UNIVERSITÀ DEGLI STUDI
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Machine Learning for Tract Segmentation in dMRI Data

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Contents

- Introduction
- State of the art (SoA)
- Problem statement
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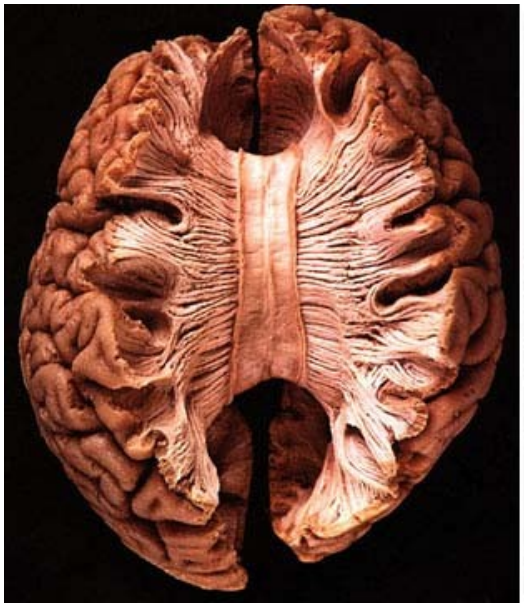
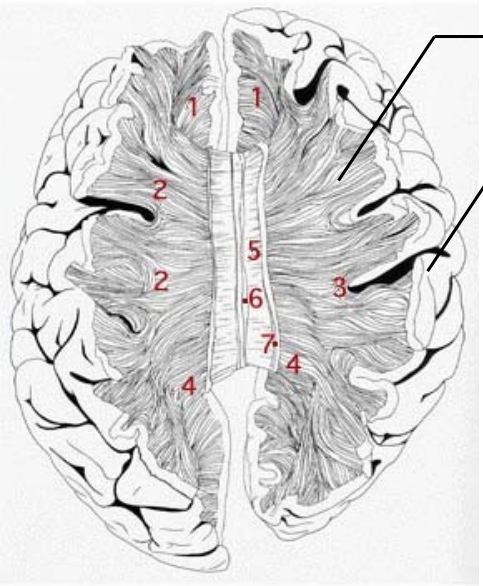
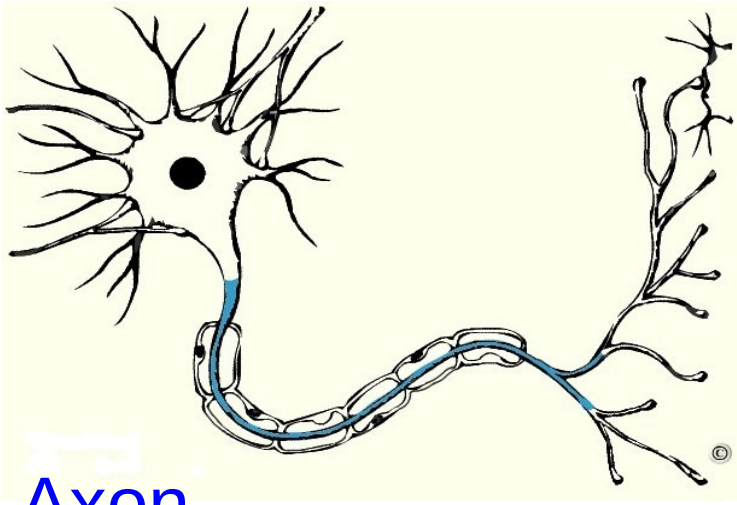
- Conclusion and Future works

White matter







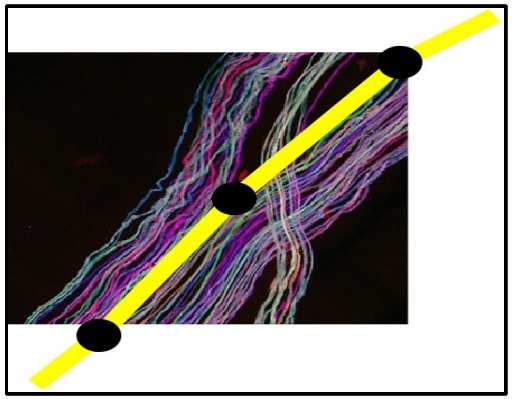
dMRI technique

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

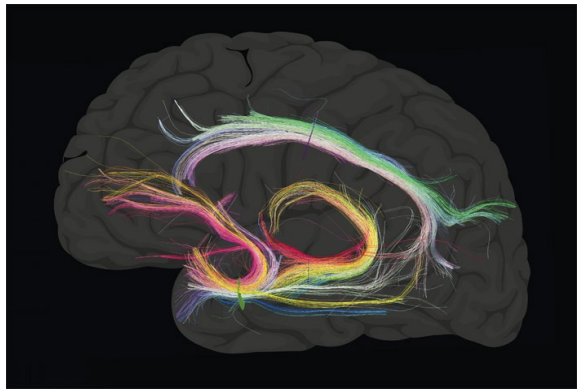
Axon

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

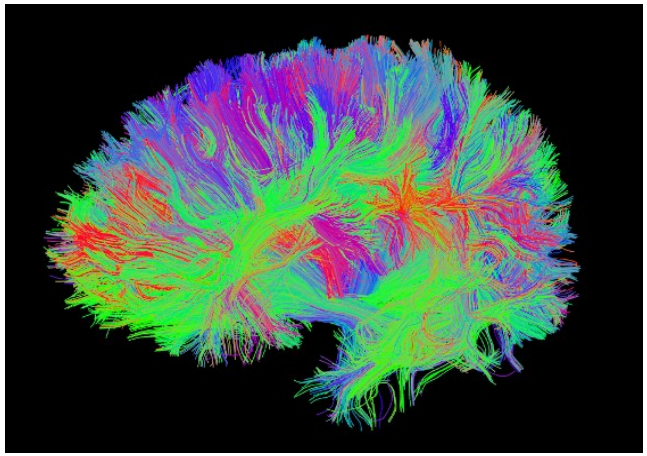
Streamline & Tractography



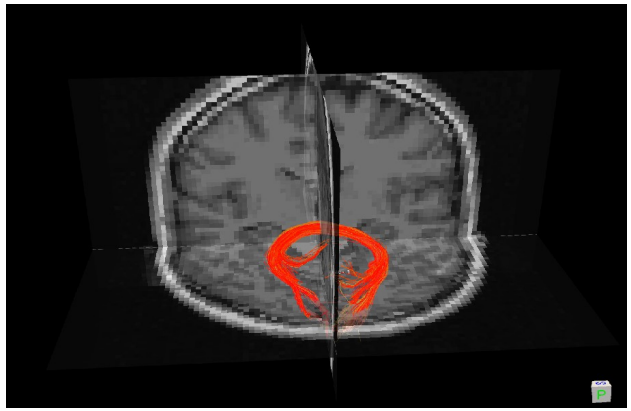
Streamline: a polyline representating thousands of axons. (fiber, track)



Bundle: a group of *'close'* streamlines

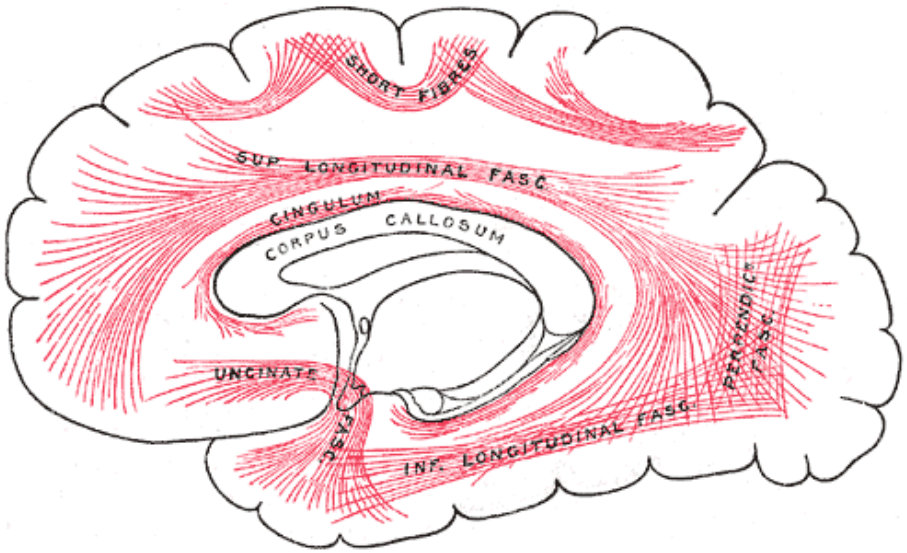


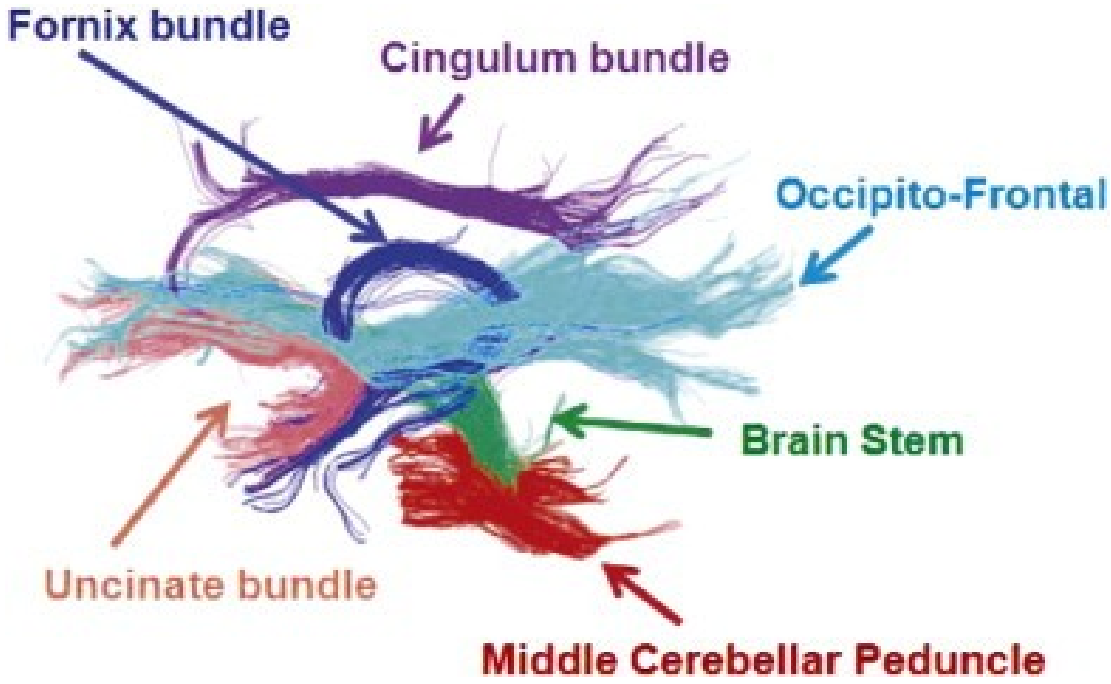
Tractography: presentation of whole brain by streamlines.



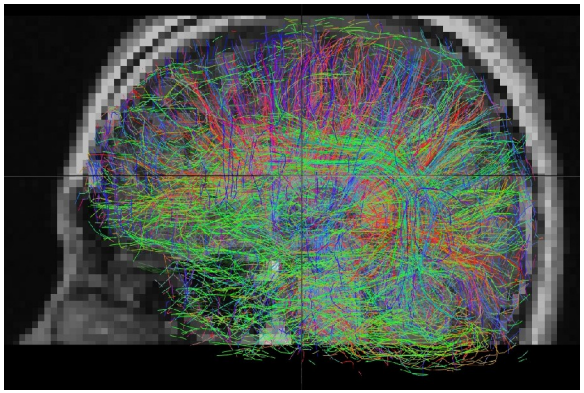
Tract: the real anatomical group of axons.

Tractography Segmentation

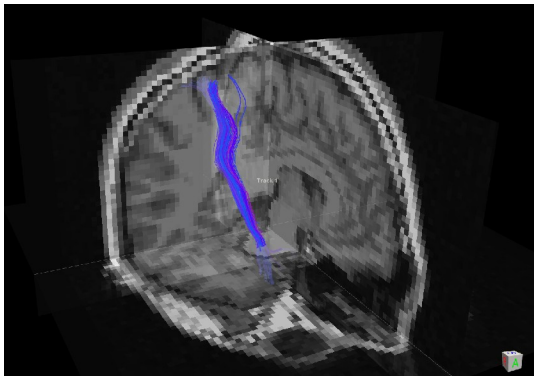




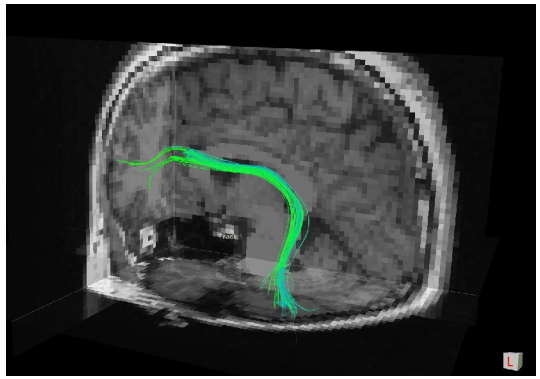
To group streamlines belonging to a common anatomical area into one segmentation



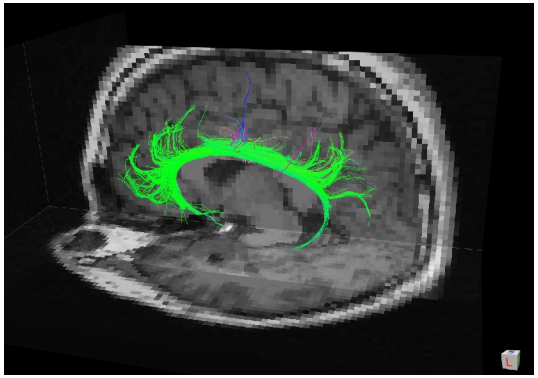
Tractography



Corticol Spnial Tract (CST)



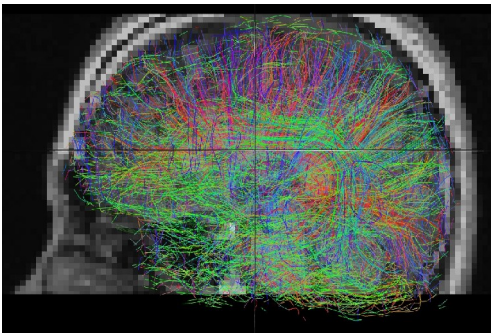
Arcuate Fasciculus Tract (AFT)



Cingulum Tract (CGT)

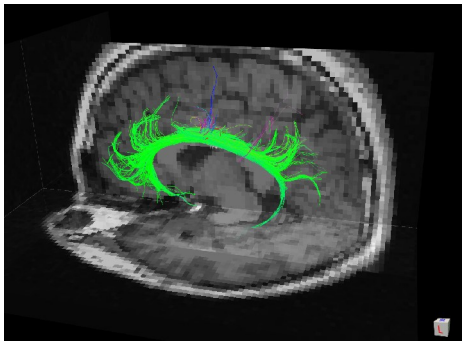
Example of
tractography segmentation

Tract segmentation approaches



tractography

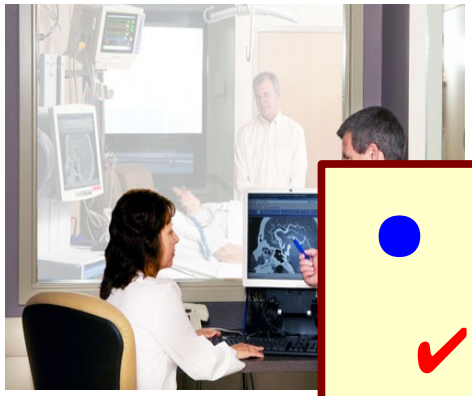
- Atlas based
- ROI based (region of interest)
- Unsupervised
- Supervised

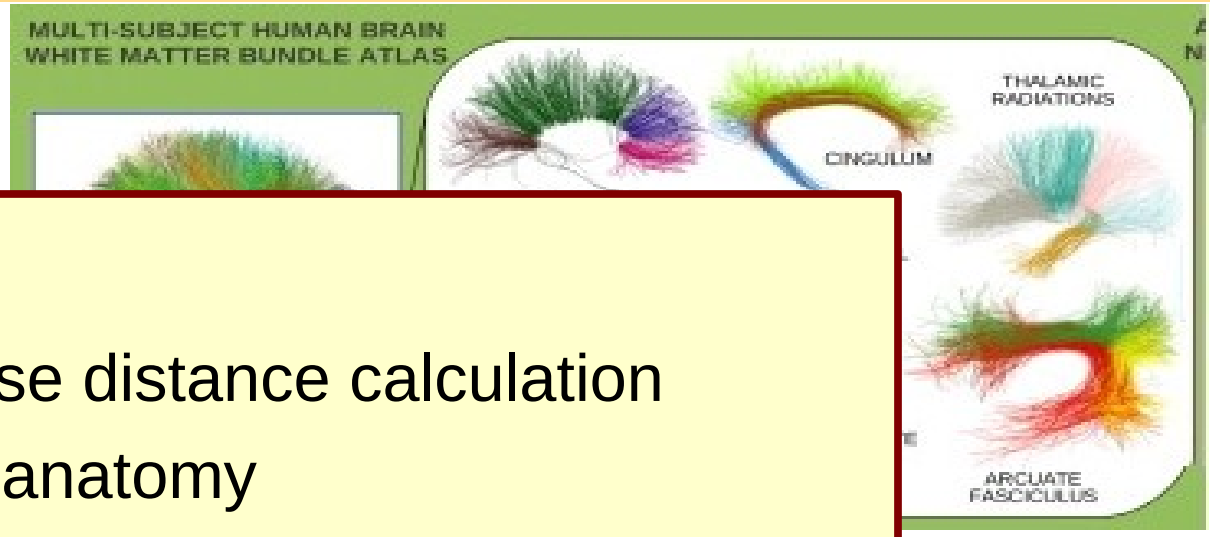


tract(s)

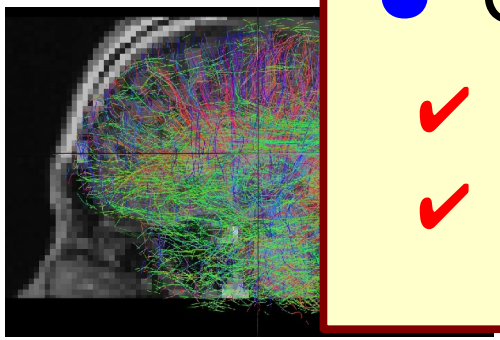
O'Donnell et al., 2007

Atlas based *Tract Segmentation*





- Pros
  - ✔ No pairwise distance calculation
  - ✔ Relate to anatomy
- Cons
  - ✔ Whole brain, not target tract
  - ✔ Brain variety → co-registration problem

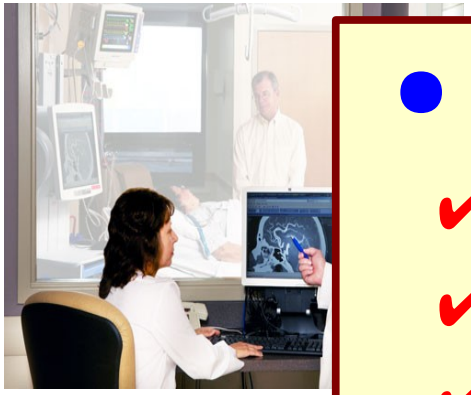


tractography

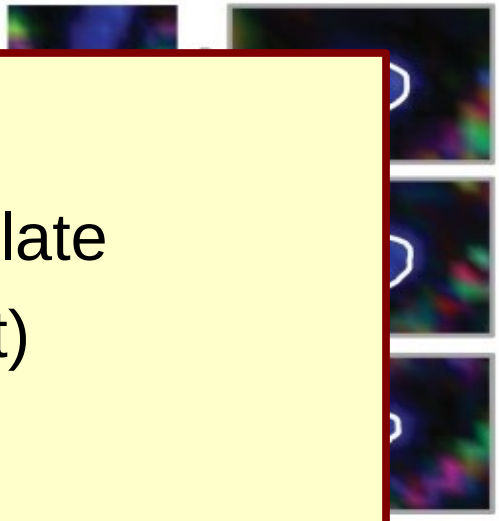
tract(s)

ROI based *Tract Segmentation*

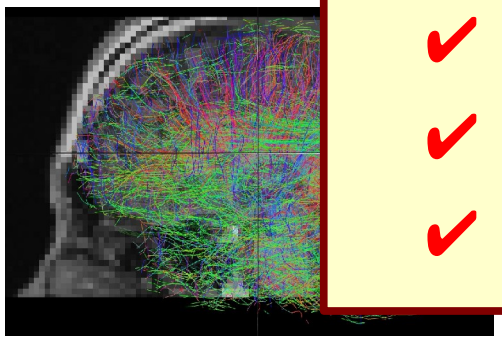
(ROI:Region of Interest)
Wakana et al., 2007



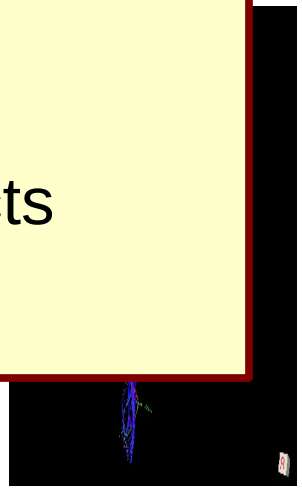
- Pros
  - ✔ No pairwise distance calculate
  - ✔ Relate to anatomy (indirect)
  - ✔ Target tract
- Cons
  - ✔ Prior knowledge of tracjectory
  - ✔ Work on well characterized tracts
  - ✔ Co-registration



ROIs are drawn



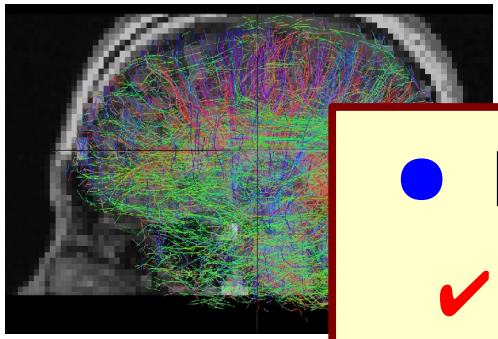
tractography



tract

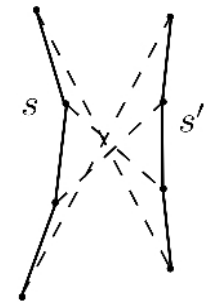
Wang et al., 2011

Unsupervised *Tract Segmentation*



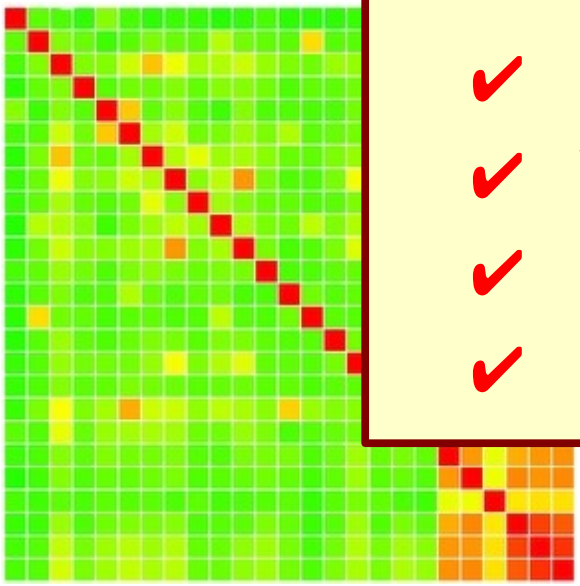
Streamlines distance

$d_{\text{mean}}(s, s')$ $d_{\text{mean}}(s', s)$ $d_{\text{direct}}(s, s')$ $d_{\text{flipped}}(s, s')$

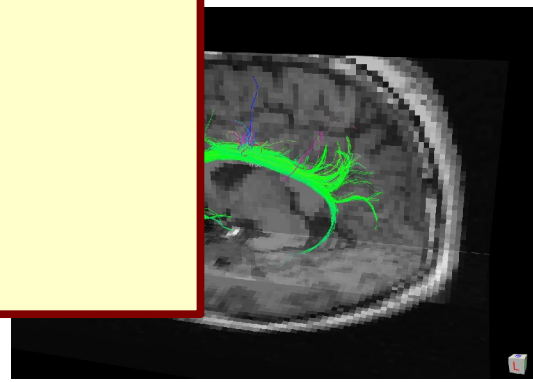


- Pros
  - ✔ No co-registration
- Cons
  - ✔ Calculate pairwaise distance
  - ✔ Whole brain not target tract
  - ✔ Not relate to anatomy
  - ✔ Number of cluster

k-means, etc.)



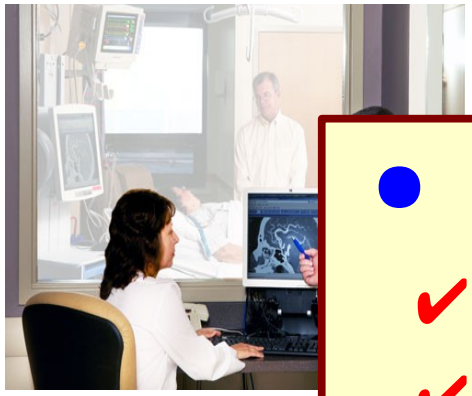
similarity matrix

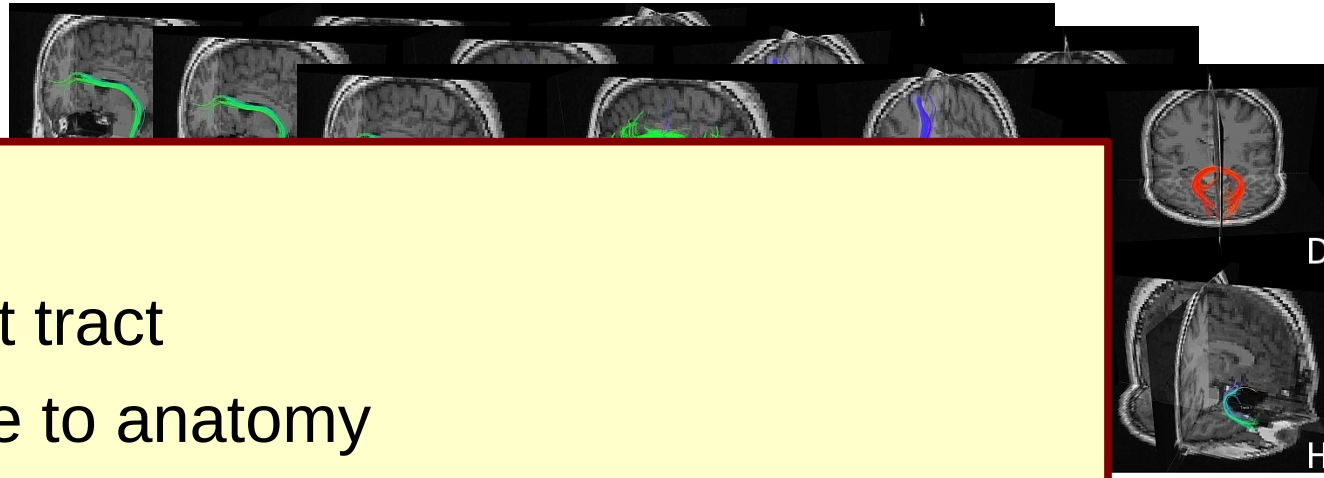


tract(s)

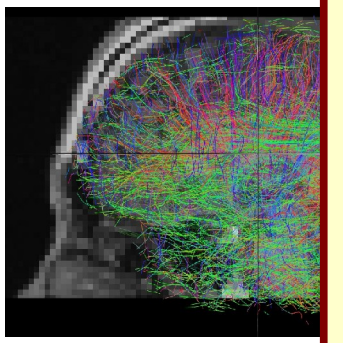
Olivetti et al., 2011

Supervised Tract Segmentation

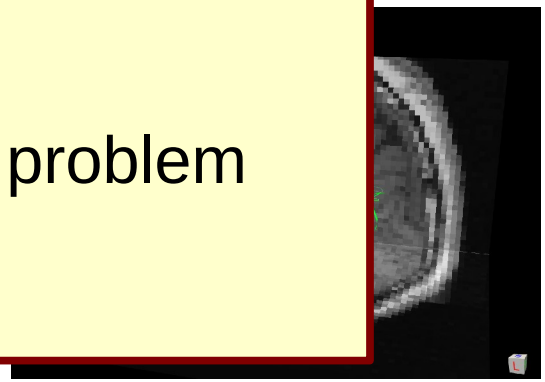




- Pros
  - ✔ Target tract
  - ✔ Relate to anatomy
- Con
  - ✔ Calculate pairwise distance
  - ✔ Brain variety → co-registration problem
  - ✔ Ground truth data



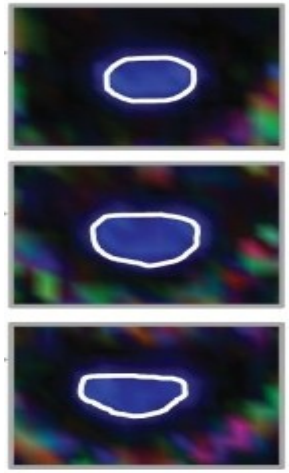
tractography

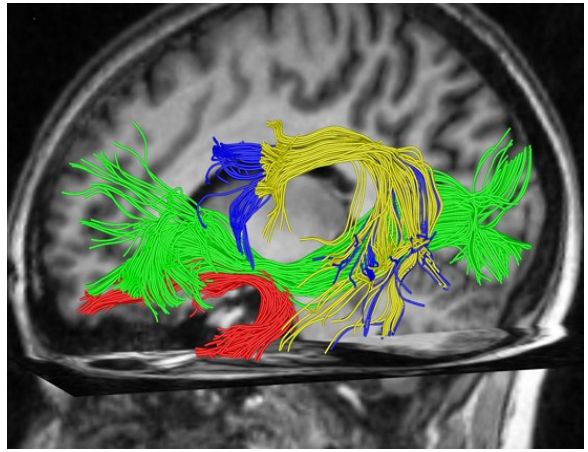


tract(s)

New strategy: BOI - Bundle of Interest

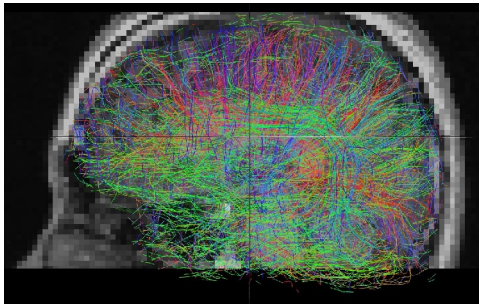
Focus directly on which bundle (cluster of streamlines) that user wants to work on



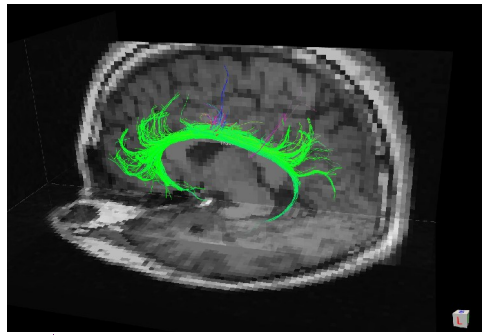


Approach	ROI	BOI
Anatomy related	Yes (indirect)	Yes
Visualization	No	Yes
Interaction	No	Yes
No prior knowledge of trajectory	No	Yes

Goals



Machine Learning (ML)

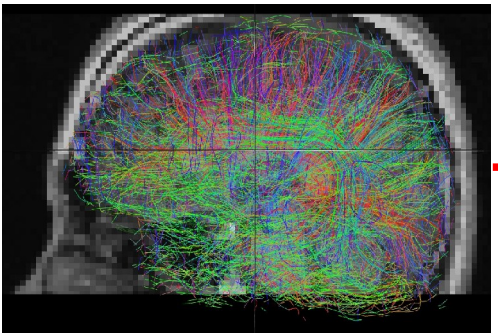


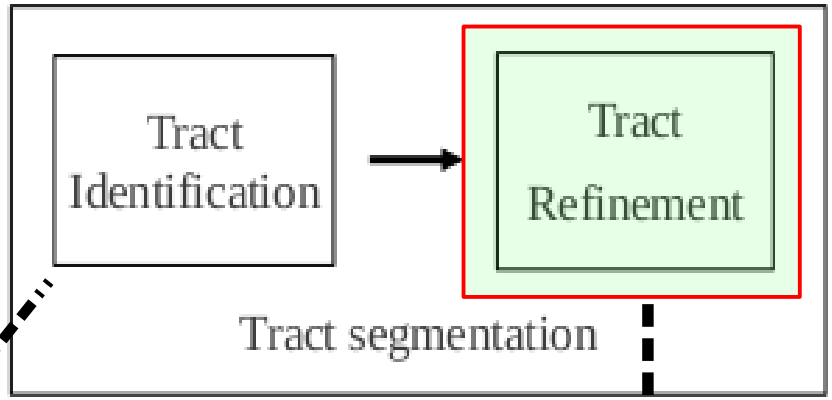
Improve the support of ML for tract segmentation

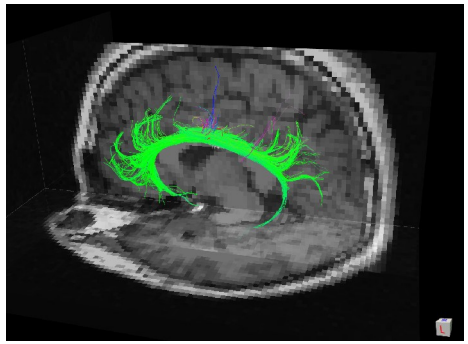
Challenges

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

Process design: *interactive segmentation*

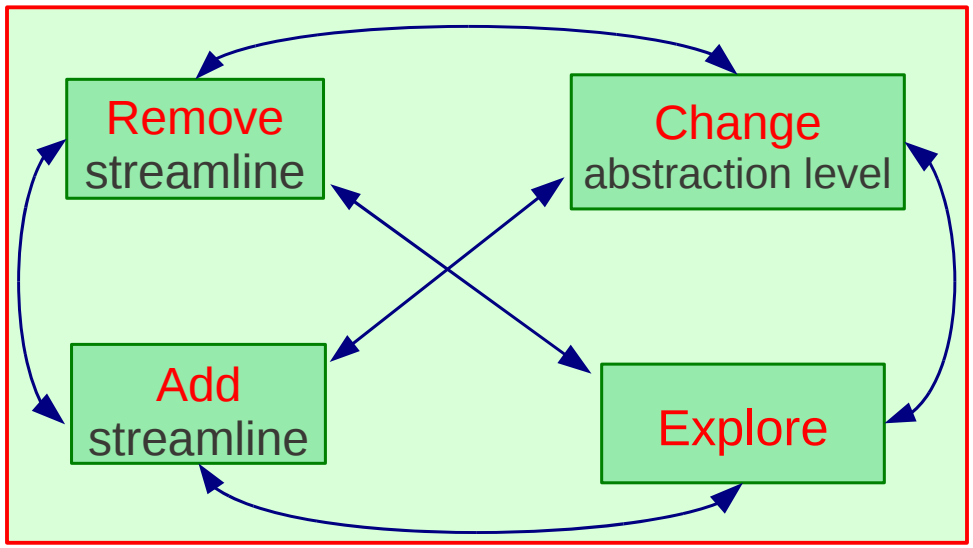






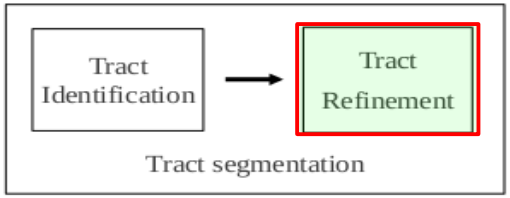
create tract candidate from set of samples

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



based on BOI

Interactive tract refinement



Demo of Spaghetti

Problem statement

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

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

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

i $C_i \neq \emptyset$, $i \in [1, .., K]$

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

iii $C_i \wedge C_j = \emptyset$, $i, j \in [1, .., K]$, $i \neq j$

Interactive clustering

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

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

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

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

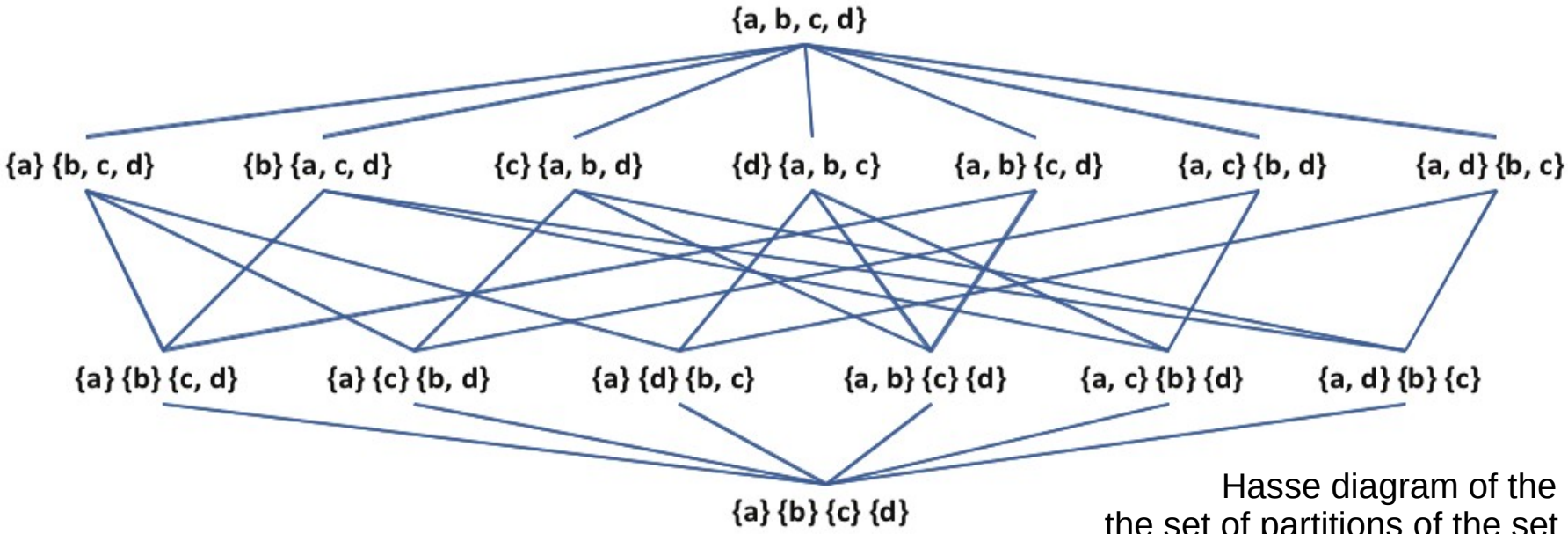
ii constraint γ: $\forall i \in [1,m-1]$, $P_i \preceq P_{i+1}$ *("nested in")*

- 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”)

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



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 $x_{r.m} \in \mathcal{X}$

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

- Add a new object x_{add}

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

$$\mathcal{P} = \{P_1, \ldots, P_m\} \quad \langle \mathcal{P}, \mathcal{X}, \gamma \rangle, \gamma: P_i \preceq P_{i+1}$$

$i \in [1, m-1]$

current partitions

$$\Longrightarrow$$

$$\mathcal{P}' = \{P'_1, \ldots, P'_m\} \quad \langle \mathcal{P}', \mathcal{X}', \gamma' \rangle, \gamma': P'_i \preceq P'_{i+1}$$

$i \in [1, m-1]$

updating partitions

Interactive clustering: add new object

- Current viewing abstraction level is *ith*
- $C(x, P_i)$: cluster in parition P_i having object x

- All upper partitions

γ'_1: $\forall j \in [i, .., m], \ \forall x \in \mathcal{X}$:

$$C(x,P'_i) = C(x_{add},P'_i) \rightarrow C(x,P'_j) = C(x_{add},P'_j)$$

- All lower partitions

γ'_2: $\forall k \in [1, .., i-1], \ \forall x \in \mathcal{X}$:

$$C(x,P'_i) \neq C(x_{add},P'_i) \rightarrow C(x,P'_k) \neq C(x_{add},P'_k)$$

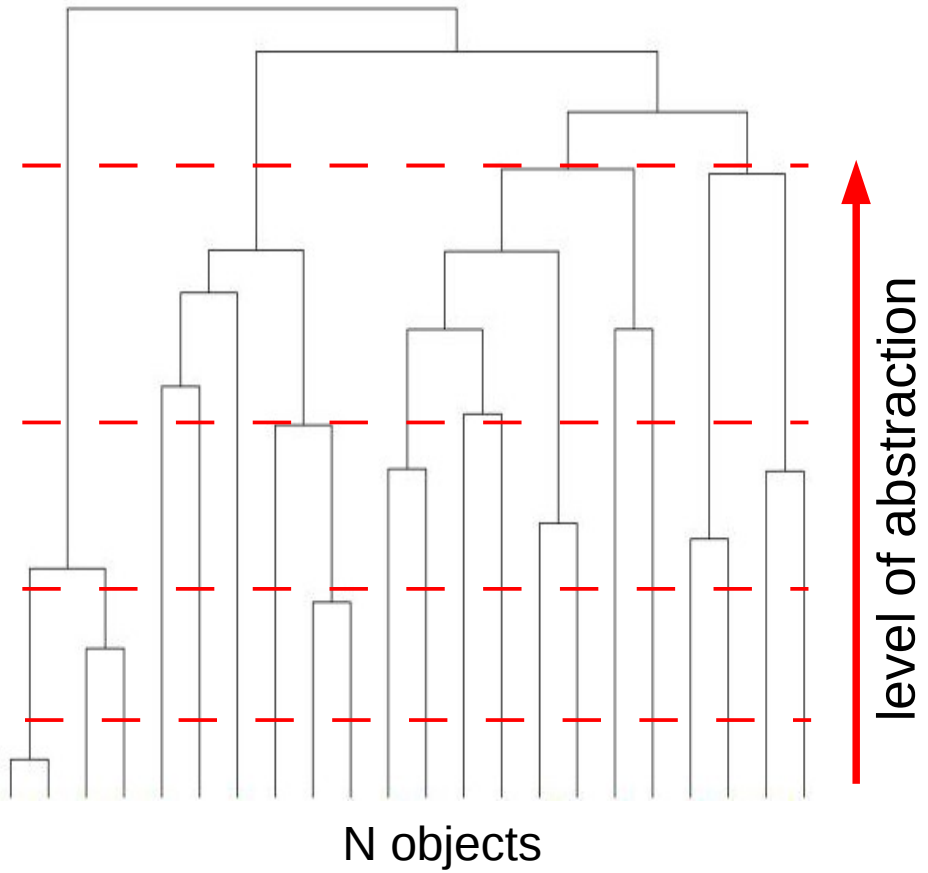
Hierarchical clustering

Johnson, 1967

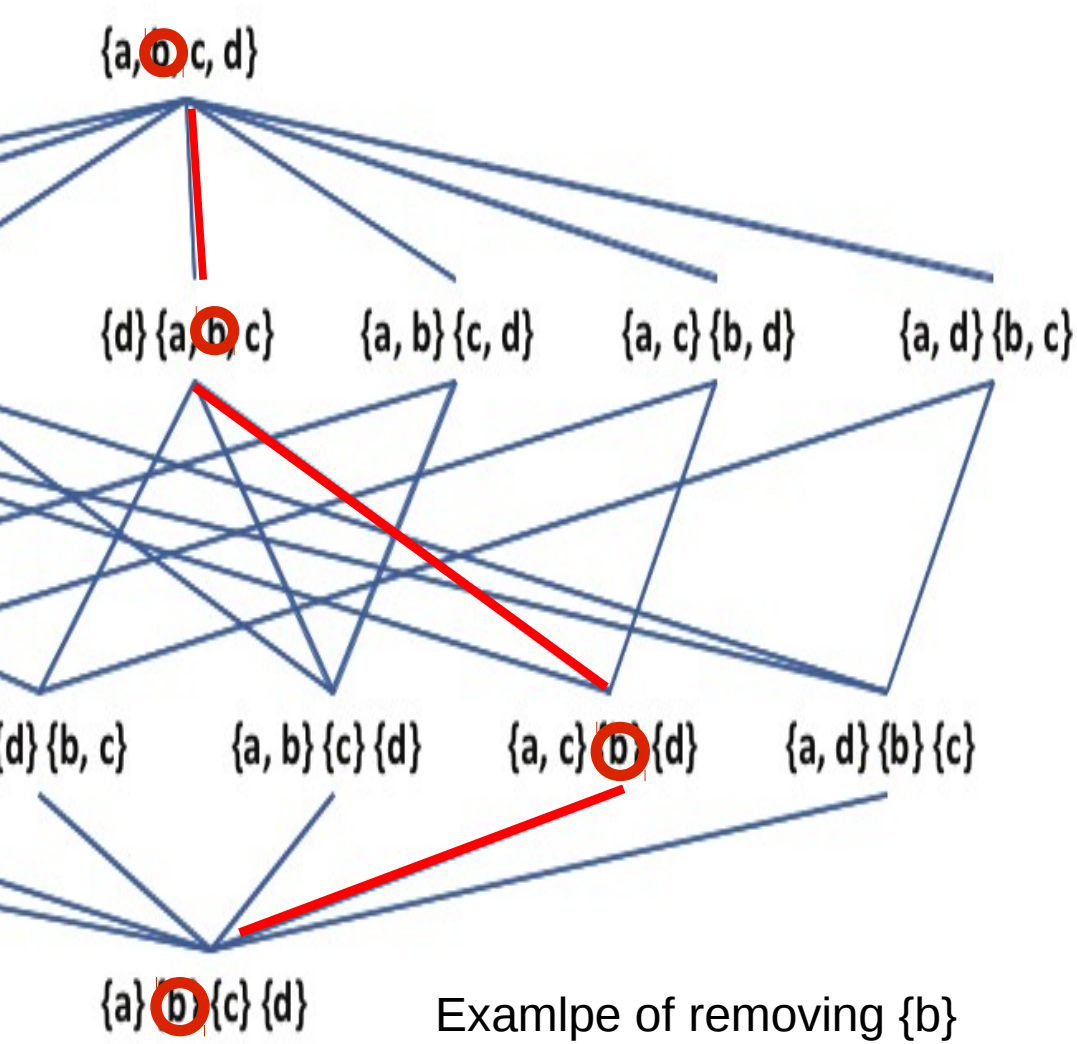
Find m partitions of $\mathcal{X}$: $\mathcal{P} = \{P_1, \ldots, P_m\}$, $P_i \prec P_{i+1}$, $i \in [1, m-1]$

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 $C^i_j = \varnothing$, $P_i = P_i \setminus \{C^i_j\}$

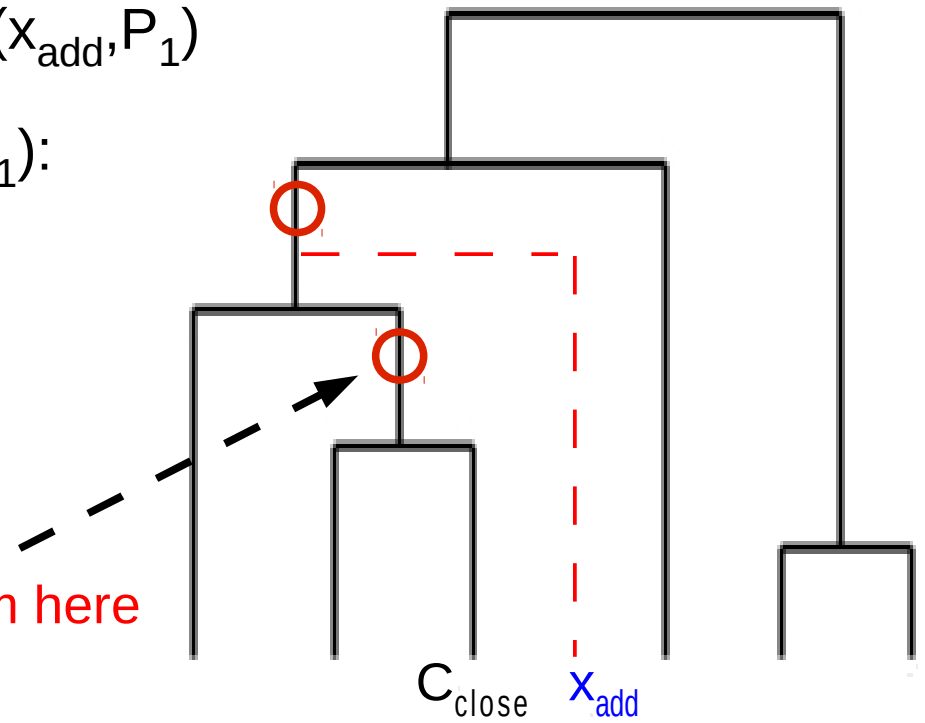
Interactive clustering: *add object*

Widyantoro et al., 2002
Gurrutxaga et al., 2009

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



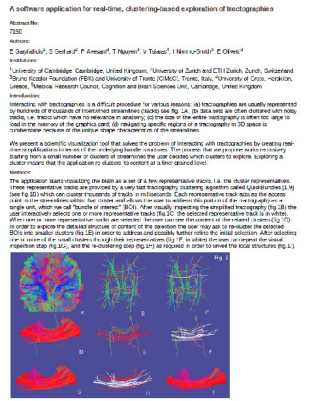
Preliminary Results

- (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, E. Olivetti,
A software application for real-time, clustering based exploration of tractographies, OHBM 2012.



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

(in preparation)

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

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Thank you!