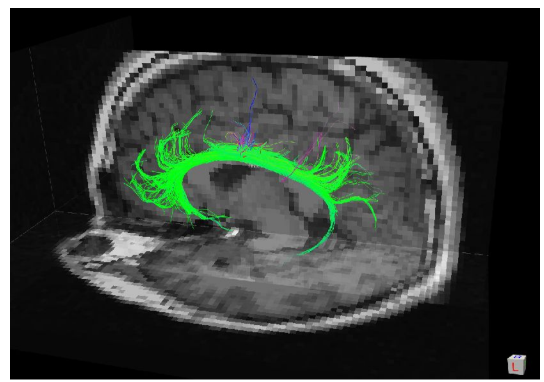
Tractography



Corticol Spnial Tract (CST)

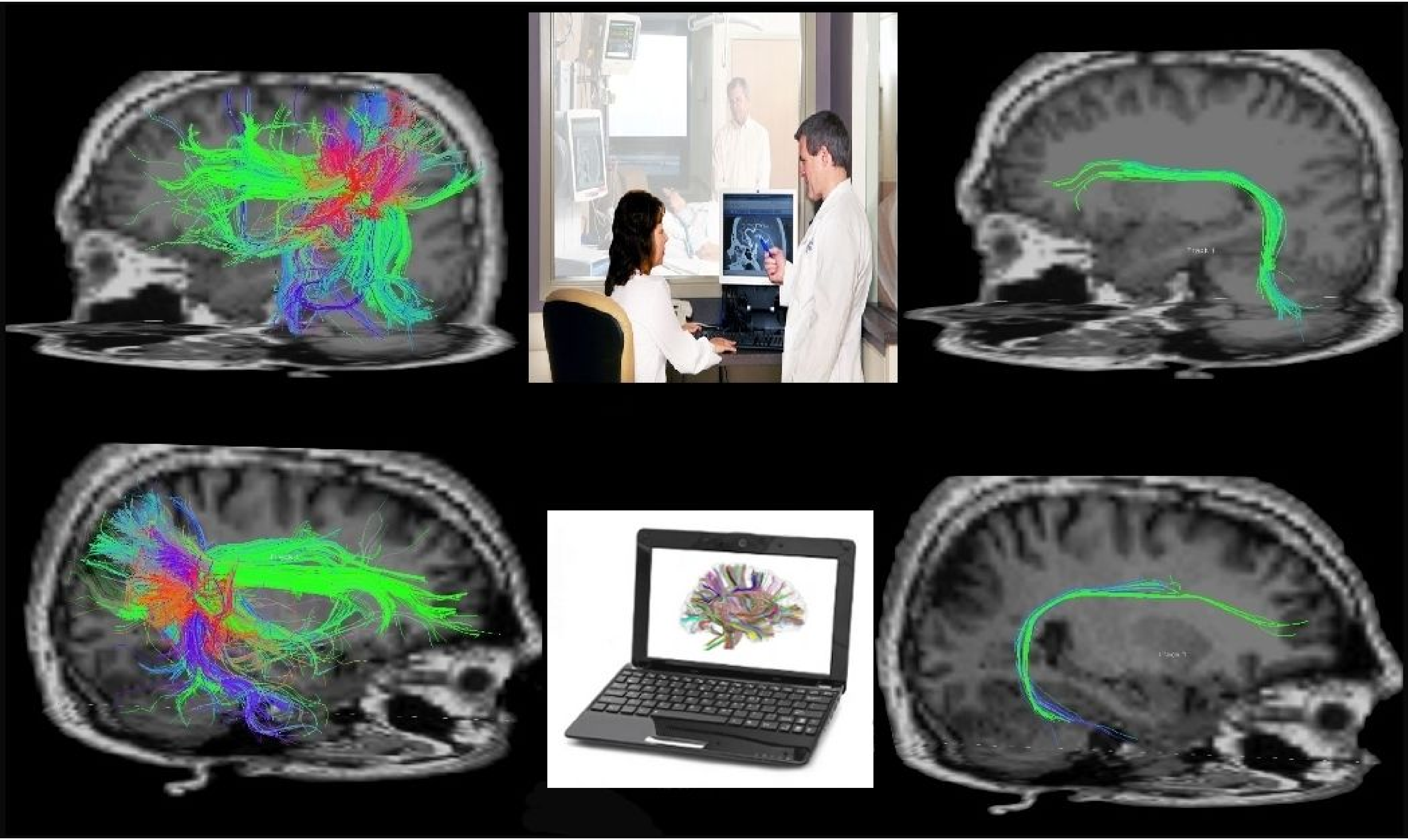


Forceps Major Tract (FMT)



Cingulum Tract (CGT)

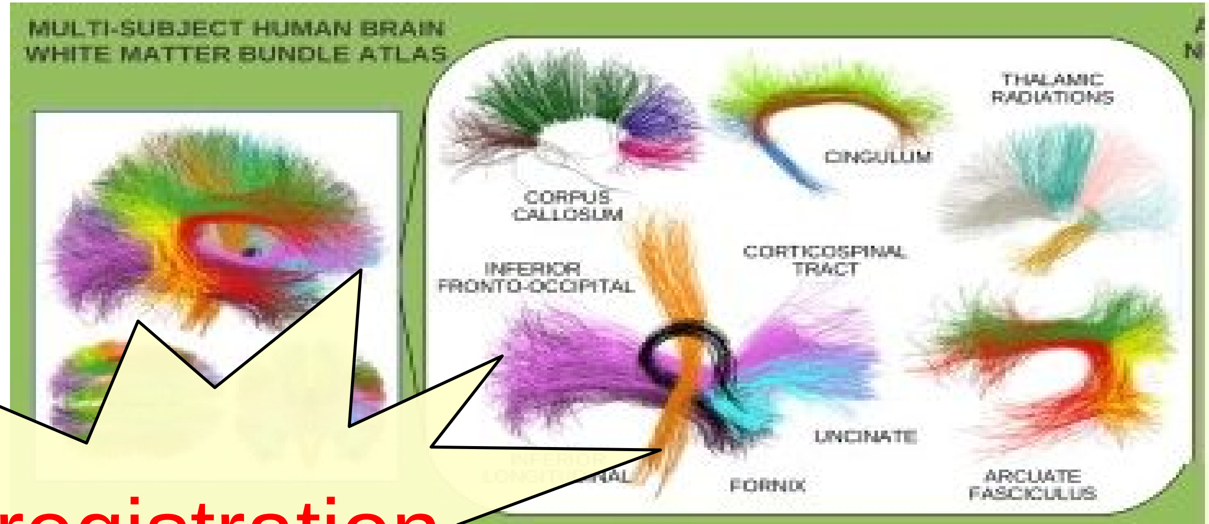
Example of
tractography segmentation



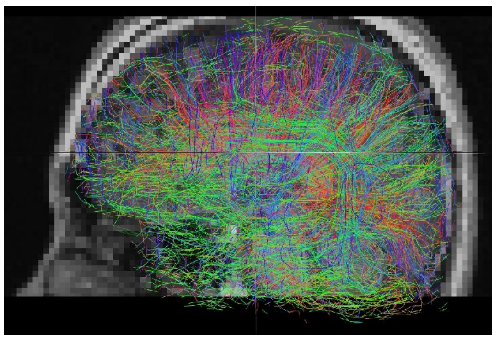
O'Donnell et al., 2007

Atlas based *Tract Segmentation*

brain variety

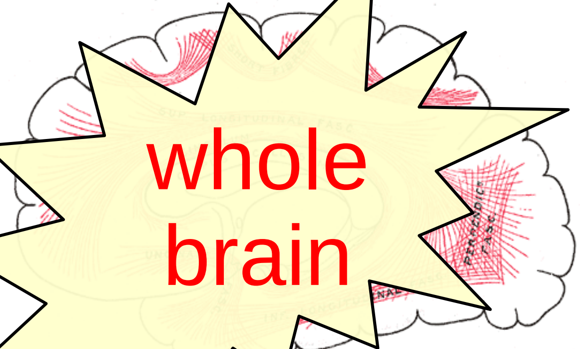


co-registration problem



tractography

clustering (nearest neighbor)

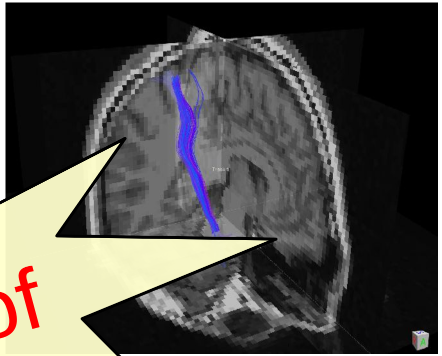


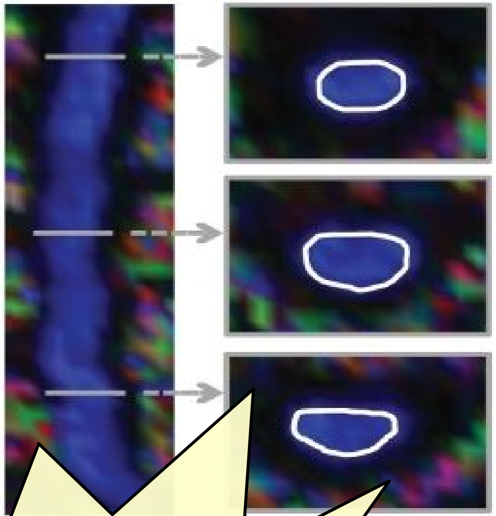
whole brain

tract(s)

ROI based *Tract Segmentation*

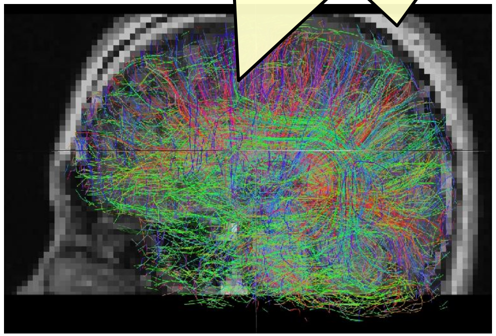
(ROI:Region of Interest)
Wakana et al., 2007



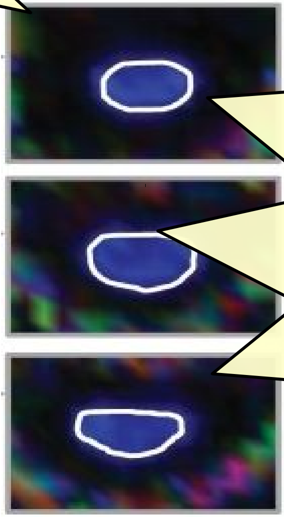


ROIs are drawn

prior knowledge of trajectory



tractography

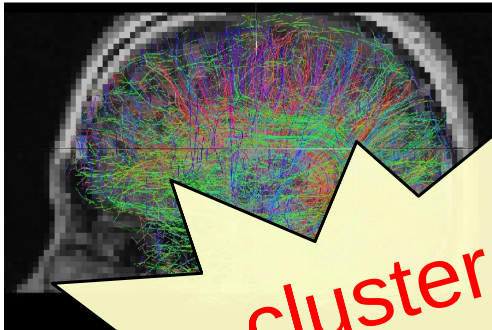


well characterized tracts

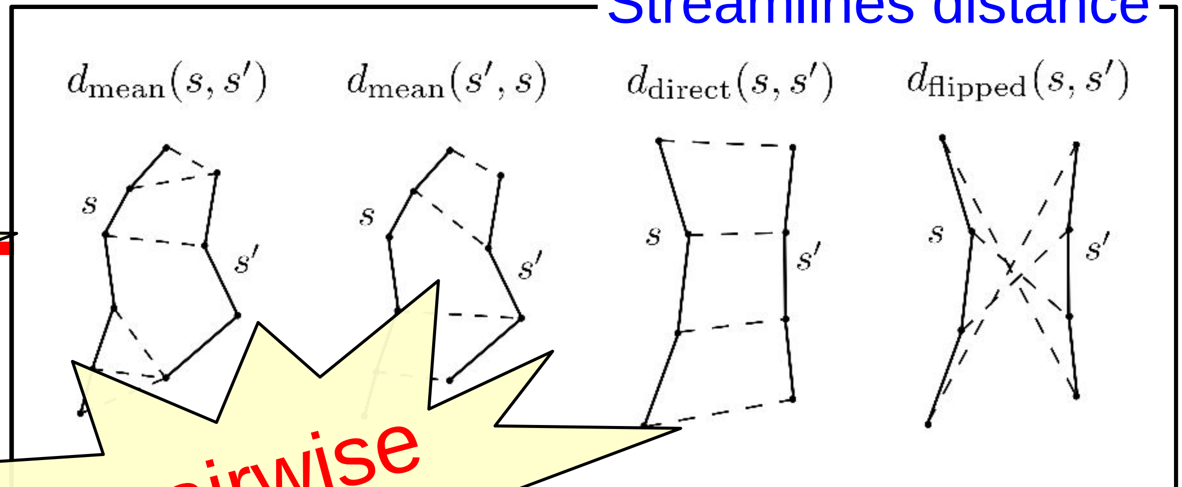
tract

Wang et al., 2011

Unsupervised *Tract Segmentation*

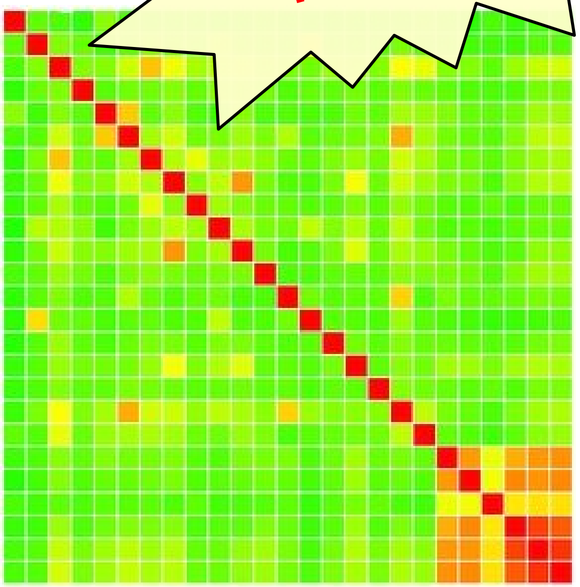


Streamlines distance



cluster number

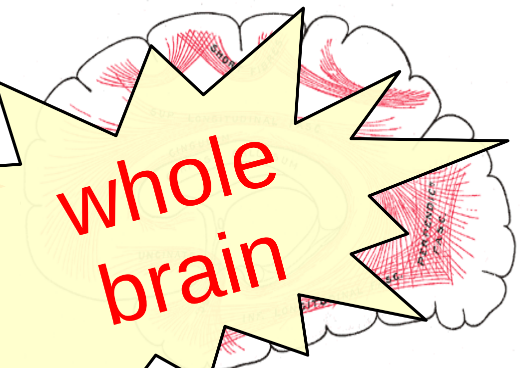
pairwise distance



similarity matrix

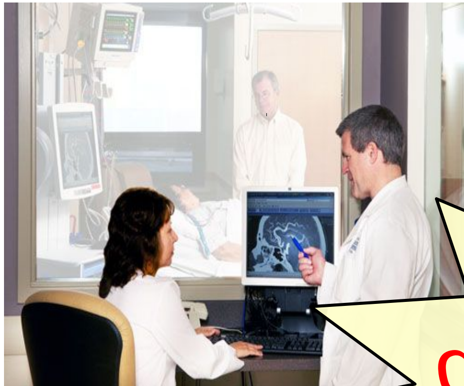
Clustering algorithm (agglomerative, k-means, etc.)

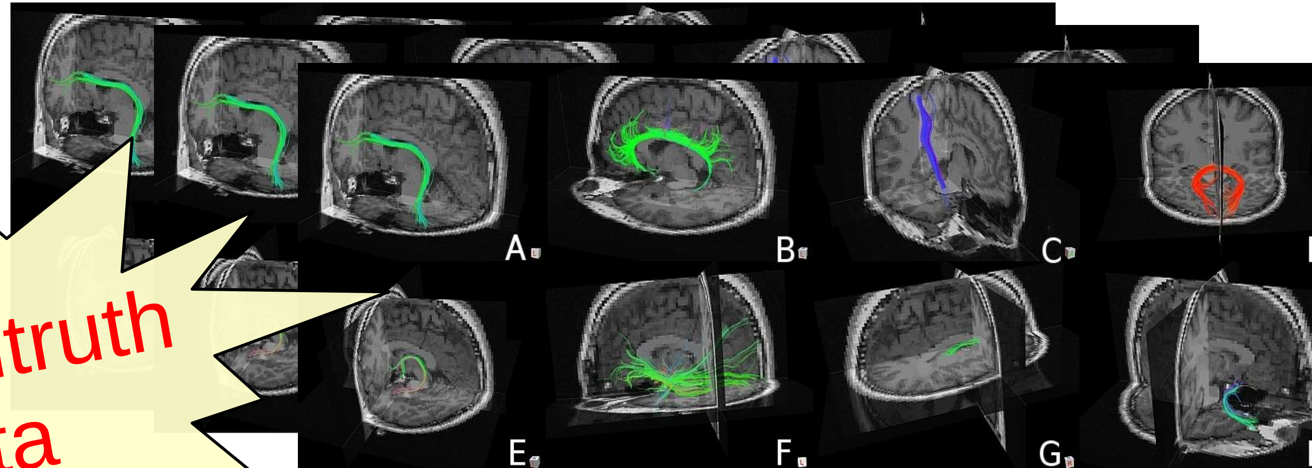
whole brain



tract(s)

Supervised Tract Segmentation

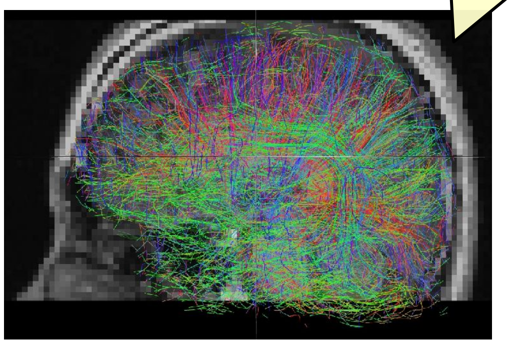




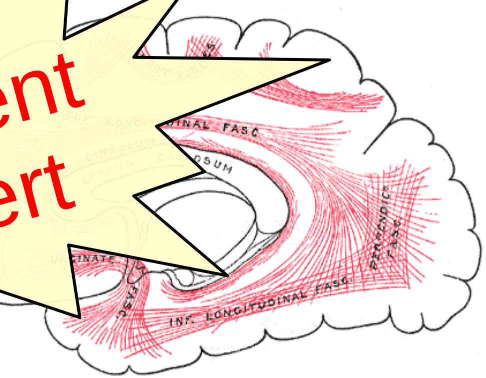
groundtruth data

Classifier
(Ada Boost, SVM, ect)

refinement of expert



tractography



tract(s)

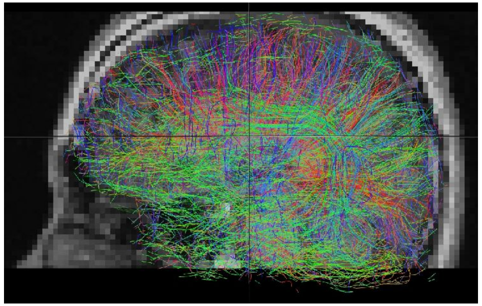
Survey of tractography segmentation methods

Approach	Target tract / Whole brain	Related anatomy	Co-registration	Pairwise distance	Visualization /Interaction
Atlas	WB	Yes	Yes	No	No
ROI	TT (indirect)	Yes (indirect)	Yes	No	No
Unsupervised	WB	No	No	Yes (costly)	No
Supervised	TT	Yes (indirect)	Yes	No	No

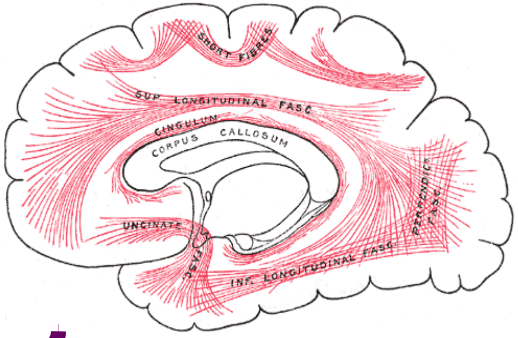
pros

con

Goals



Machine Learning (ML)



Improve the support of ML for tract segmentation

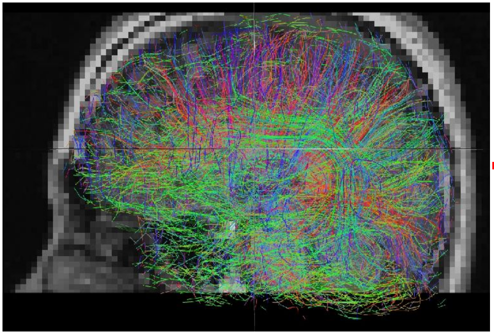
Challenges

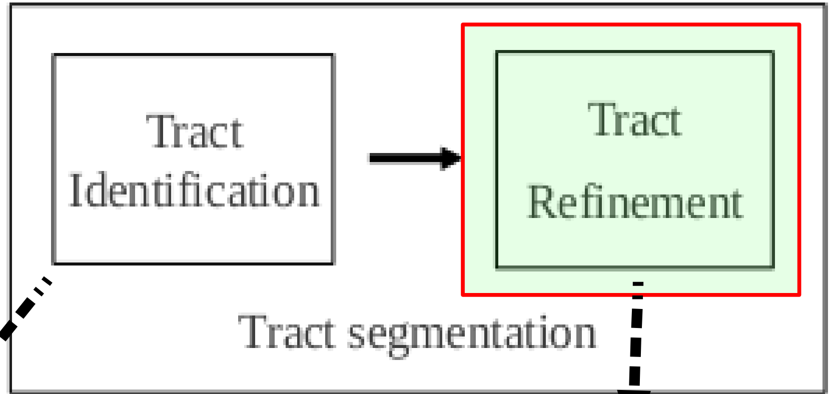
- design an effective method for tract segmentation
- overcome disadvantages of Atlas, ROI
- combine both un-supervised and supervised

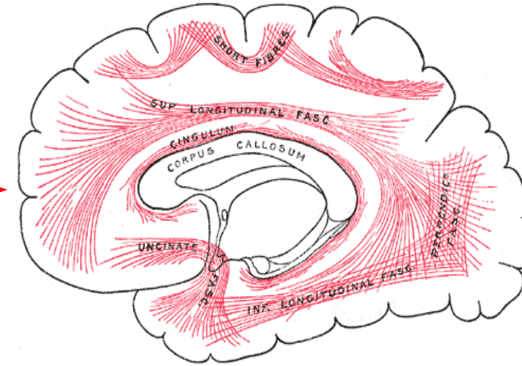
Comparison

Approach	Target tract / Whole brain	Related anatomy	Co-registration	Pairwise distance	Visualization /Interaction
Atlas	WB	Yes	Yes	No	No
ROI	TT (indirect)	Yes (indirect)	Yes	No	No
Unsupervised	WB	No	No	Yes (costly)	No
Supervised	TT	Yes (indirect)	Yes	No	No
Ours	TT	Yes	Yes(*)	No	Yes

Process design: *interactive segmenation*

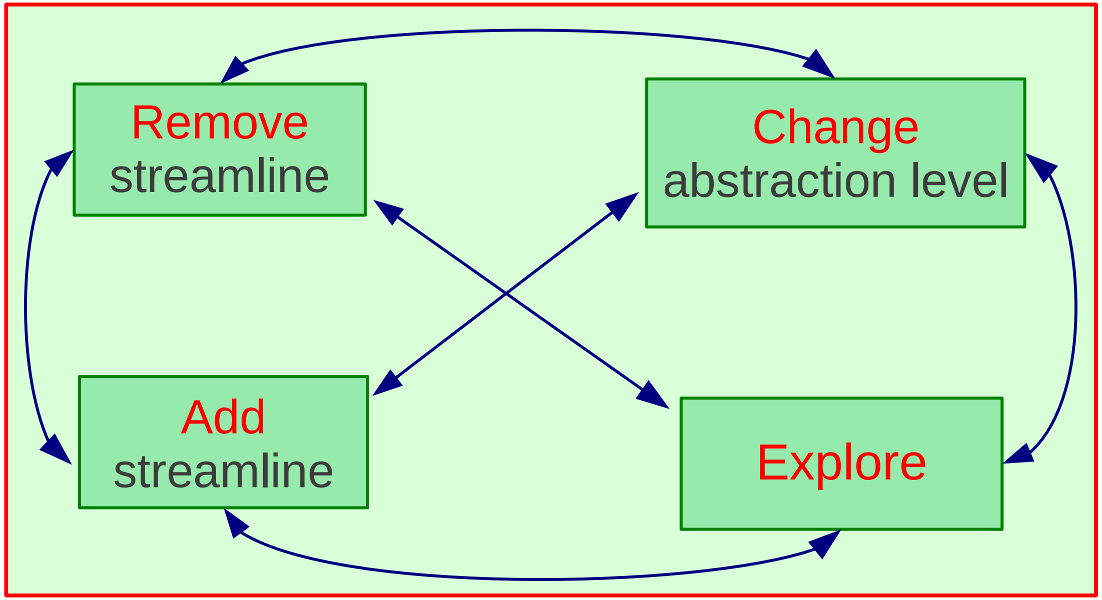






Create tract candidate from set of samples

Olivetti et al., *Supervised segmentation of fiber tracts,* SIMBAD 2011



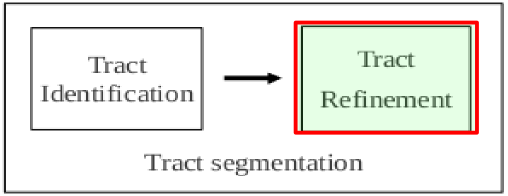
based on BOI

BOI - bunble of interest

- Focus dirrectly on which bundle (cluster of streamlines) that user wants to work on
- Related to anatomy
- Easy to visualize and to interact

Approach	ROI	BOI
Anatomy related	Yes (indirect)	Yes
Visualization	No	Yes
Interaction	No	Yes
Prior knowledge of trajectory	Yes	No

Interactive tract refinement



Demo of Spaghetti

Problem statement

- Given a set of N objects $\mathcal{X} = \{x_1, \dots, x_N\}$
- Traditional clustering: find one partition of $\mathcal{X}$

$$C = \{C_1, \dots, C_K\} \text{ with } K \leq N$$

with C_i is a cluster of $\mathcal{X}$: $C_i = \{x^i_1, \dots, x^i_j\}, j \leq N$

i $C_i \neq \emptyset, i = 1, \dots, K$

ii $\bigcup_{i=1}^{K} C_i = \mathcal{X}$

Interactive clustering

- Our approach: find a set m partitions of $\mathcal{X}$

$$\mathcal{P} = \{ P_1 , . . . , P_m \}$$

where P_i is one partition of $\mathcal{X}$: $P_i = \{C^i_1 , . . . , C^i_{d_i}\}$

i P_i represents the *ith abstraction level* of $\mathcal{X}$

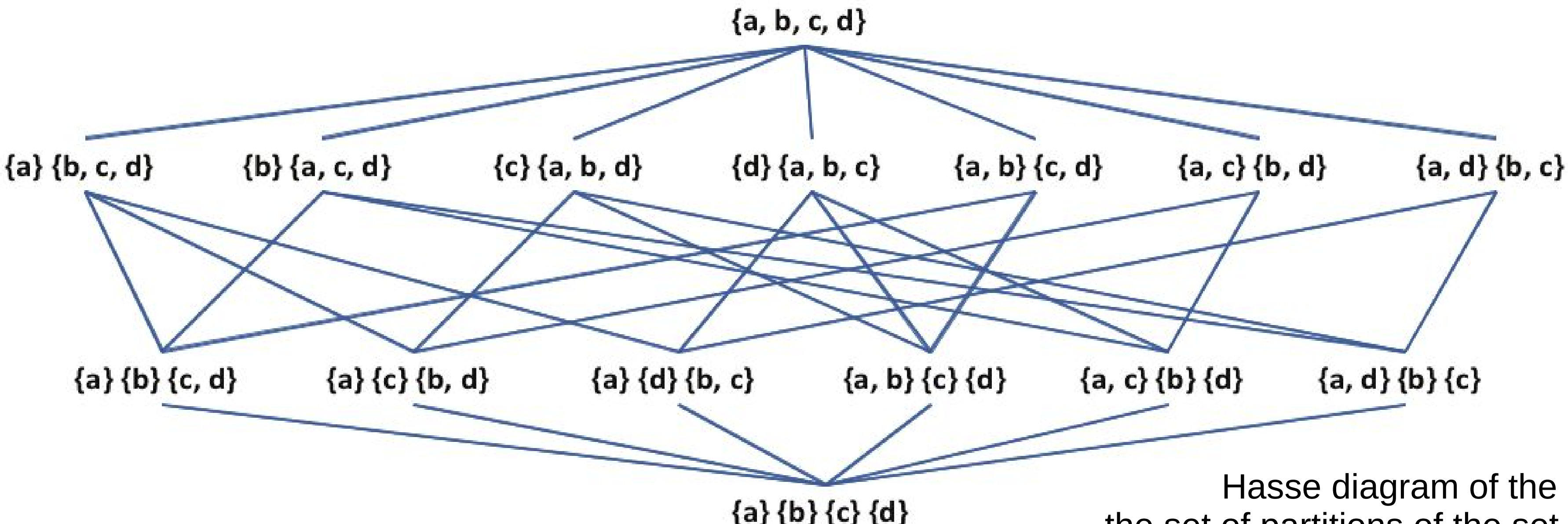
ii constraint γ: $\forall i \in [1,m-1]$, $P_i \preceq P_{i+1}$ *("nested in")*

- Denoted as a triple $\langle \mathcal{P}, \mathcal{X}, \gamma \rangle$

Interactive clustering: partial order relation

- $\mathcal{P}_{\mathcal{X}}$: set of all possible partitions of $\mathcal{X}$
- Over $\mathcal{P}_{\mathcal{X}}$, a partial order relation $\preceq$ ("nested in")

$$\forall P_a, P_b \in \mathcal{P}_{\mathcal{X}},\ P_a \preceq P_b \leftrightarrow \forall\, C^b_i \in P_b, \exists C^a_{i_1},..,C^a_{i_k} \in P_a: \mathbf{C^b_i = \cup^k_{t=1} C^a_{i_t}}$$



Hasse diagram of the lattice of
the set of partitions of the set {a,b,c,d}

Interactive clustering: update partitions

- Remove an old object $x_{r.m} \in \mathcal{X}$

$\mathcal{X} = \{x_1, \ldots, x_N\}$ $\Rightarrow$ $\mathcal{X}' = \mathcal{X} \setminus \{x_{r.m}\}$

- Add a new object x_{add}

$\mathcal{X} = \{x_1, \ldots, x_N\}$ $\Rightarrow$ $\mathcal{X}' = \mathcal{X} \cup \{x_{add}\}$

---

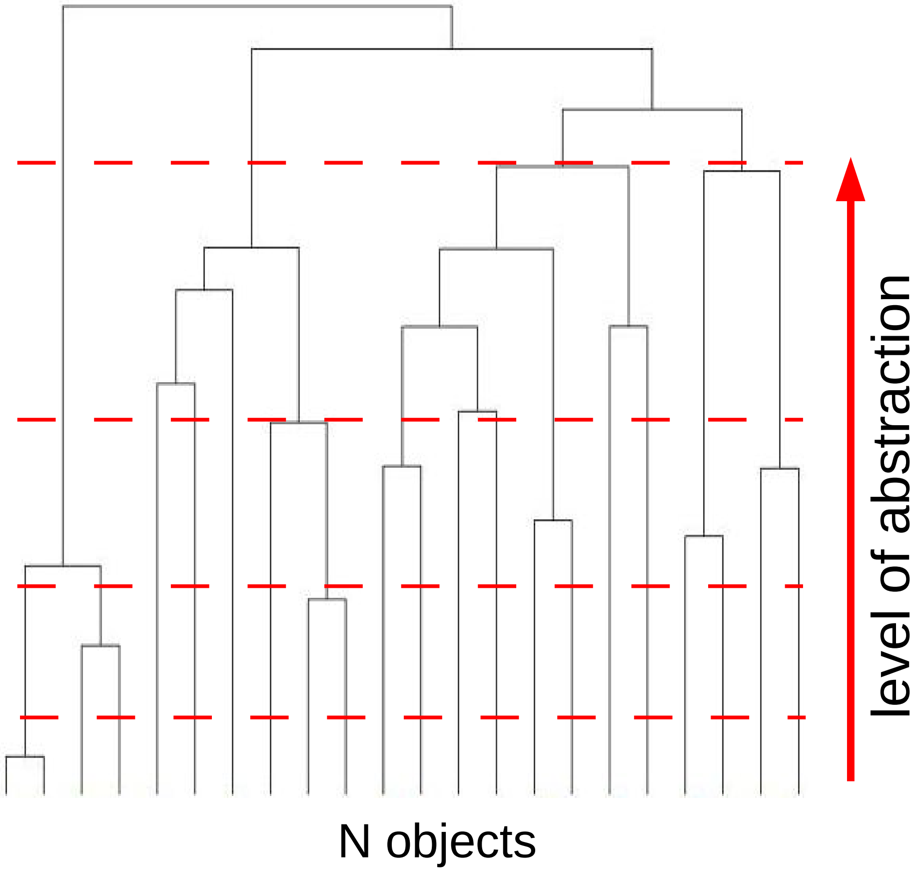
current partitions		updating partitions
$\mathcal{P} = \{P_1, \ldots, P_m\}$	$\Rightarrow$	$\mathcal{P}' = \{P'_1, \ldots, P'_m\}$
$\langle \mathcal{P}, \mathcal{X}, \gamma \rangle$, γ: $P_i \preceq P_{i+1}$ $i \in [1, m-1]$		$\langle \mathcal{P}', \mathcal{X}', \gamma' \rangle$, γ': $P'_i \preceq P'_{i+1}$ $i \in [1, m-1]$

Hierarchical clustering

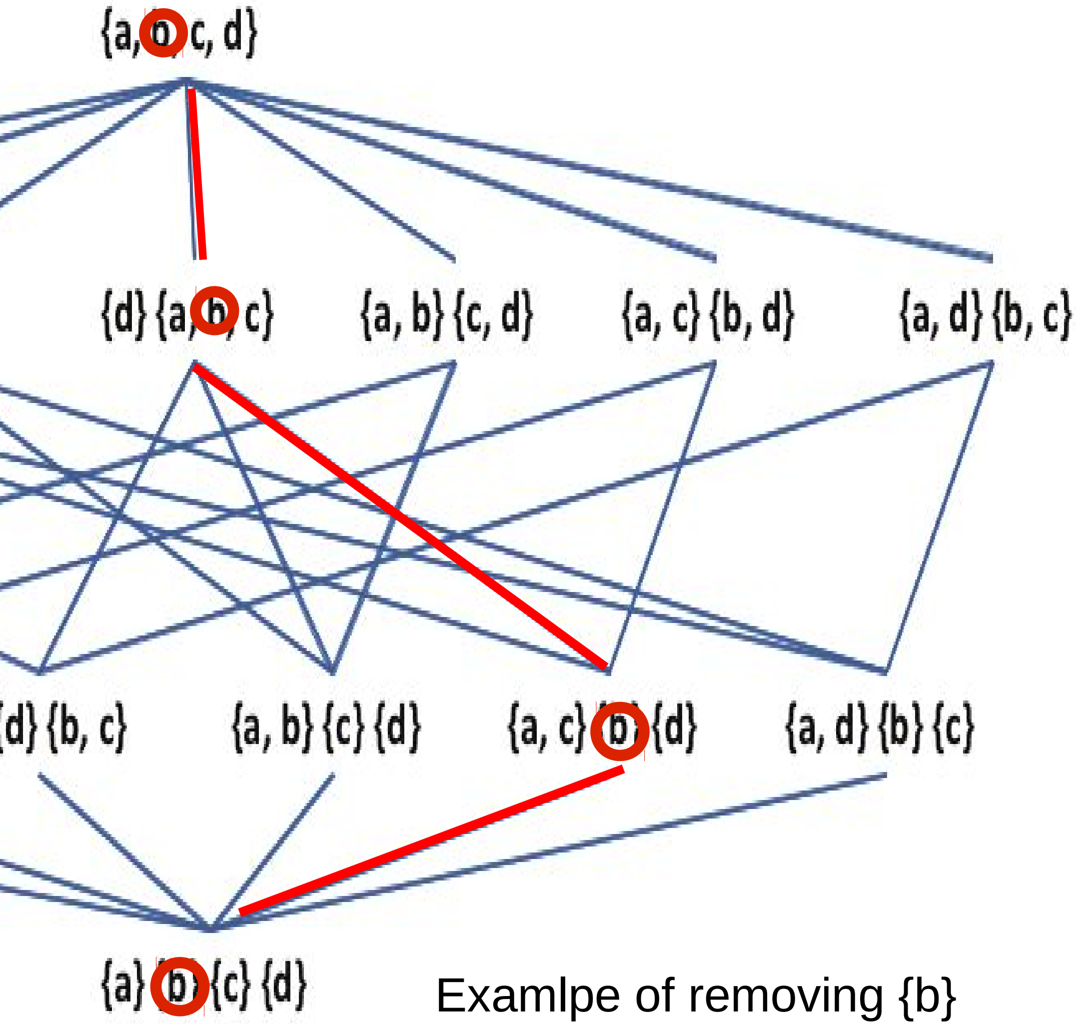
Find m partitions of $\mathcal{X} : \mathcal{P} = \{P_1, \ldots, P_m\}$, $P_i \preceq P_{i+1}$, $i \in [1, m-1]$

Algorithm

1. Assign each s_i to one cluster
2. Merge two closest clusters
3. Compute distances
4. Repeat until all in one cluster



Interactive clustering: *remove object*



Examlpe of removing {b}

Removing object $x_{r.m}$ from all partitions

$\forall P_i$, $i \in [1,..,m]$,

$\forall j \in [1,..,d_i]$:

if $x_{r.m} \in C^i_j$ then

$C^i_j = C^i_j \setminus \{x_{r.m}\}$,

if $C^i_j = \emptyset$, $P_i = P_i \setminus \{C^i_j\}$

Interactive clustering: *add object*

Denote δ_{max} as the maximum distance in cluster C_i

$$\delta_{max}(C_i) = \max \{d(x,x')\}, \forall x,x' \in C_i, x \neq x'$$

1. Find the closet cluster of x_{add} in P_1: $C_{close}(x_{add},P_1)$

2. Start from the direct parent of $C_{close}(x_{add},P_1)$:

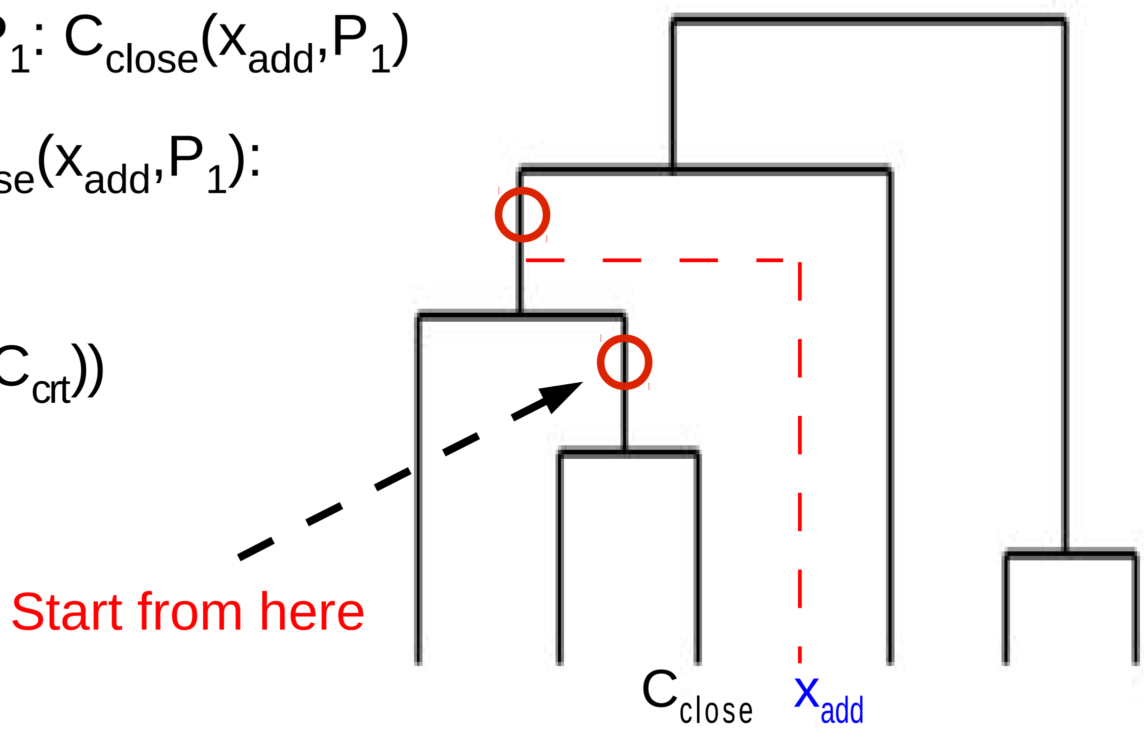
   $C_{crt} = C_{close}(x_{add},P_1).parent$

3. If $(C_{crt} = \emptyset) \vee (d(x_{add}, C_{crt}) < \delta_{max}(C_{crt}))$

   3.1. Merge: $C_{crt} = C_{crt} \cup \{s_a\}$

   3.2. Stop

4. $C_{crt} = C_{crt}.parent$



Preliminary Results

- (method) Dissimilarity representation

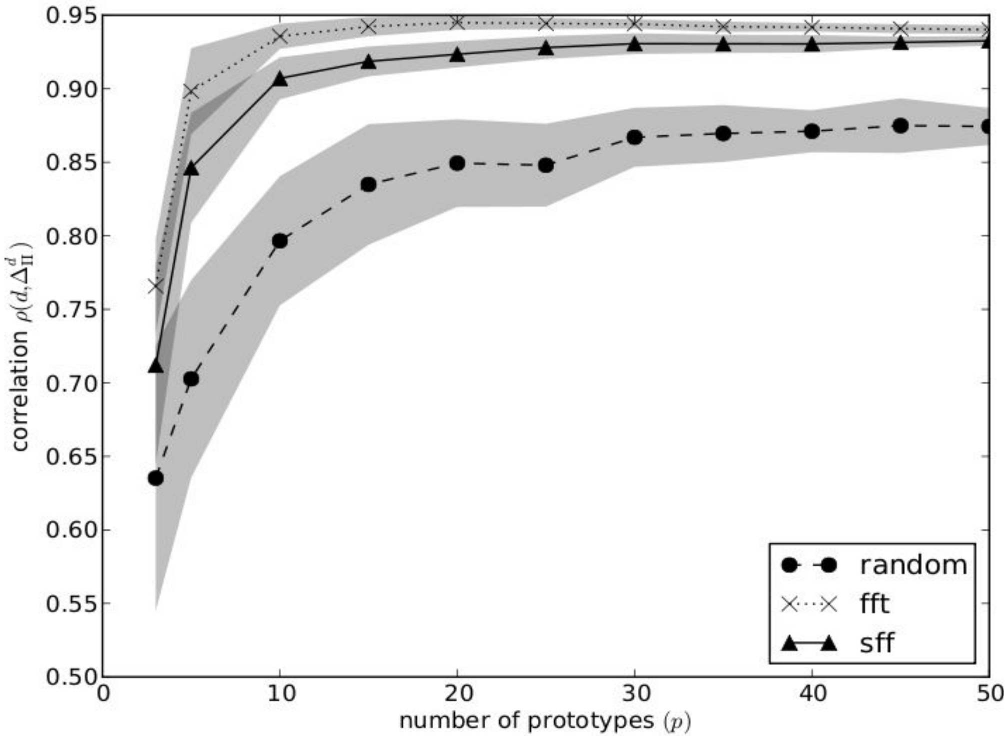
  E. Olivetti, **T. B. Nguyen**, E. Garyfallidis, *The Approximation of the Dissimilarity Projection*, Pattern Recognition in NeuroImaging, PRNI 2012.

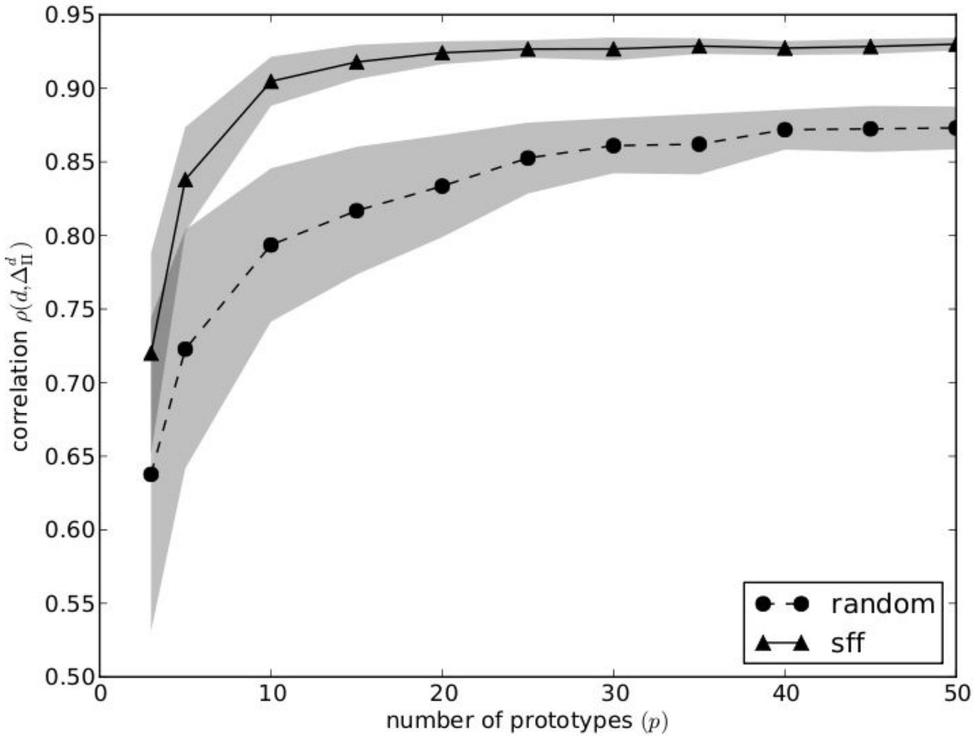
- (software/tool) Spaghetti: an interactive visualization tool for segmentation tractography

  E. Garyfallidis, S. Gerhard, P. Avesani, **T. B. Nguyen**, V. Tsiaras, I. N. Smith, and E. Olivetti, *A software application for real-time, clustering-based exploration of tractographies*, OHBM 2012.

- (case study) ALS (amyotrophy lateral sclerosis) disease

(dis)Similarity approximation for tractography





FFT: < 1secs, SFF: 2 secs (one iteration)

Tractography of 10^3 streamlines

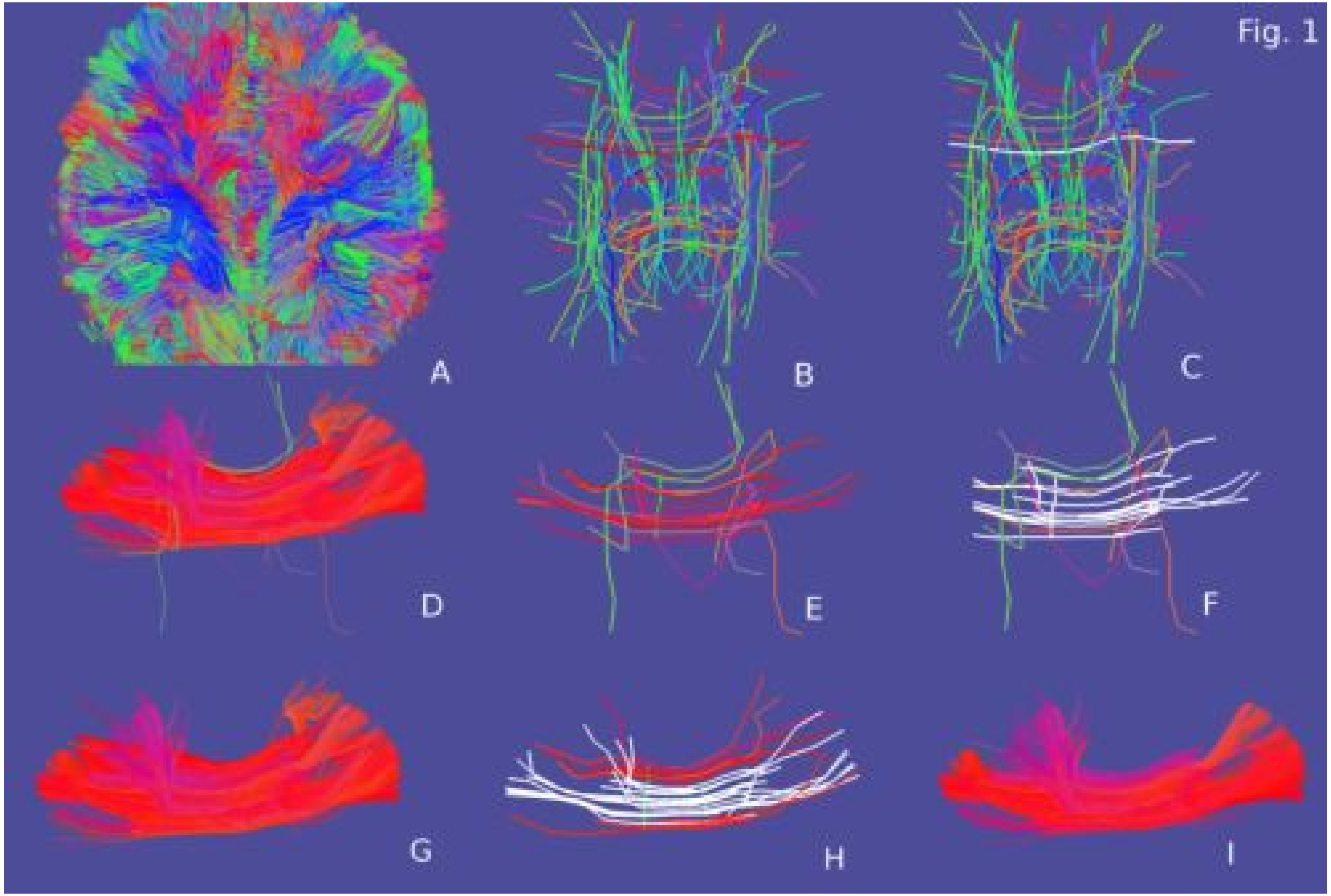
FFT: 15mins, SFF: 2 secs (one iteration)

Tractography of $3x10^5$ streamlines

E. Olivetti, **T. B. Nguyen**, E. Garyfallidis, *The Approximation of the Dissimilarity Projection*, PRNI 2012.

Spaghetti

- **Refinement**, not support the tract candidate step
- "cluster" – recluster, not change partition

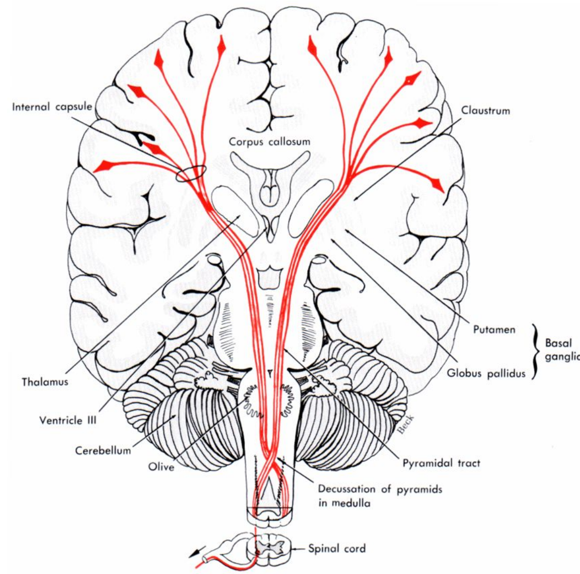


E. Garyfallidis, S. Gerhard, P. Avesani, **T. B. Nguyen**, V. Tsiaras, I. N. Smith, and E. Olivetti, *A software application for real-time, clustering-based exploration of tractographies*, OHBM 2012.

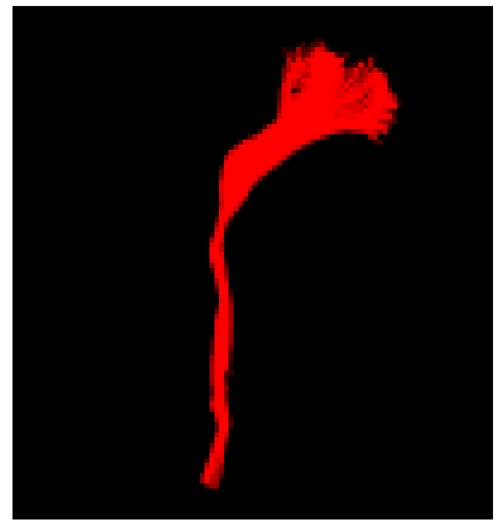
Case study: ALS disease

- Aim: the difference of CST between healthy and ALS (Amyotrophy Lateral Smytrophic) diseased brains
- Based on tractography approach

ALS disease



Cortical spinal tract (CST)



CST segmentation using Sphagetti

Conclusion

- An effective method for tract segmentation:
  tract candidate (supervised) and tract refinement (clustering)
- An interactive visualization tool for tract segmentation
- ALS case study

Future works

- Implement the modified HAC for tractography
- Revise the solution for 'adding object' to partitions
- Integerate tract candidate (supervised) into Spaghetti

Credits

- **Nivedita Agarwal**, *S.Chiara Trento Hospital, Italy; University of Utah, USA*
- **Eleftherios Garyfallidis**, *University of Cambridge, UK; University of Sherbrooke, Canada*
- **Emanuele Olivetti**, *Fondazione Bruno Kessler, Italy*
- **Paolo Avesani**, *Fondazione Bruno Kessler, Italy*
- **Luigi Cattaneo**, *CiMeC, University of Trento, Italy*
- **Francesca Maule**, *CiMeC, University of Trento, Italy*

Thank you!