Open challenges in tractography: addressing tractography biases and tackling the false-positive problem

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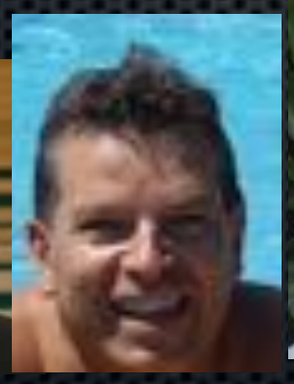
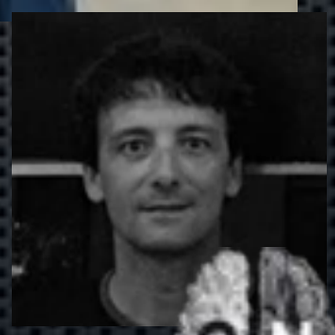
Université de Sherbrooke

UNIVERSITÉ DE SHERBROOKE

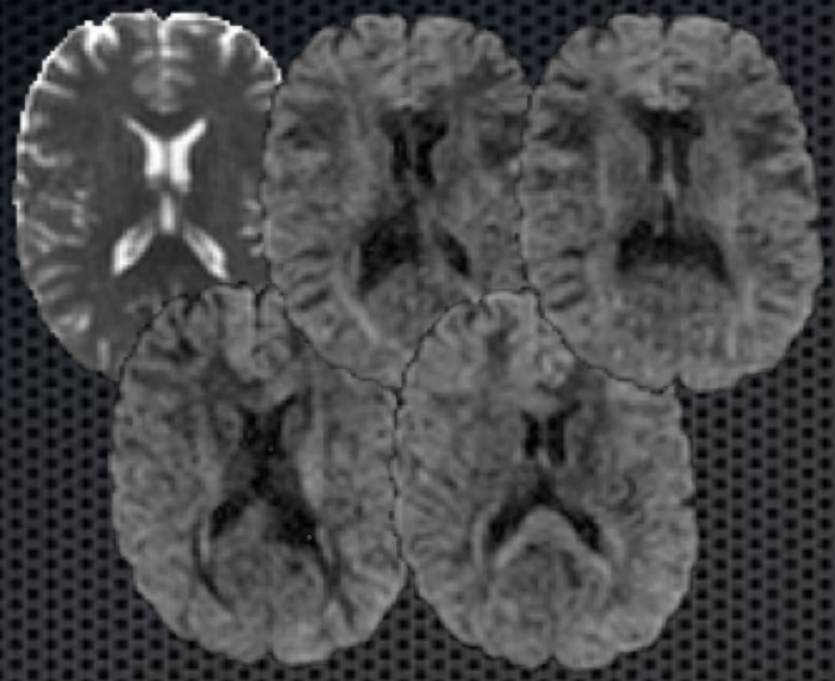
Sherbrooke Connectivity Imaging Lab (SCIL)

Thanks!





2 branches in diffusion MRI



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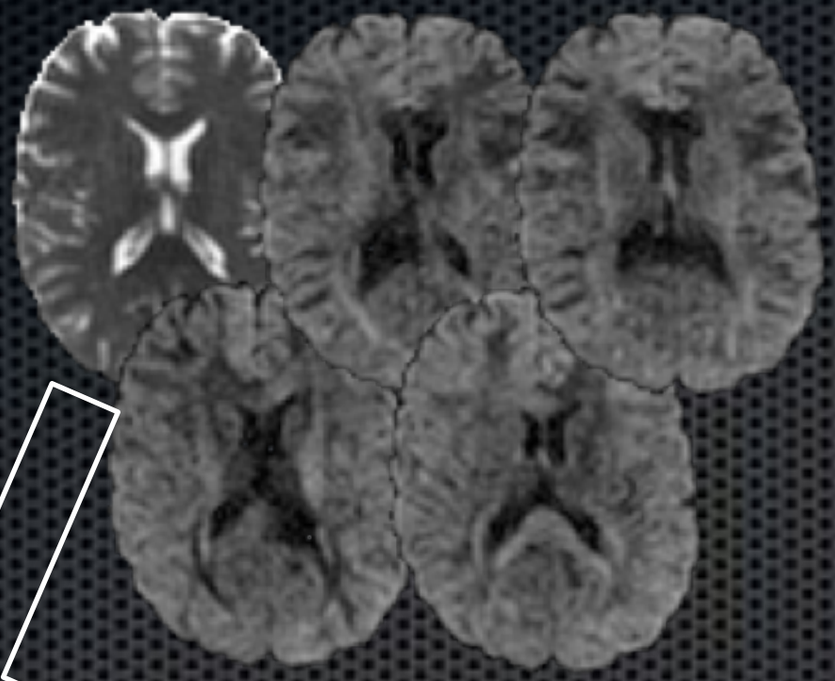
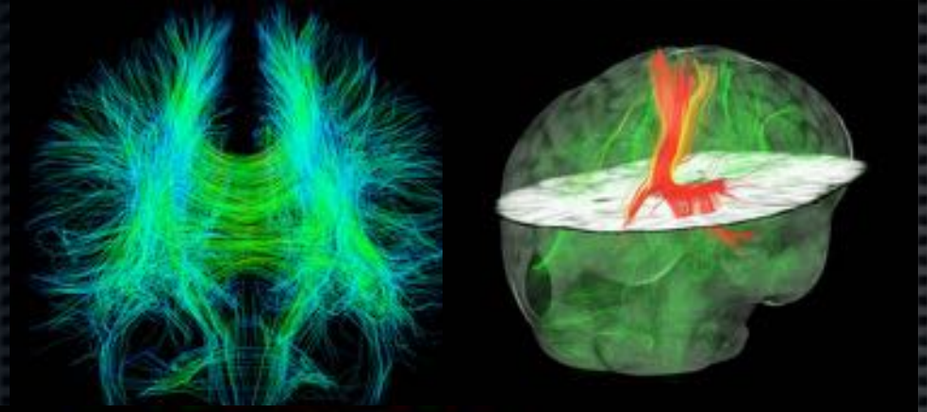
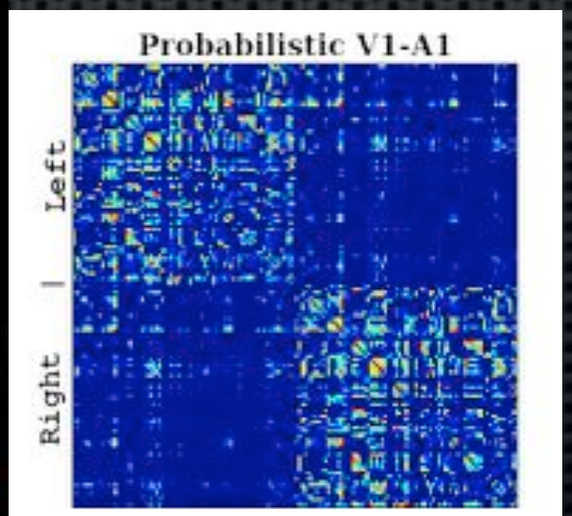


Tract-based
Tractography
Tractometry
Connectomics





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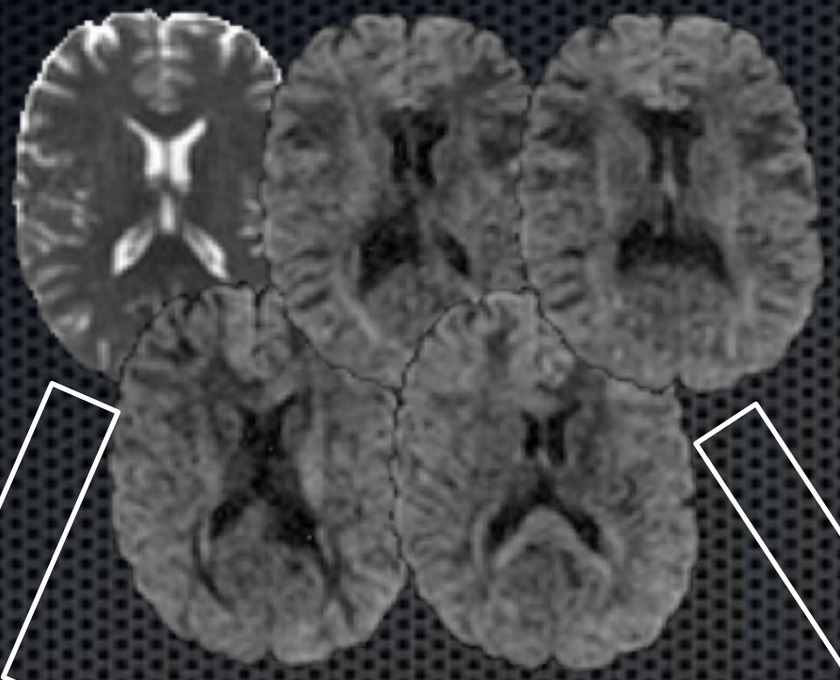

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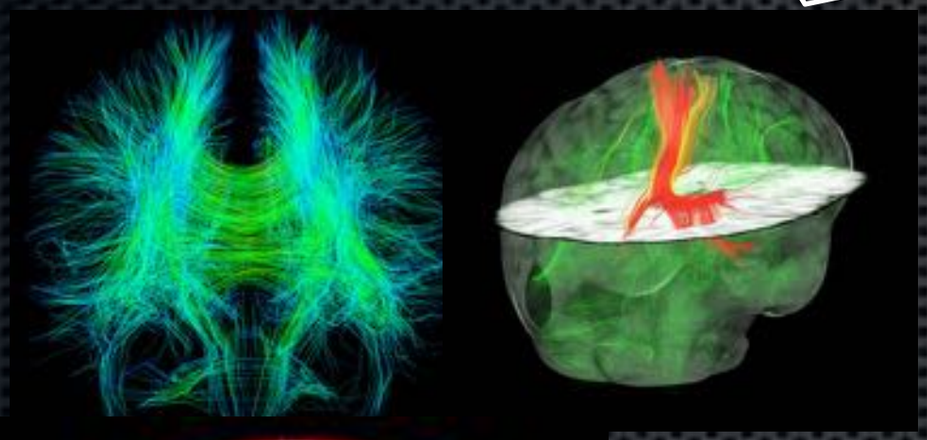
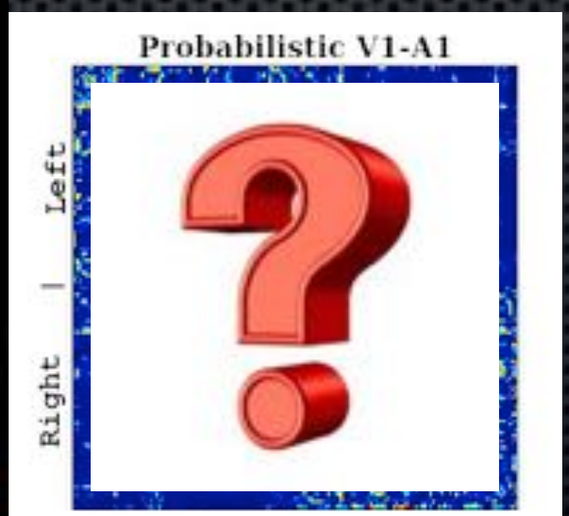
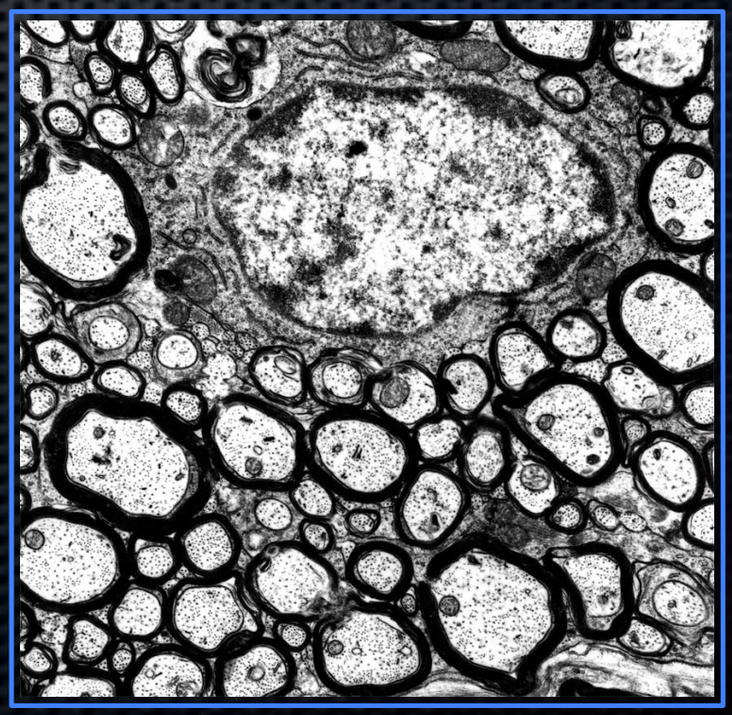
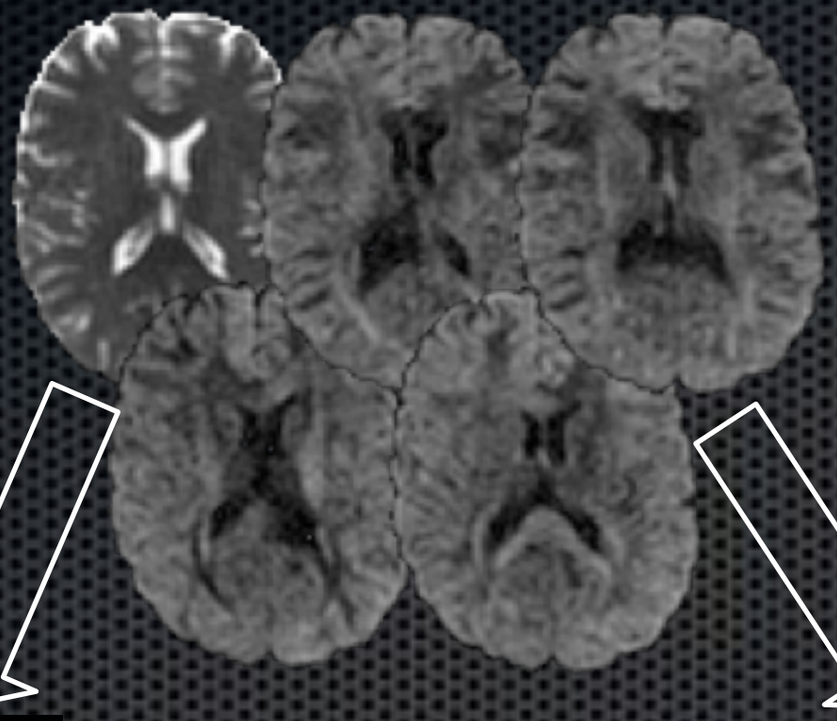




Tissue properties
local modelling
microstructure
(axon diameter,
intra/extra
axonal VF, g-ratio)



Towards quantitative connectomics



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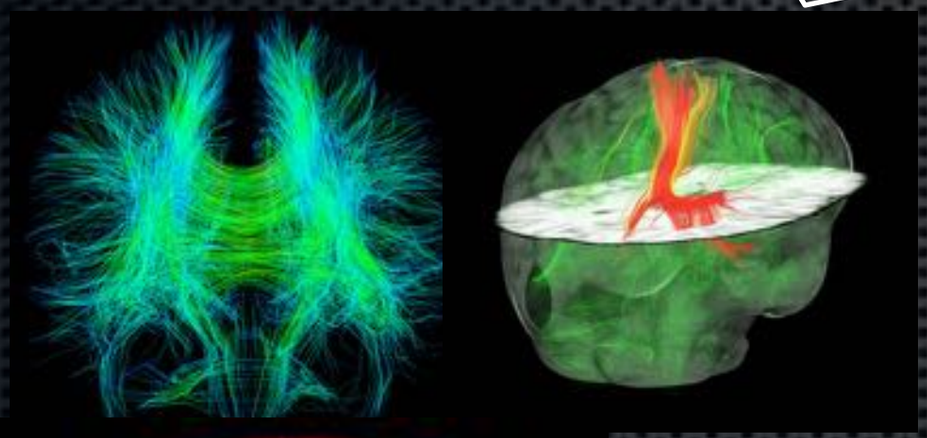

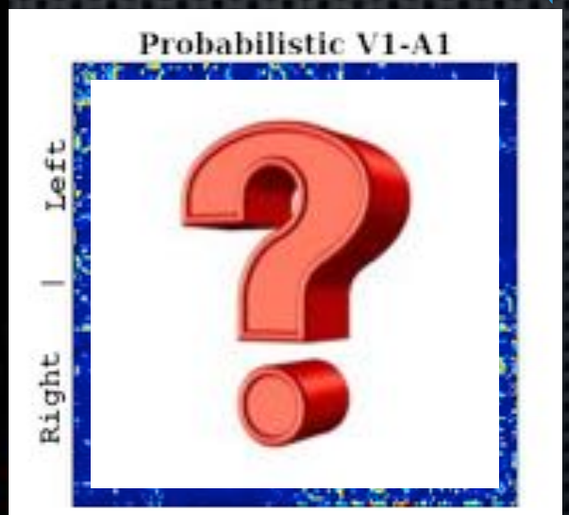

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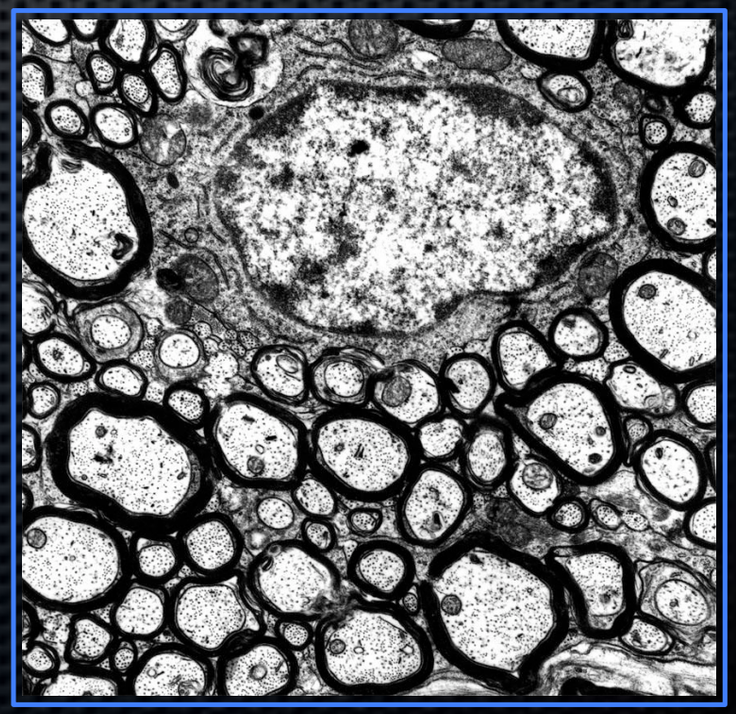
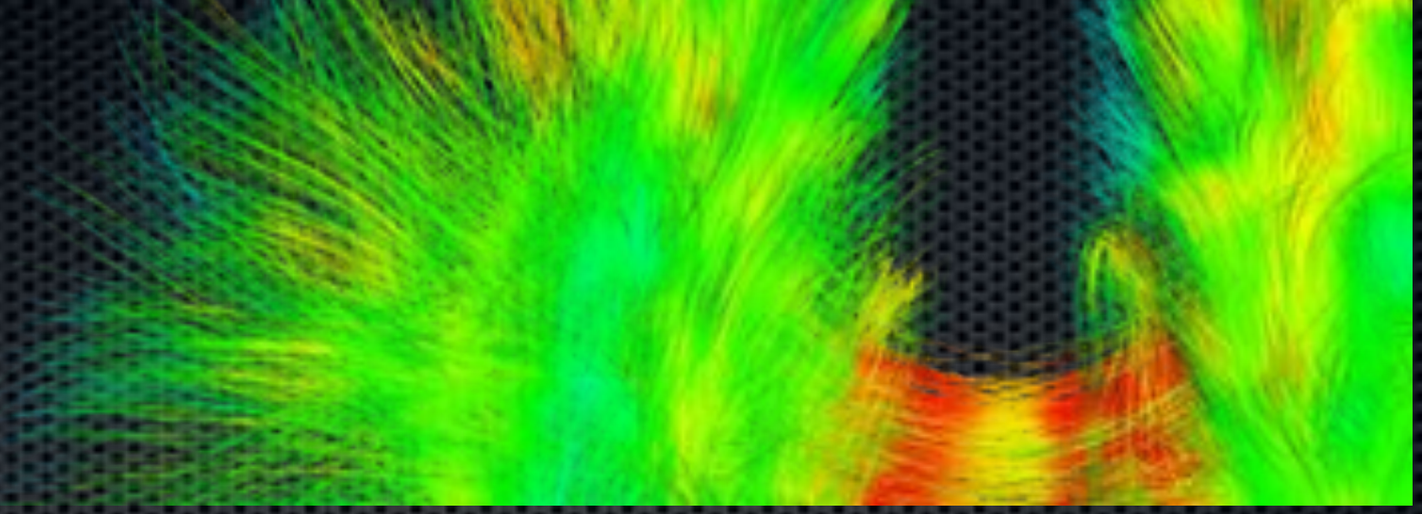


[Daducci, Descoteaux et al. Frontiers 2016]

Different family of algorithms

- Streamline deterministic
- Streamline probabilistic
- Probabilistic
- Global techniques

[e.g. Aganj et al., MIA, 2010; Behrens et al., Nimg, 2007; Cambell et al., Nimg, 2005; Collins et al., ACCV, 2010; Descoteaux et al., TMI, 2009; Fillard et al., MICCAI, 2009; Fillard et al., NImg, 2011; Iturria-Medina et al., Nimg, 2008; Jbabdi et al., NImg, 2007; Jbabdi et al., J. Bio. Img., 2008; Jeurissen et al., Hum. Brain Mapp., 2011; Jones, TMI, 2008; Merlet et al., MICCAI, 2012; Oguz et al., MICCAI, 2012; Pontabry and Rousseau, MICCAI, 2011; Reisert et al., NImg, 2010; Sherboody et al., MICCAI, 2010; Satiropoulos et al., Nimg, 2010; Smith et al., Nimg, 2013; Tournier et al., Nimg, 2007; Tournier et al., J. Img. Sys. 2012; Takemura et al., Plos Comp. Bio., 2016; Zalesky et al., TMI, 2008]



Tractography challenges & open questions

Tractography challenges

- **No connections**
- **Tractography biases**
  - Length bias
  - Size bias
  - Shape bias
  - Position bias (gyral bias, partial volume areas)
- **Invalid connections**

Shape/length/size bias

[Jbabdi Brain Connectivity 2011
Jones et al 2013
Chamberland Frontiers 2014]

Shape/length/size bias

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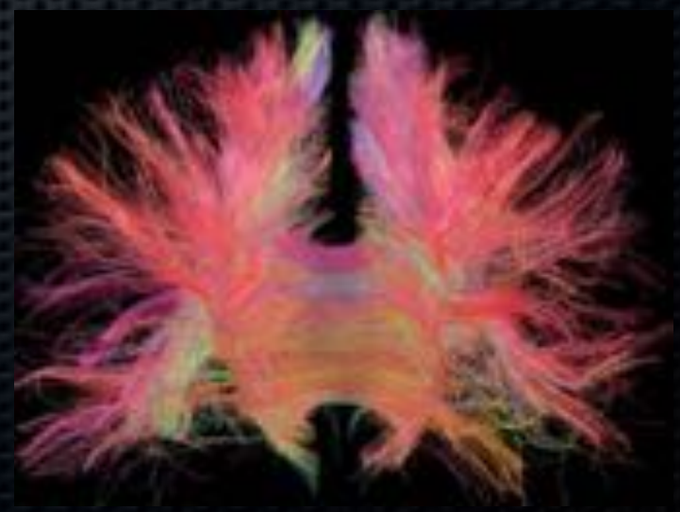
- Some bundles are easier/harder to track
- Optimal tracking parameters vary across the brain



[Jbabdi Brain Connectivity 2011
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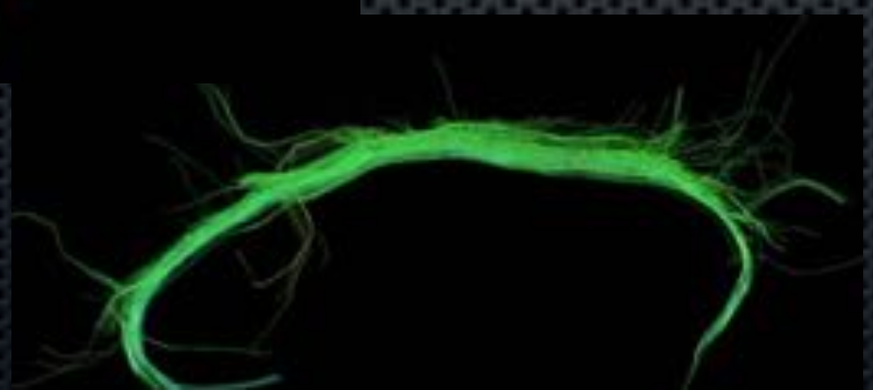
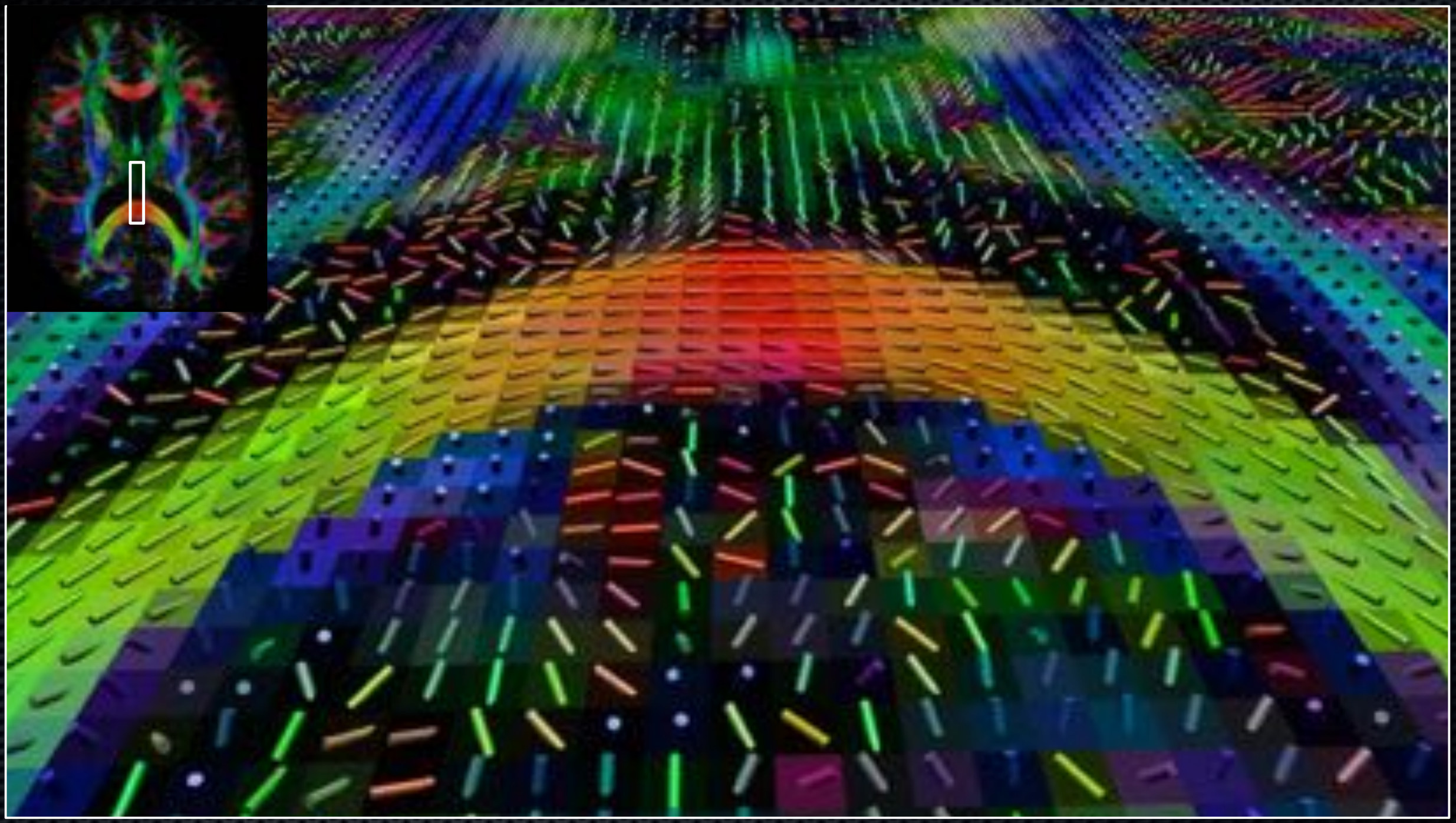
Shape/length/size bias

- Some bundles are easier/harder to track
  - Optimal tracking parameters vary across the brain
- Bigger, longer, straighter bundles
  - have more seeds in them



Seeding/shape bias of tractography



"seeding the *whole* white matter"

[Slide Curtesy A Leemans]

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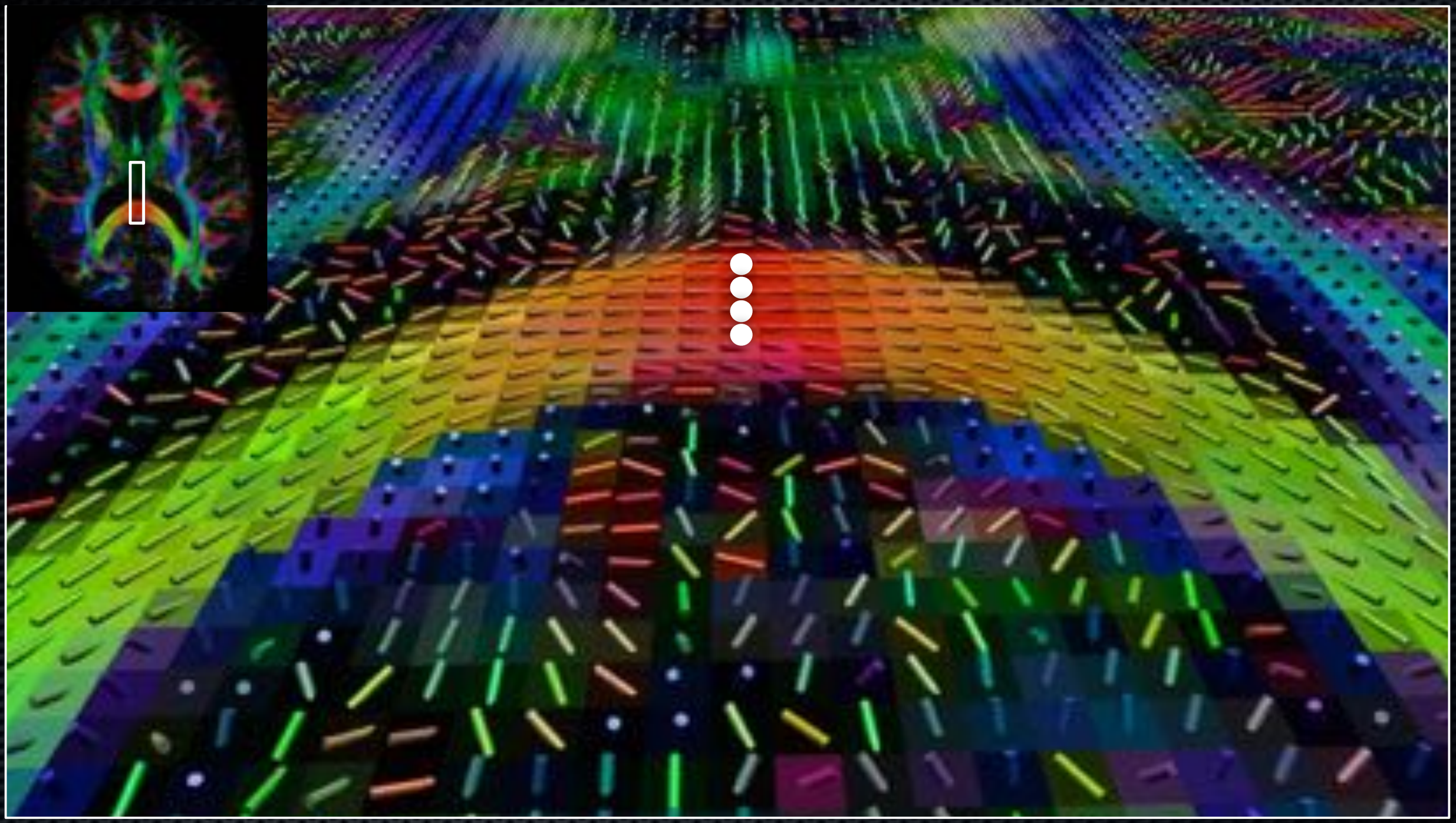

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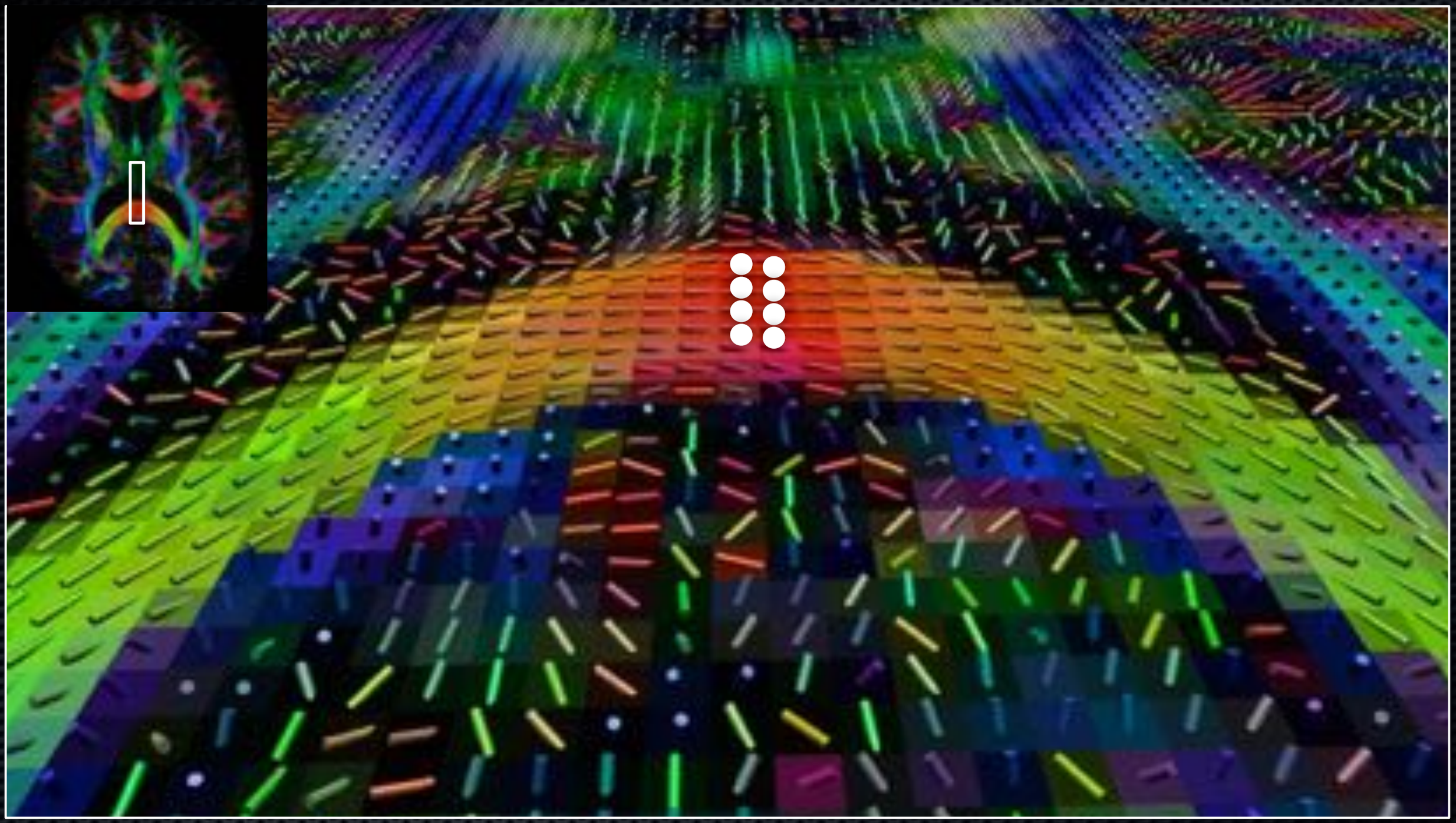

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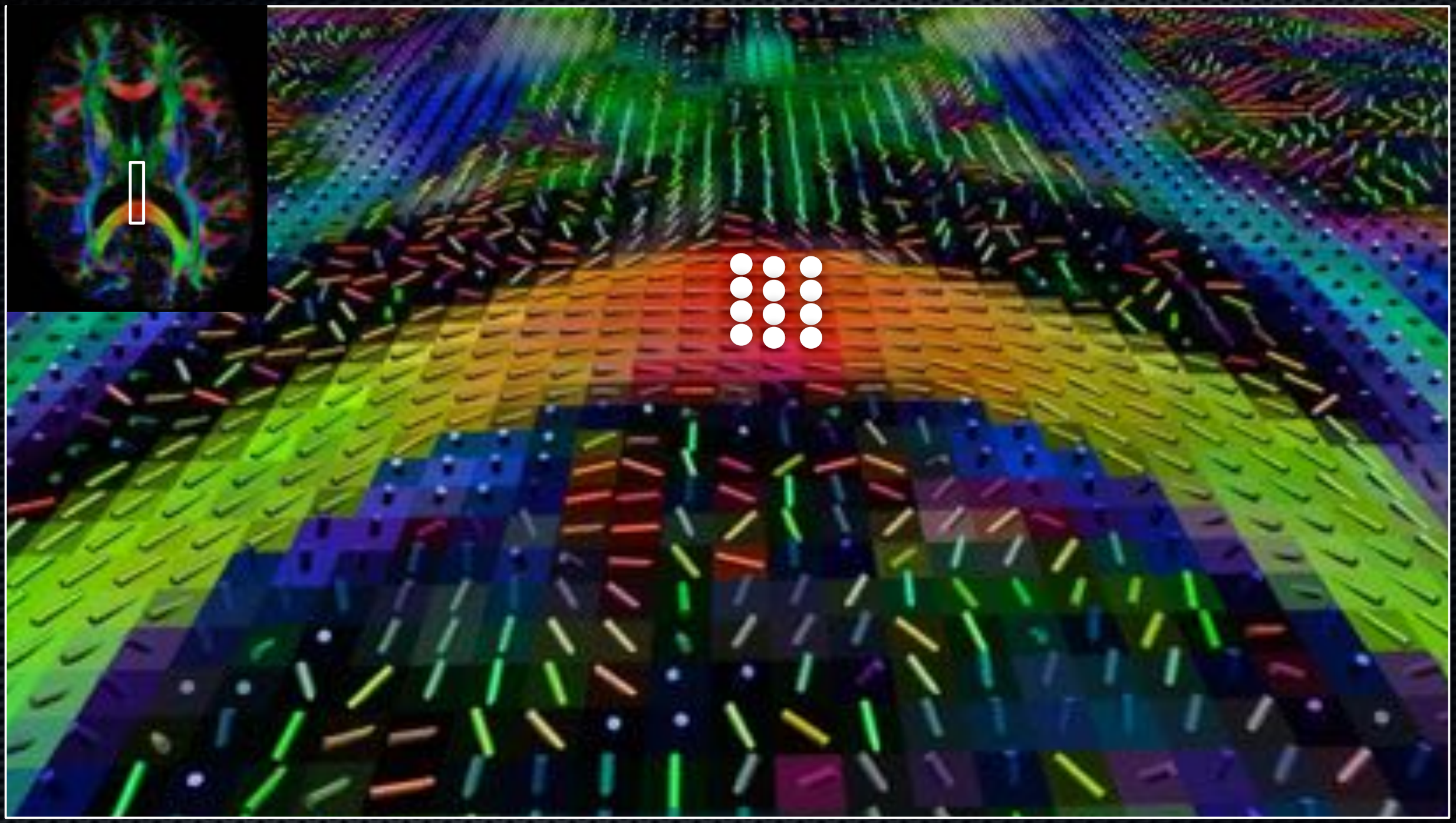

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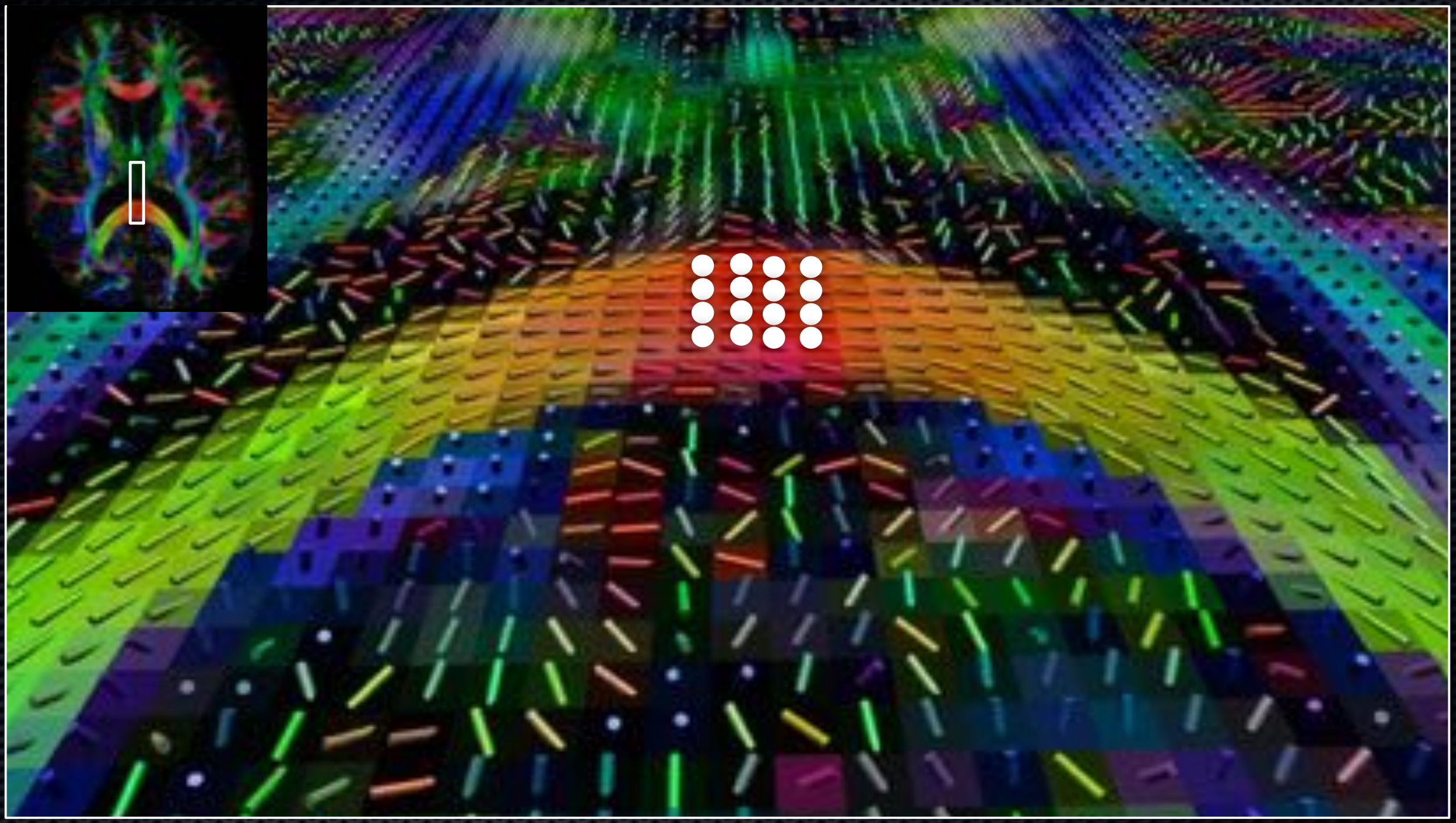

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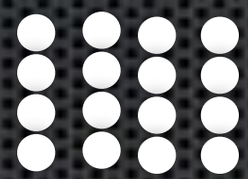


Large and **long** bundles
are *OVER*-represented

"seeding the *whole* white matter"

[Slide Curtesy A Leemans]

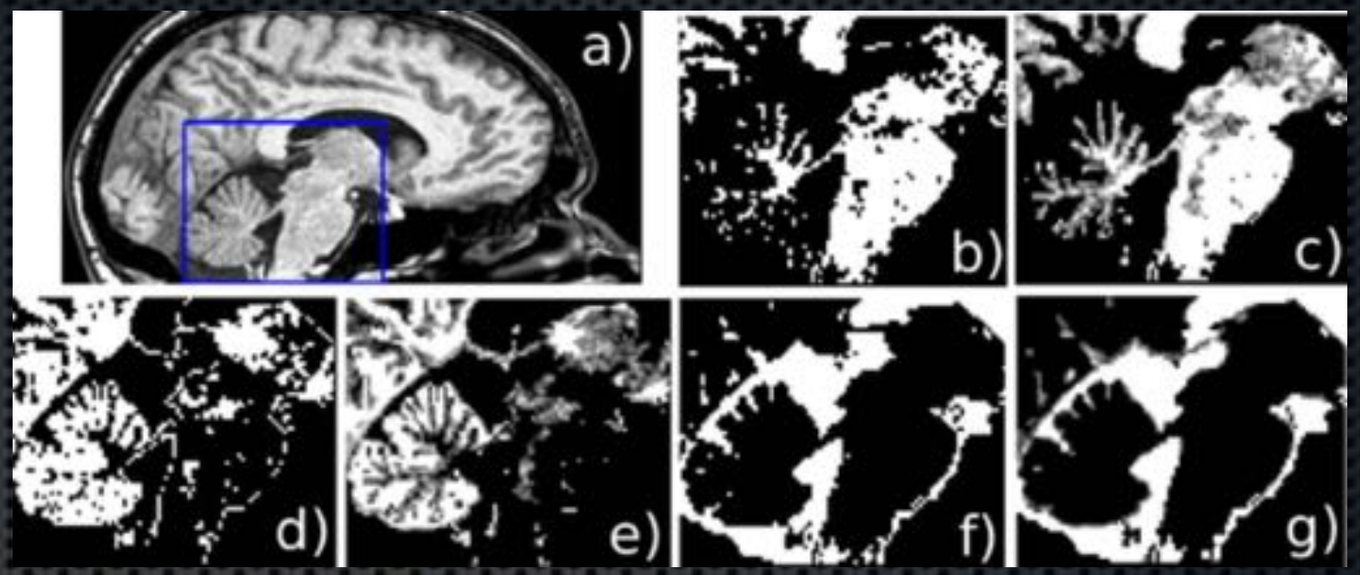
Solution: gm/wm interface seeding

- Seeding from the wm/gm interface

  reduces the shape, size & length biases

[Smith et al. NeuroImage 2012-2014] [Girard et al. NeuroImage 2014]

Position bias

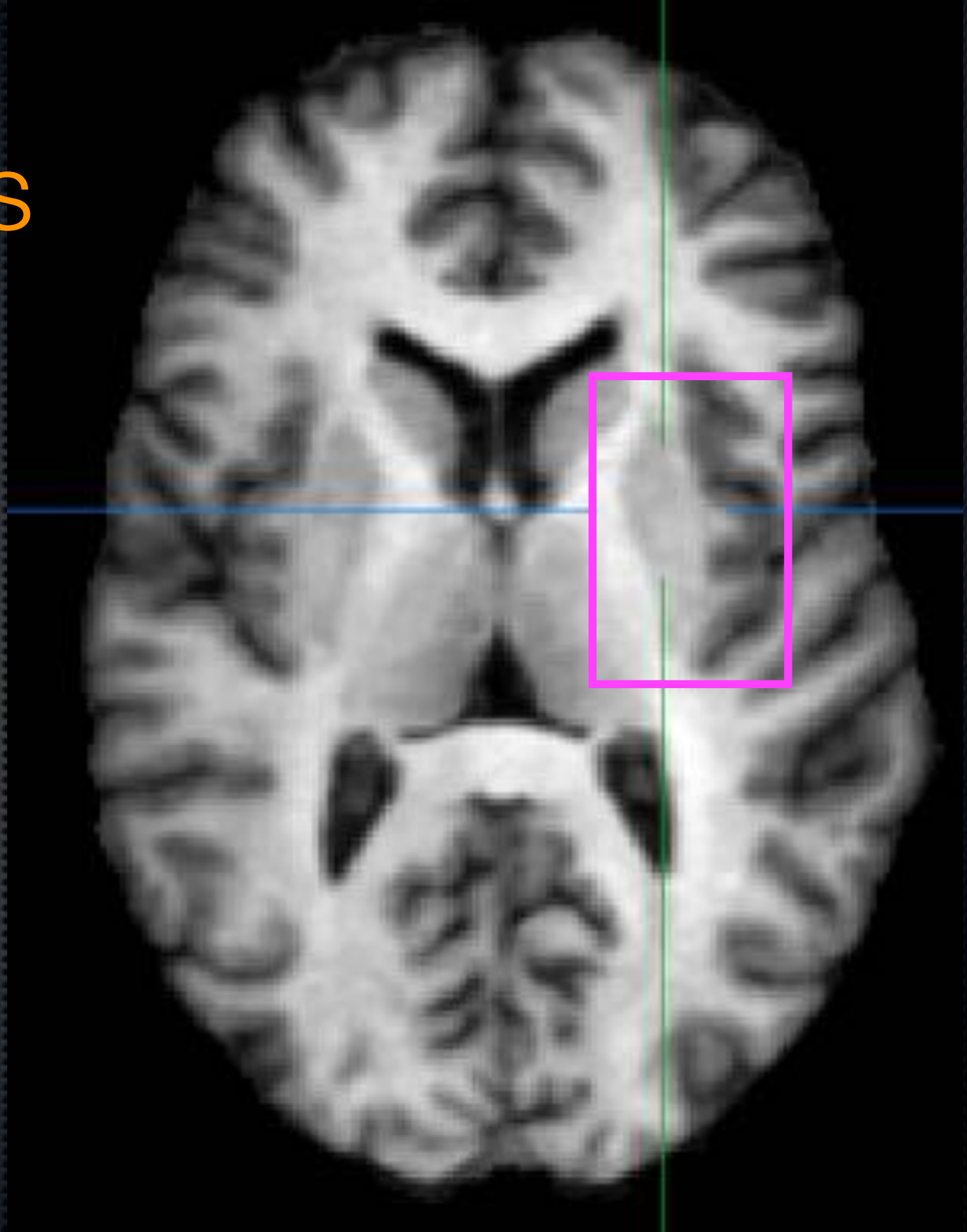


- Streamlines
  - near the cortex
  - in deep structures (nucleii, brainstem)
  - in & out of the cerebellum

  are an **open challenge**:
    - harder to track
    - under-represented in the tractogram

Position bias

Position bias



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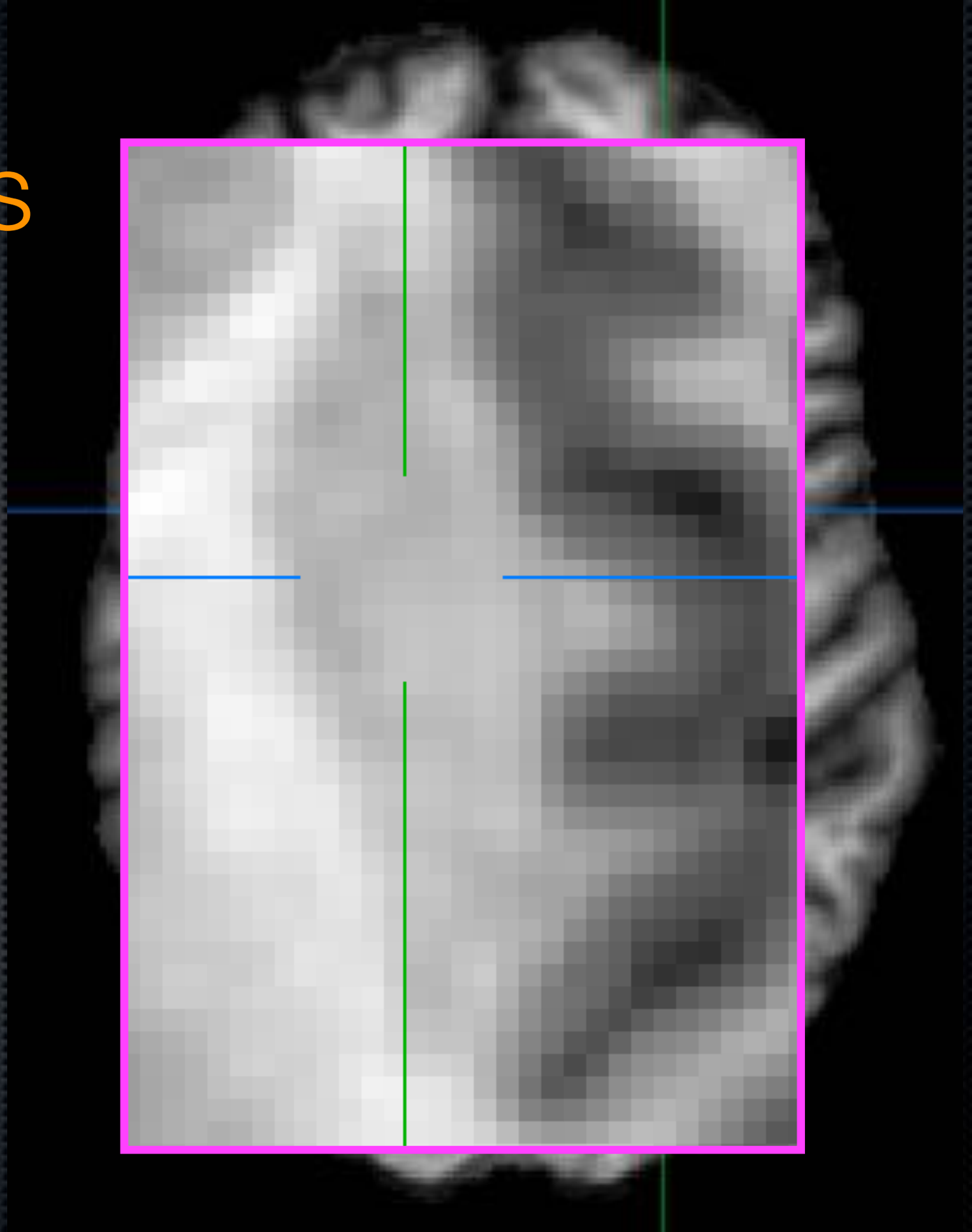

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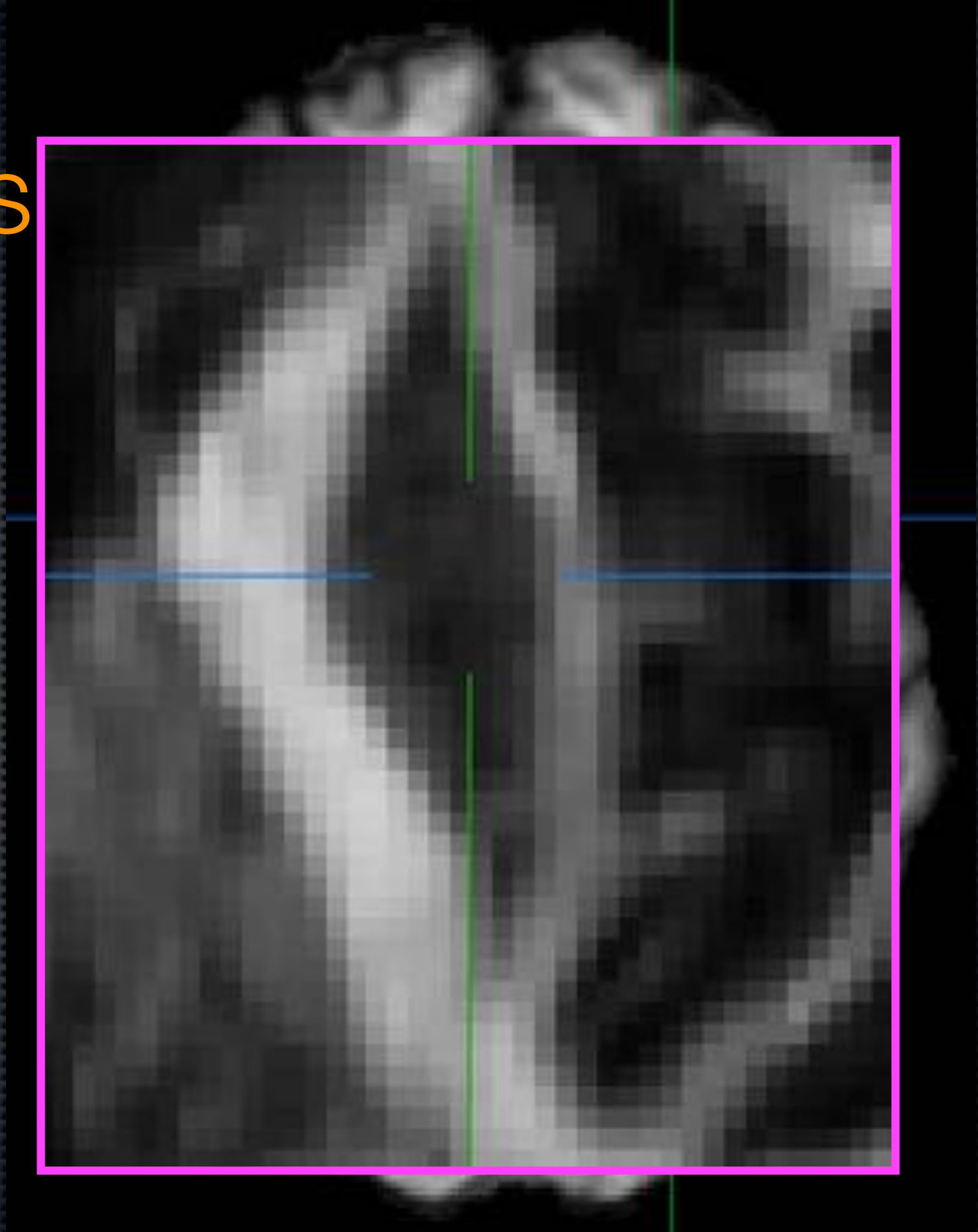
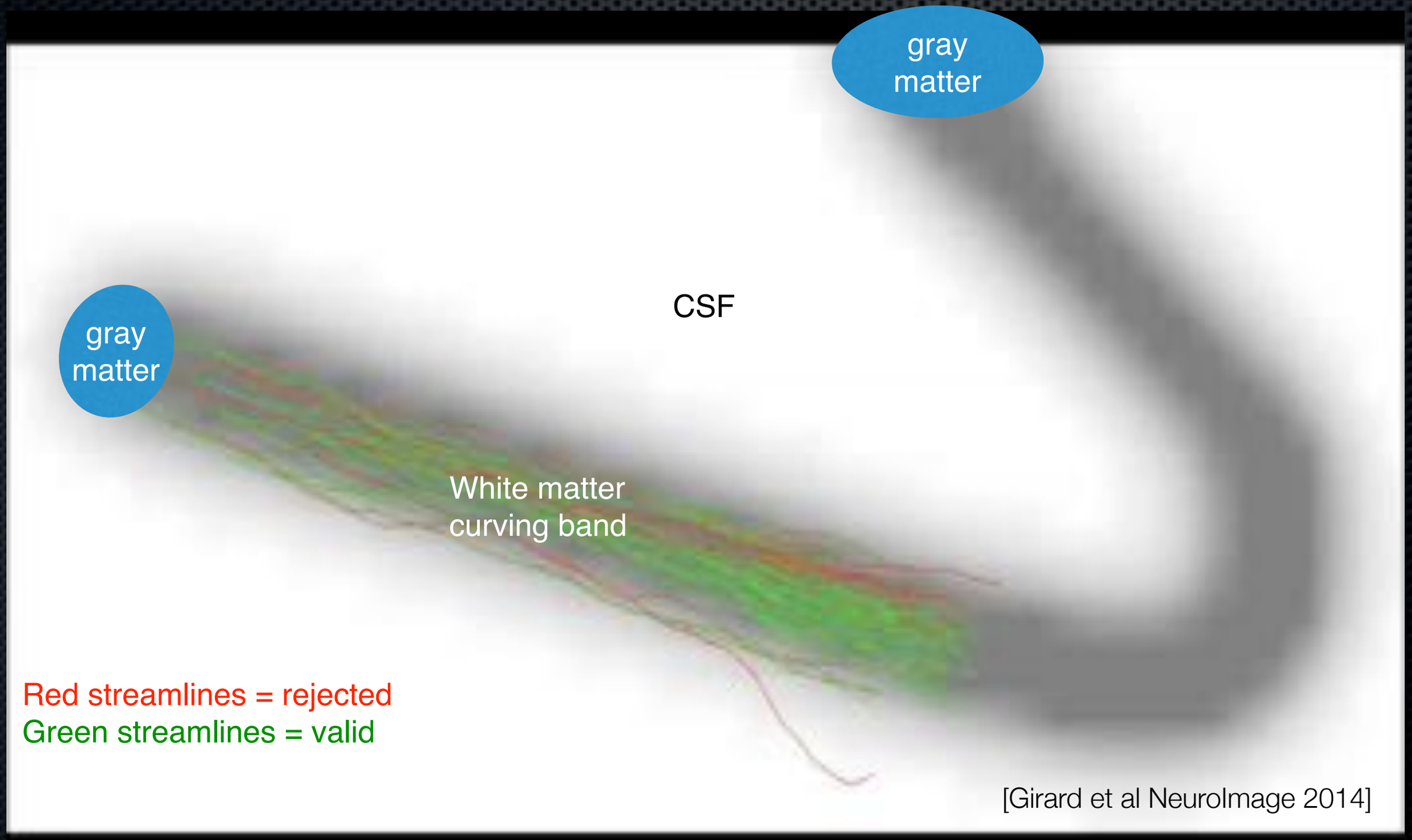


Particle filtering tractography (PFT)

Reducing shape bias

- Better management of boundaries, curving & stopping criteria



[Girard et al NeuroImage 2014]

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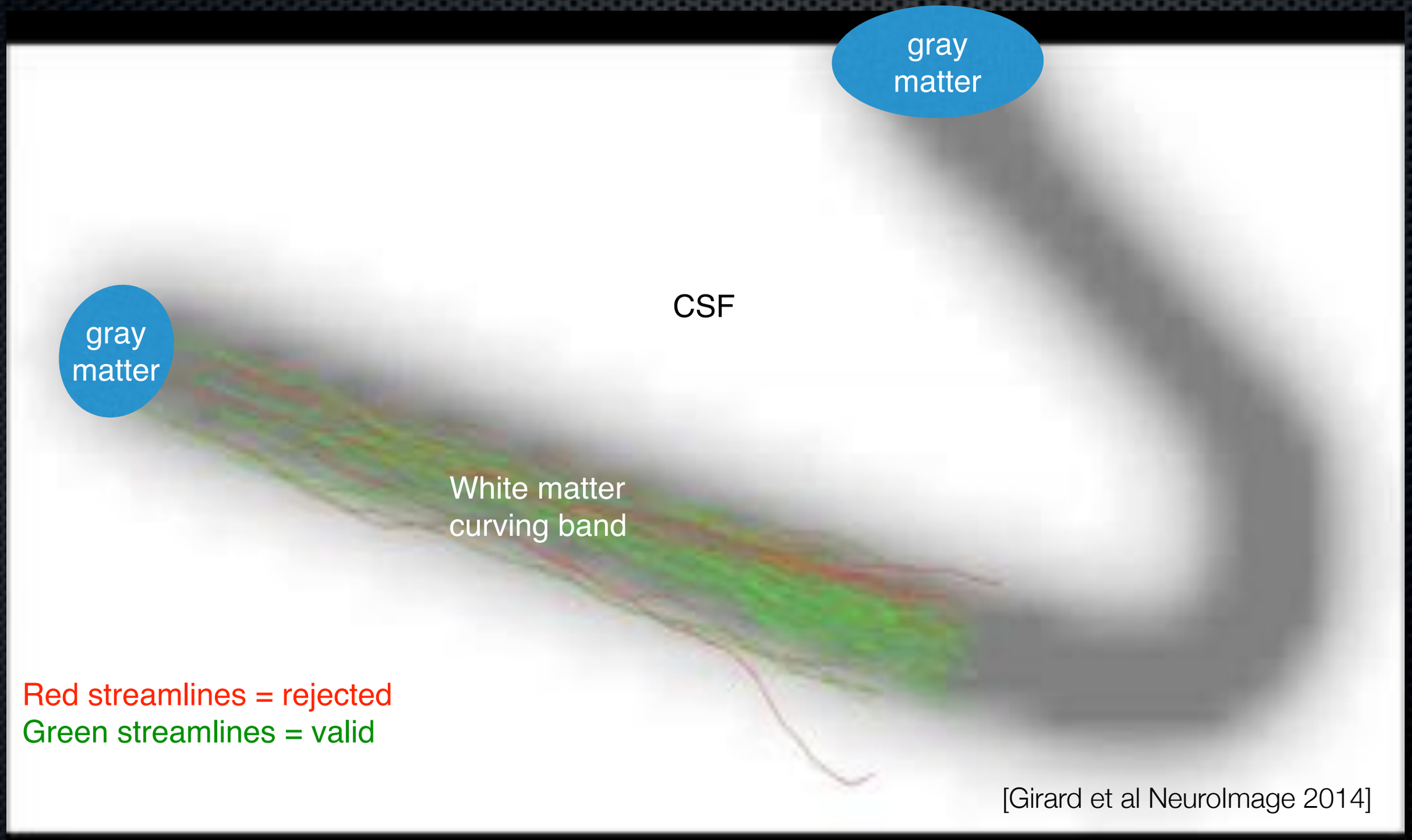


[Girard et al NeuroImage 2014]

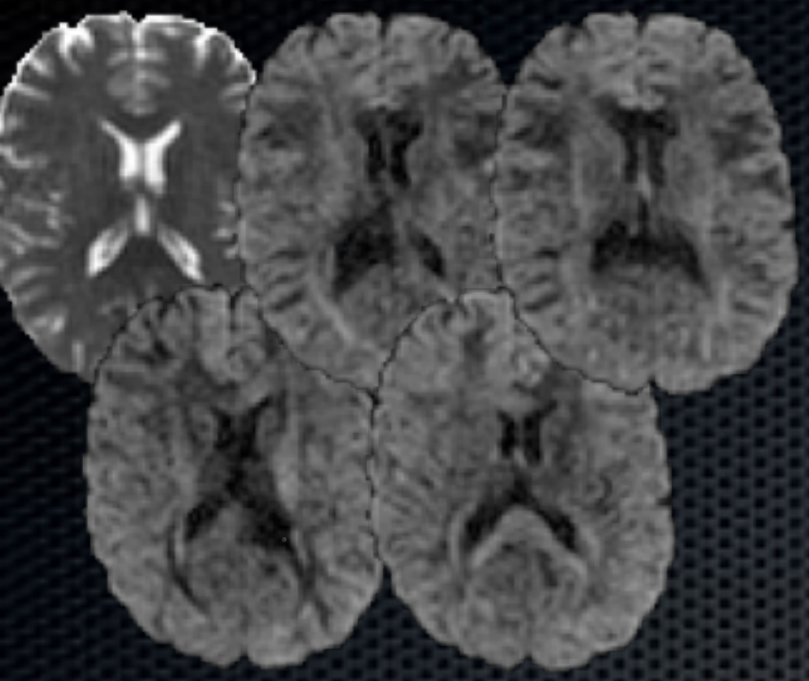
Particle filtering tractography (PFT)
with anatomical priors
with interface seeding
with PVE maps for stopping

[Gabriel Girard]

helps to reduce the positional bias

[Girard et al NeuroImage 2014]

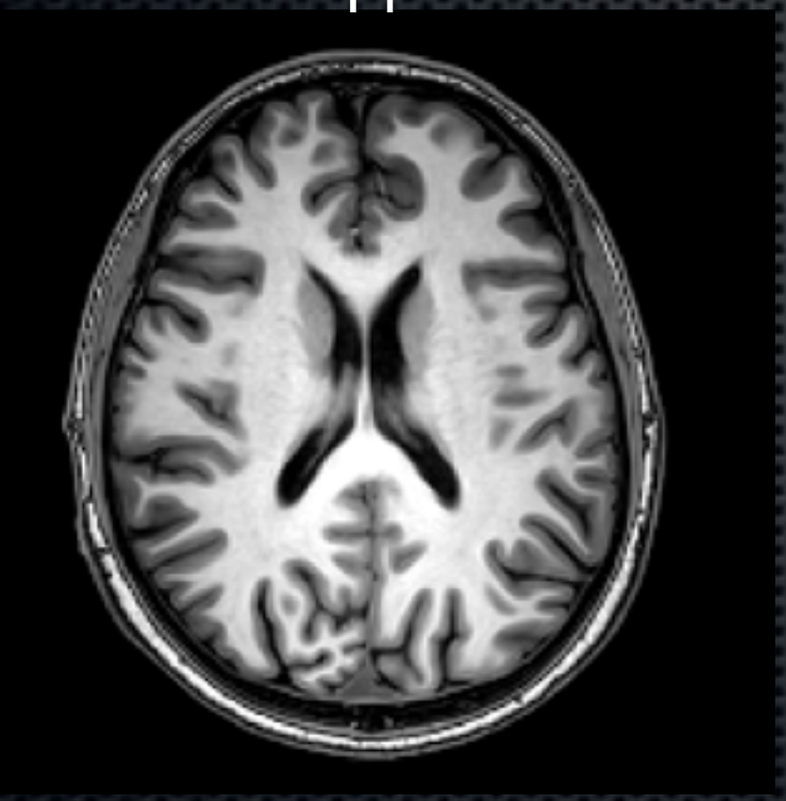
Connectomics - Structural connectivity



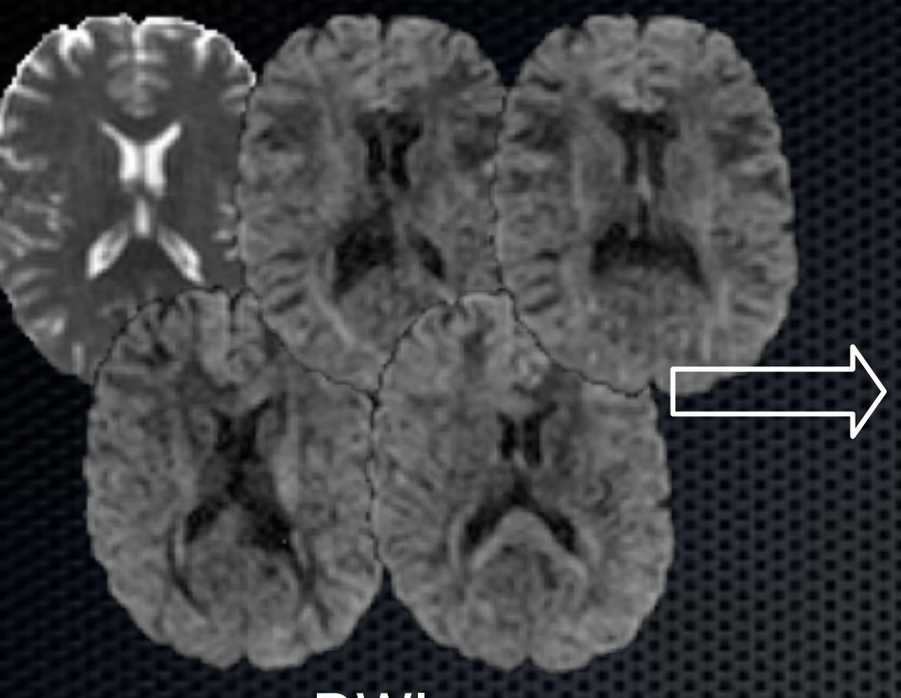
DWI

+

T1



tractogram



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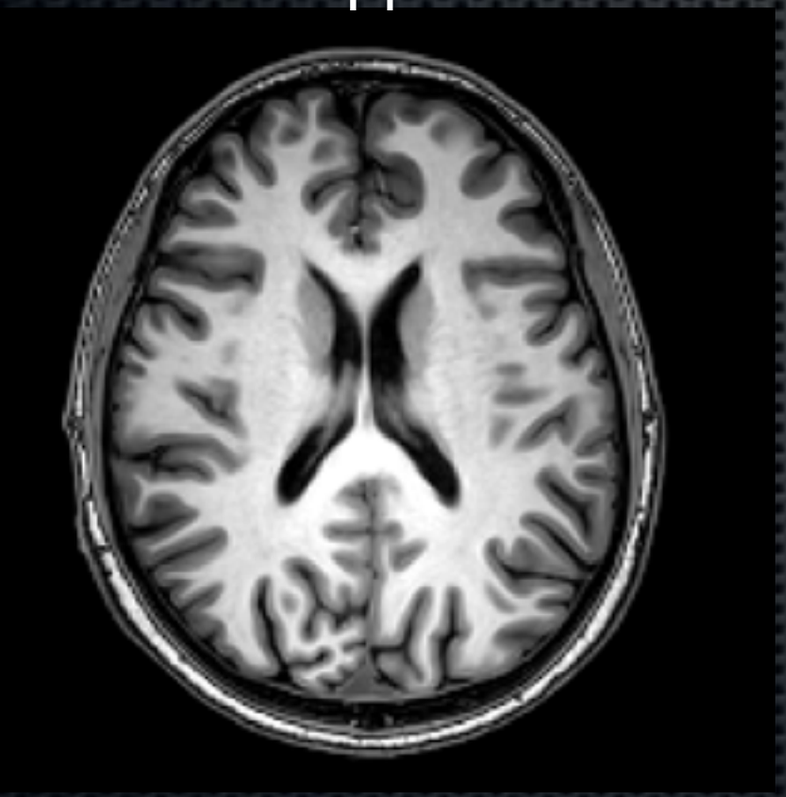

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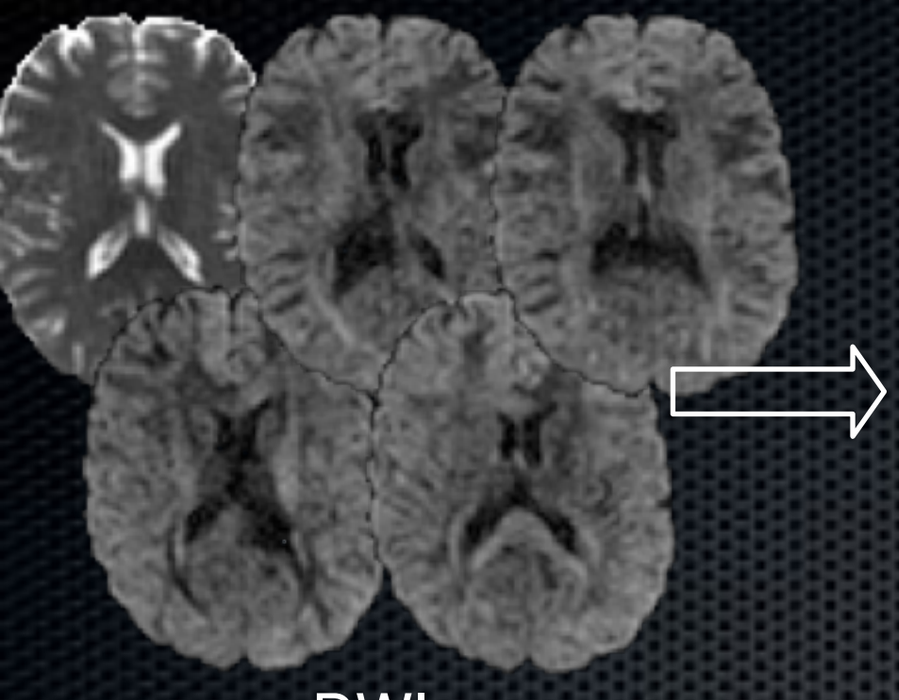

DWI

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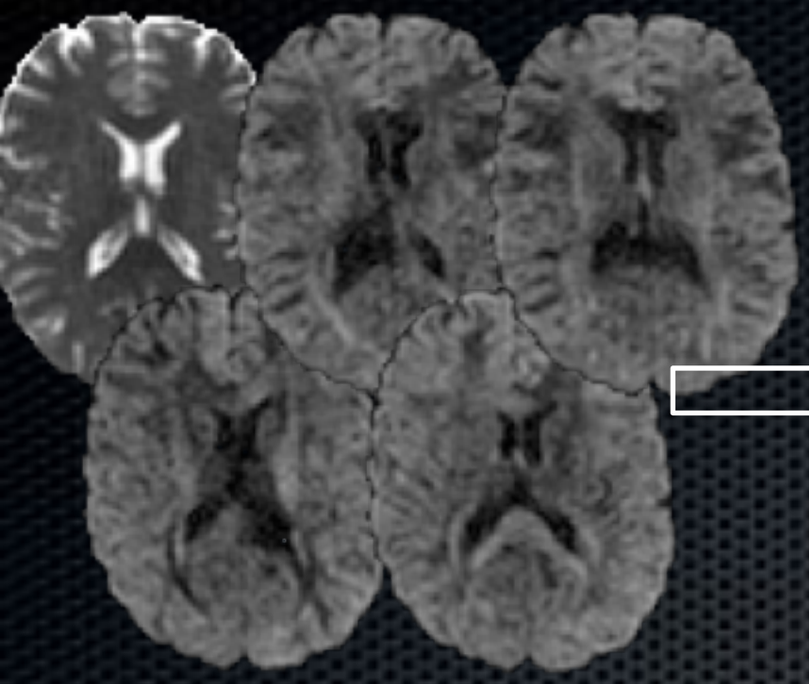
T1

Cortical parcellation

tractogram



DWI

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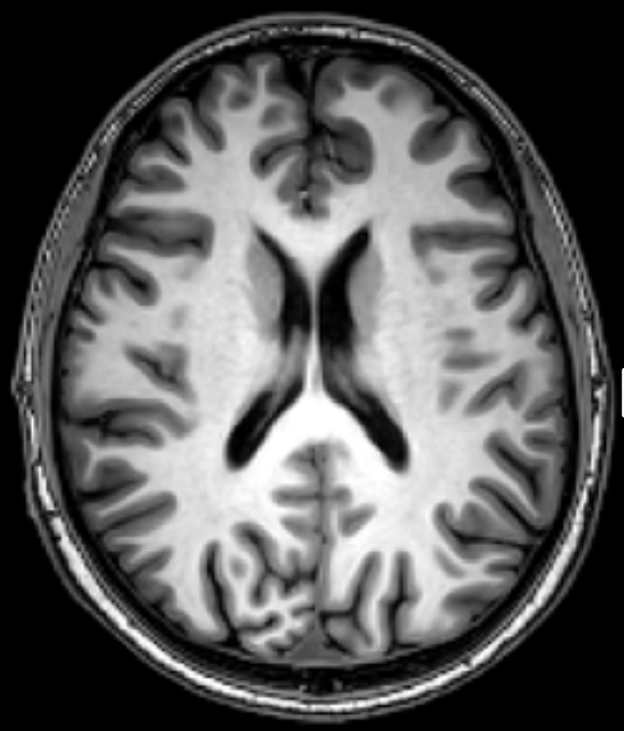
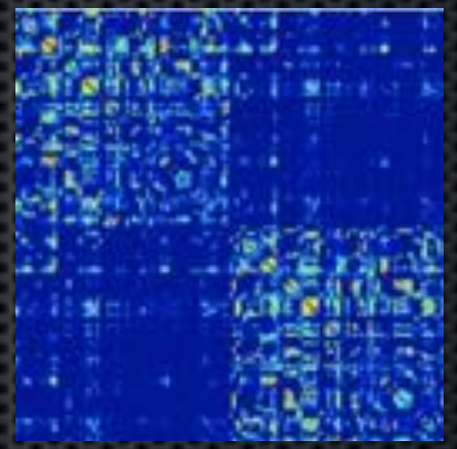
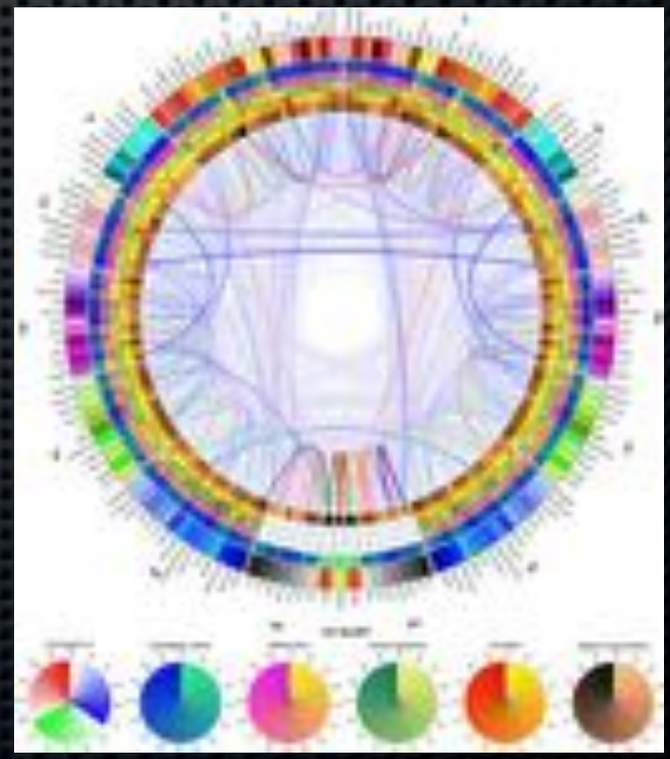
T1







Structural connectome

Cortical parcellation

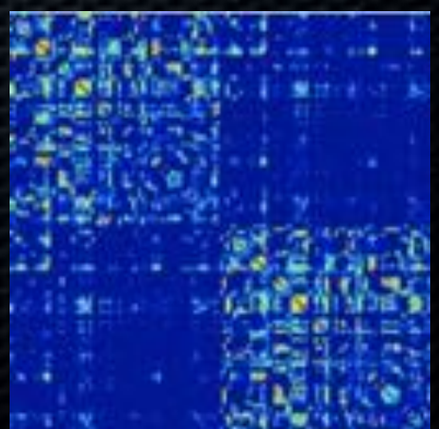
Structural connectivity reproducibility through multiple acquisitions

Authors:
Girard, G., Whittingstall, K., Deriche, R., Descoteaux, M.

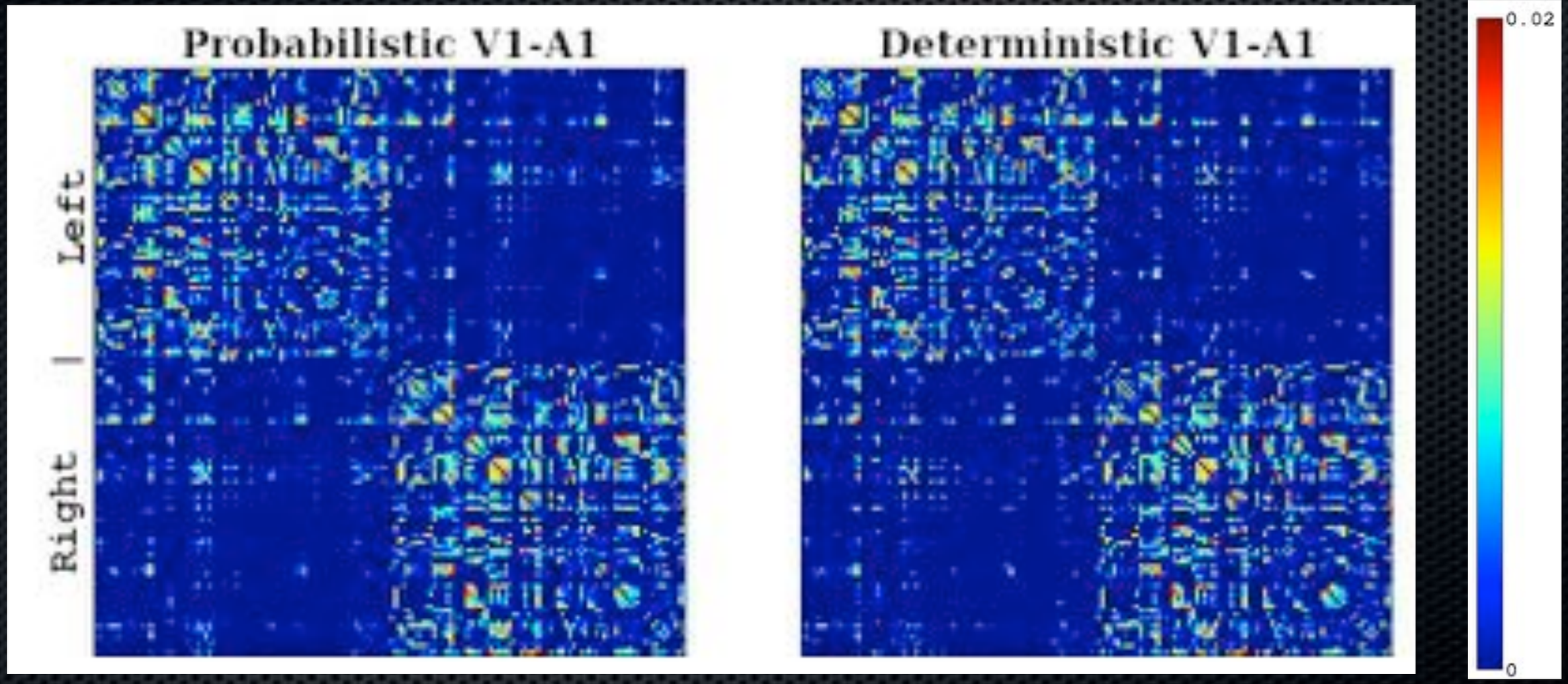
[Gabriel Girard]

- 11 subjects - 3 times points
- Tractography (det/prob, wm/int)
- 150 cortical regions dilated by 2mm of the Destrieux atlas (*Freesurfer*) *without subcortical areas*

- *Count tracts between ROIs* to produce 150x150 connectivity matrix



Normalized tract count
sum(C_{ij}) = 1



C_{ij} C_{ij}

[Girard, Descoteaux et al., HBM 2015]

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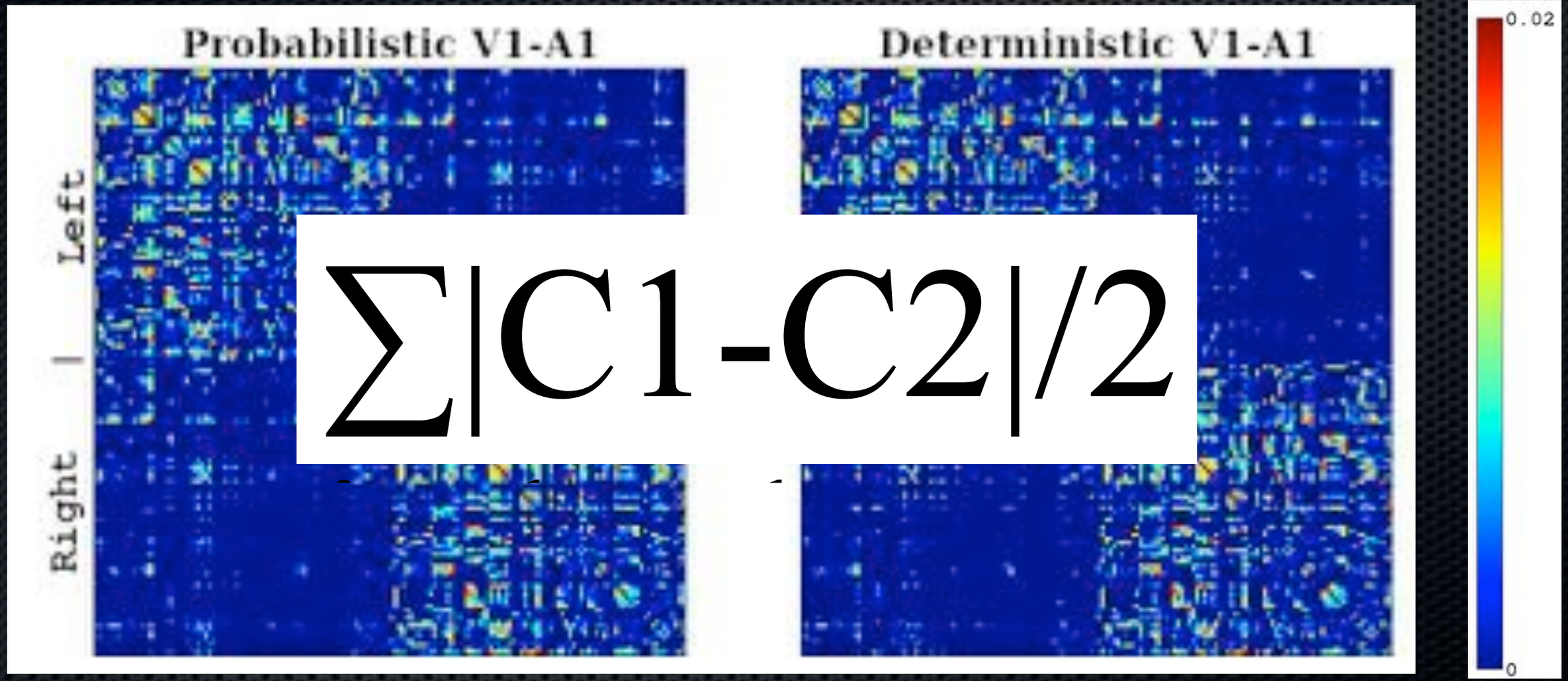

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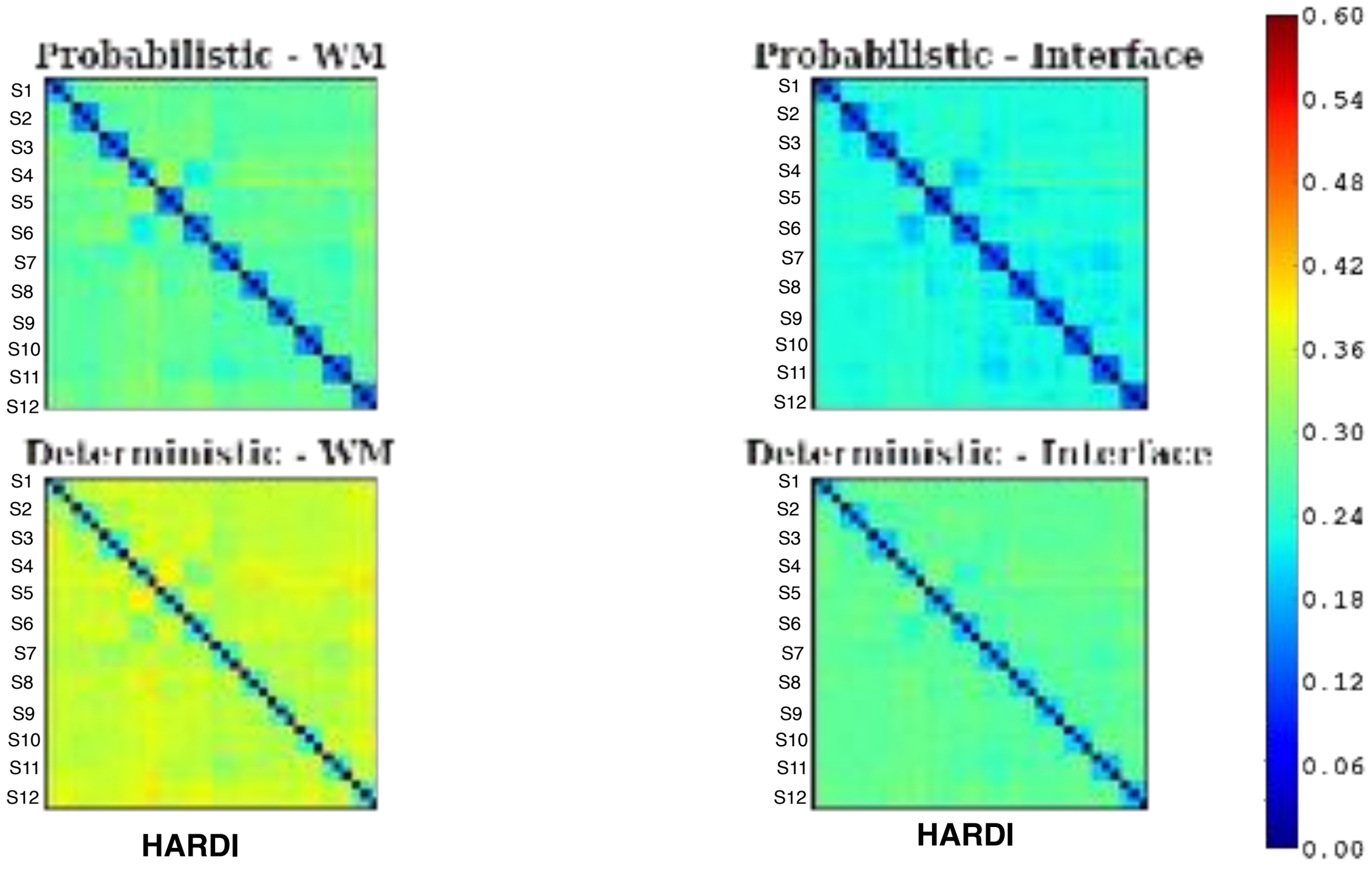
One of the 11 subjects scanned 1 year later - Can you find him?



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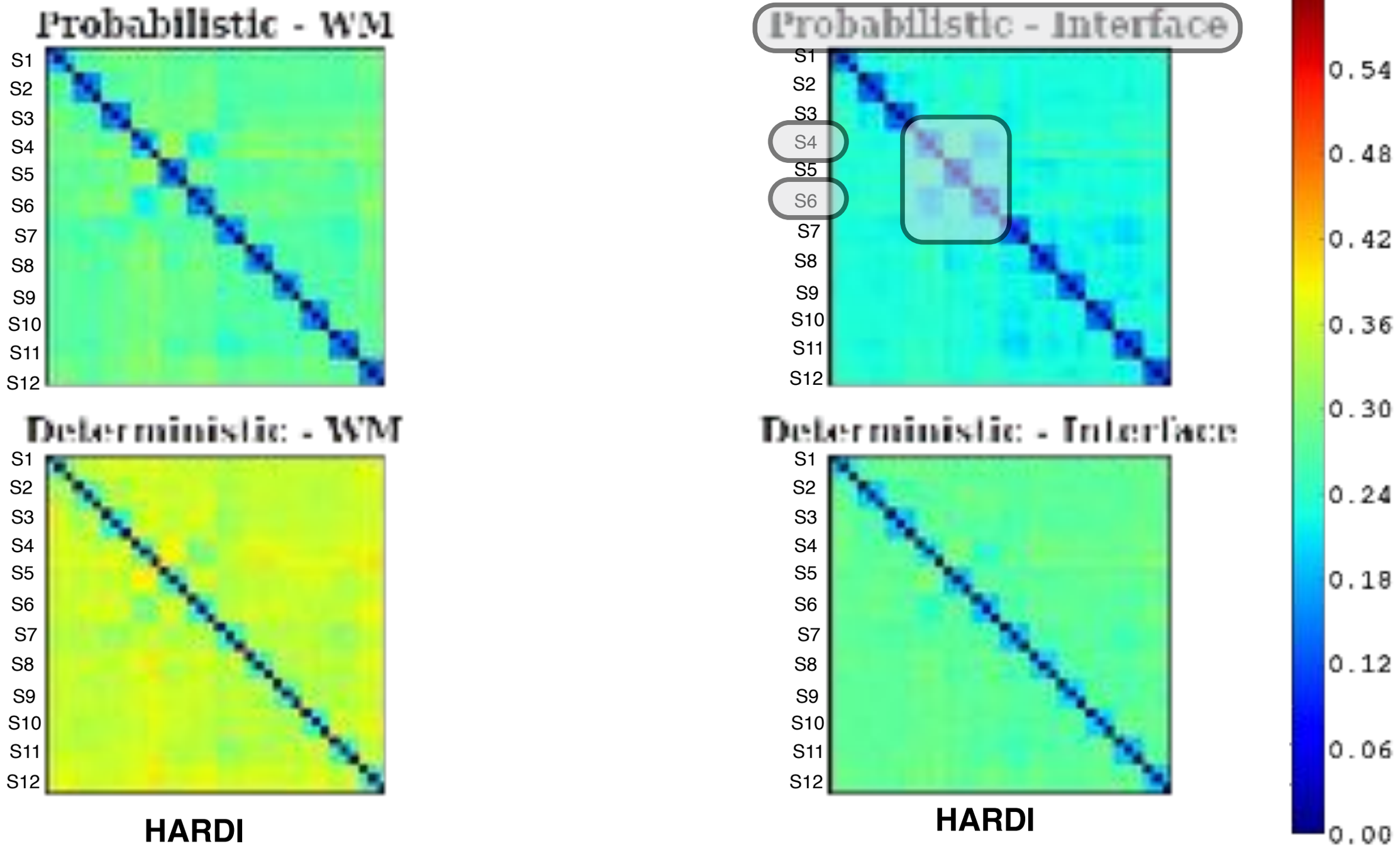

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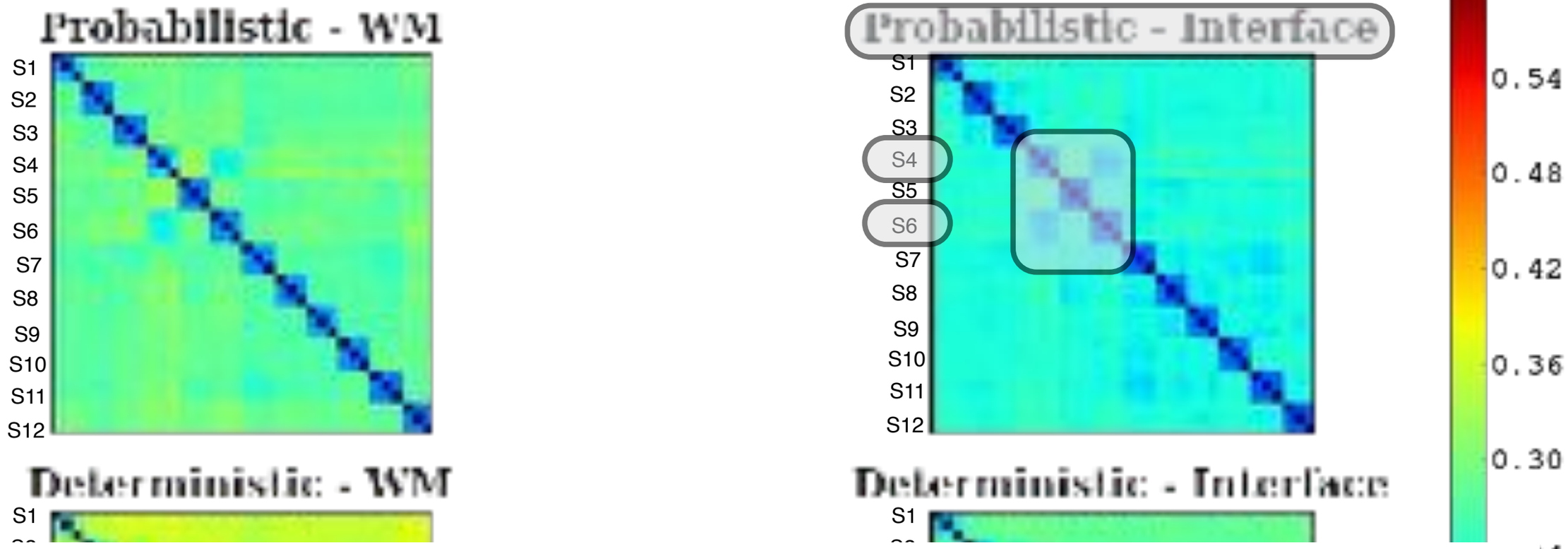
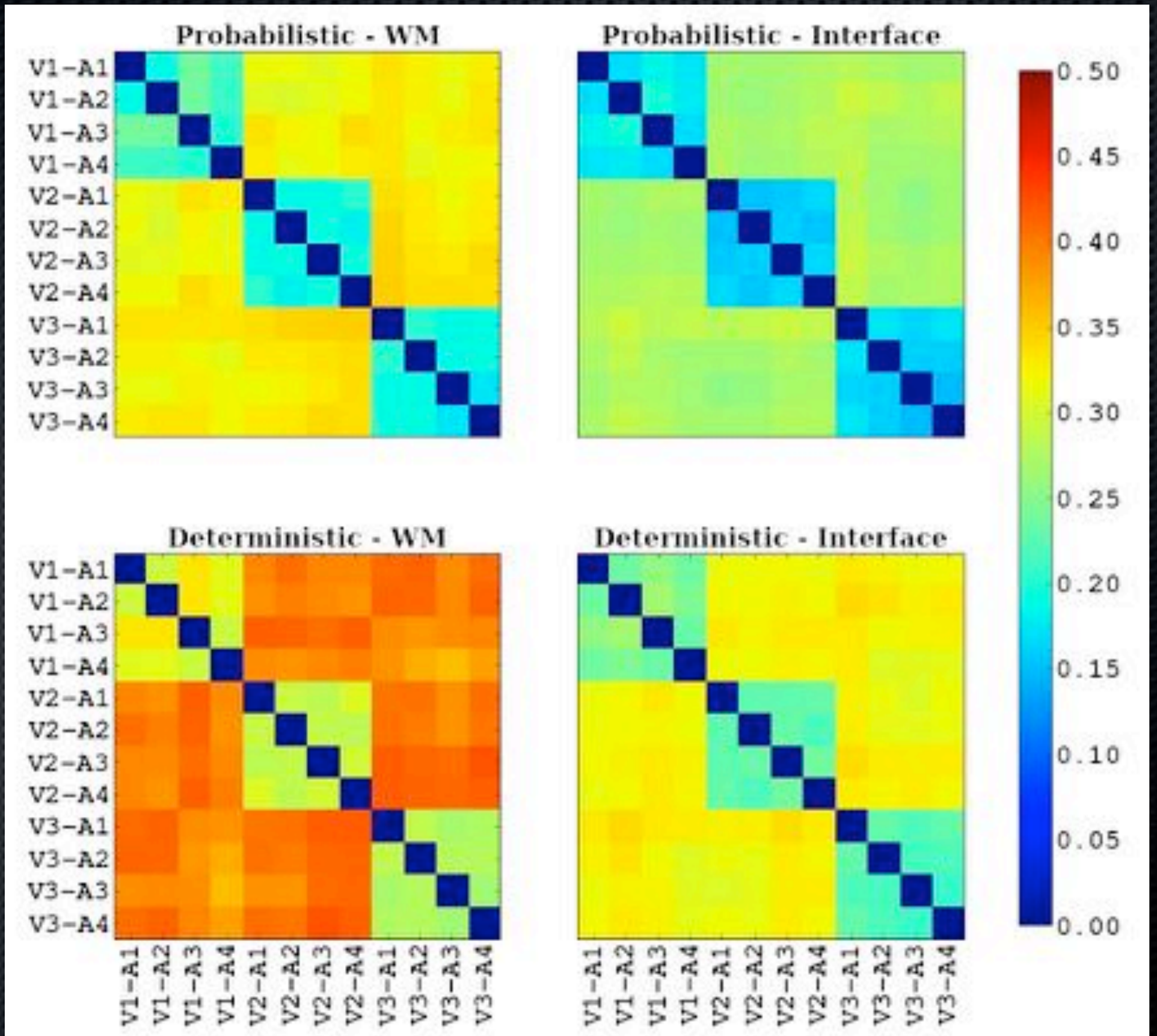


	Tractography			
	Deterministic		Probabilistic	
	WM	Interface	WM	Interface
Inter-subject distance	39.9%	32.3%	32.7%	27.3%
Intra-subject distance	29.4%	23.2%	19.9%	16.8%
Dunn index	1.36	1.39	**1.64**	**1.63**

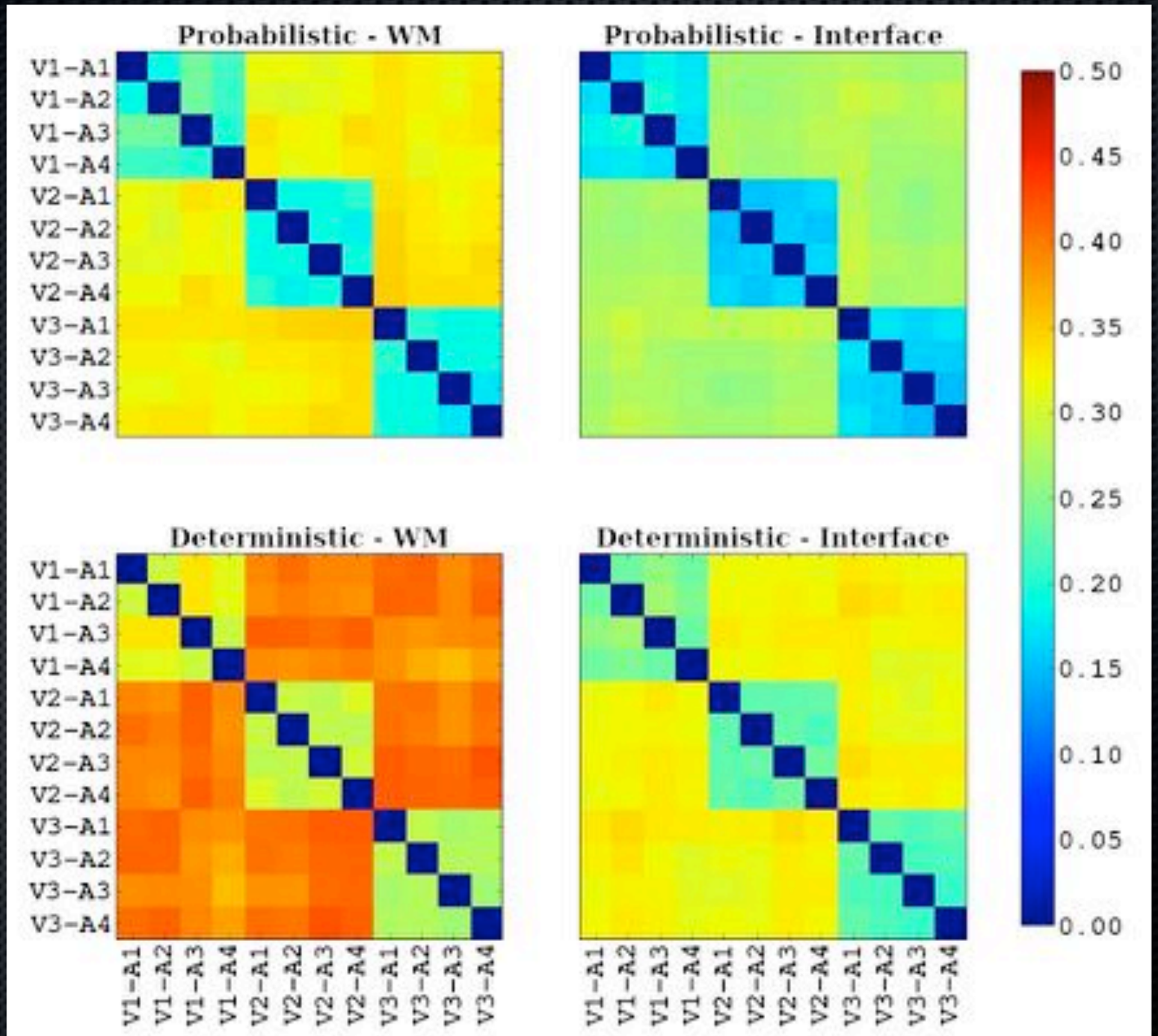
3 subjects
4 time points



3 subjects
4 time points

At best,
15% from
myself

30% from
neighbor



Open challenge! Reducing variability

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4 time points

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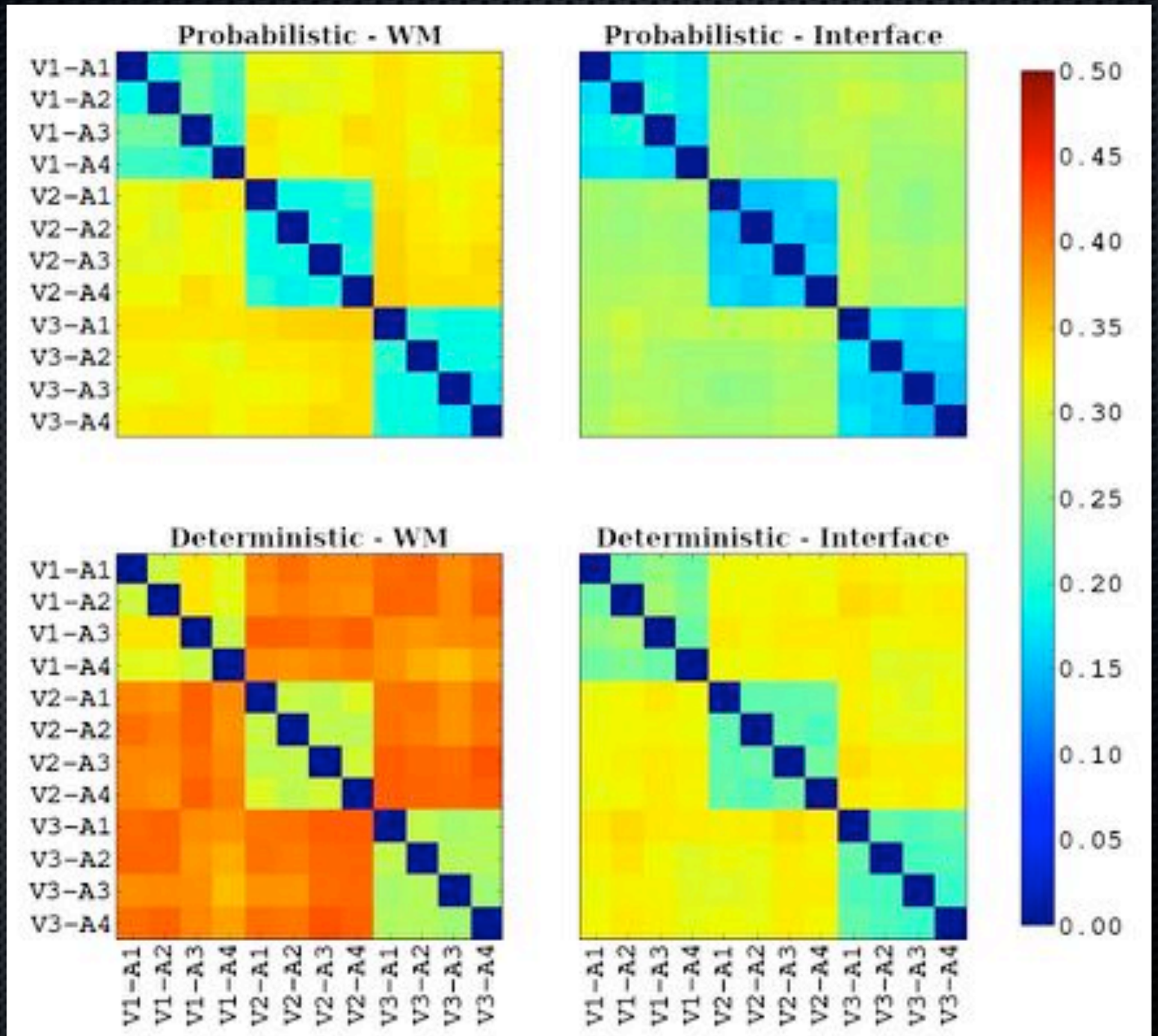

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- **No connections**
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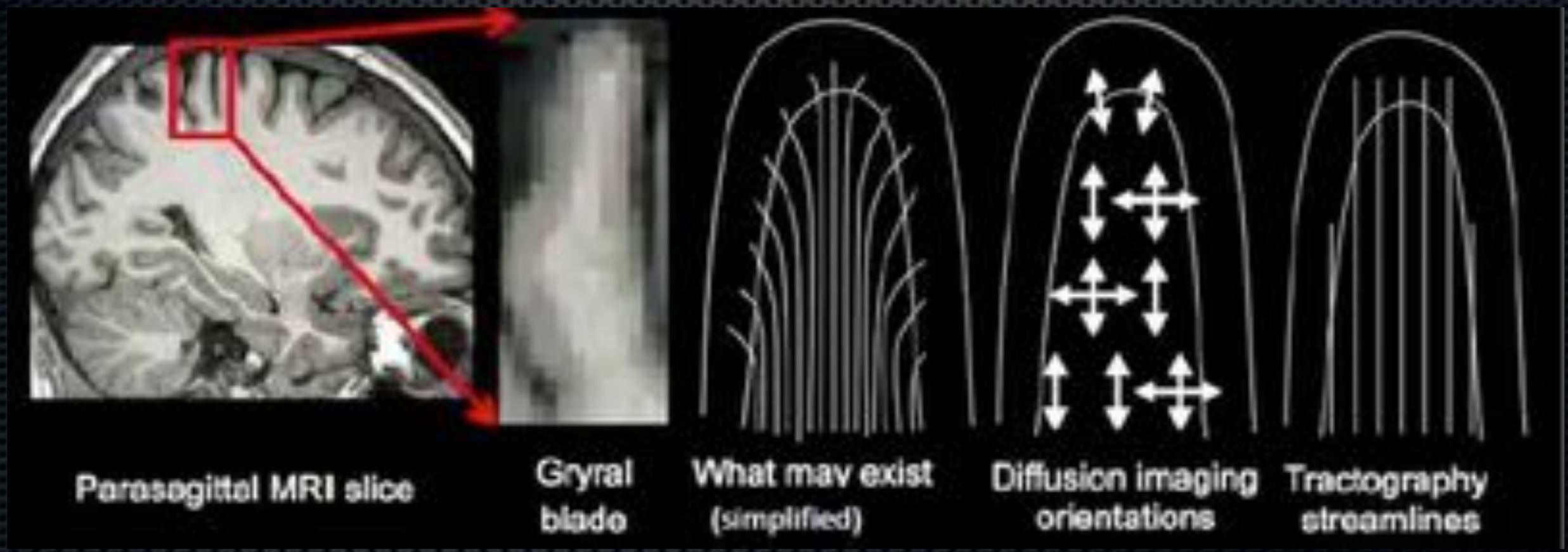
  - Shape bias
  - Position bias (gyral bias, partial volume areas)
- **Invalid connections**

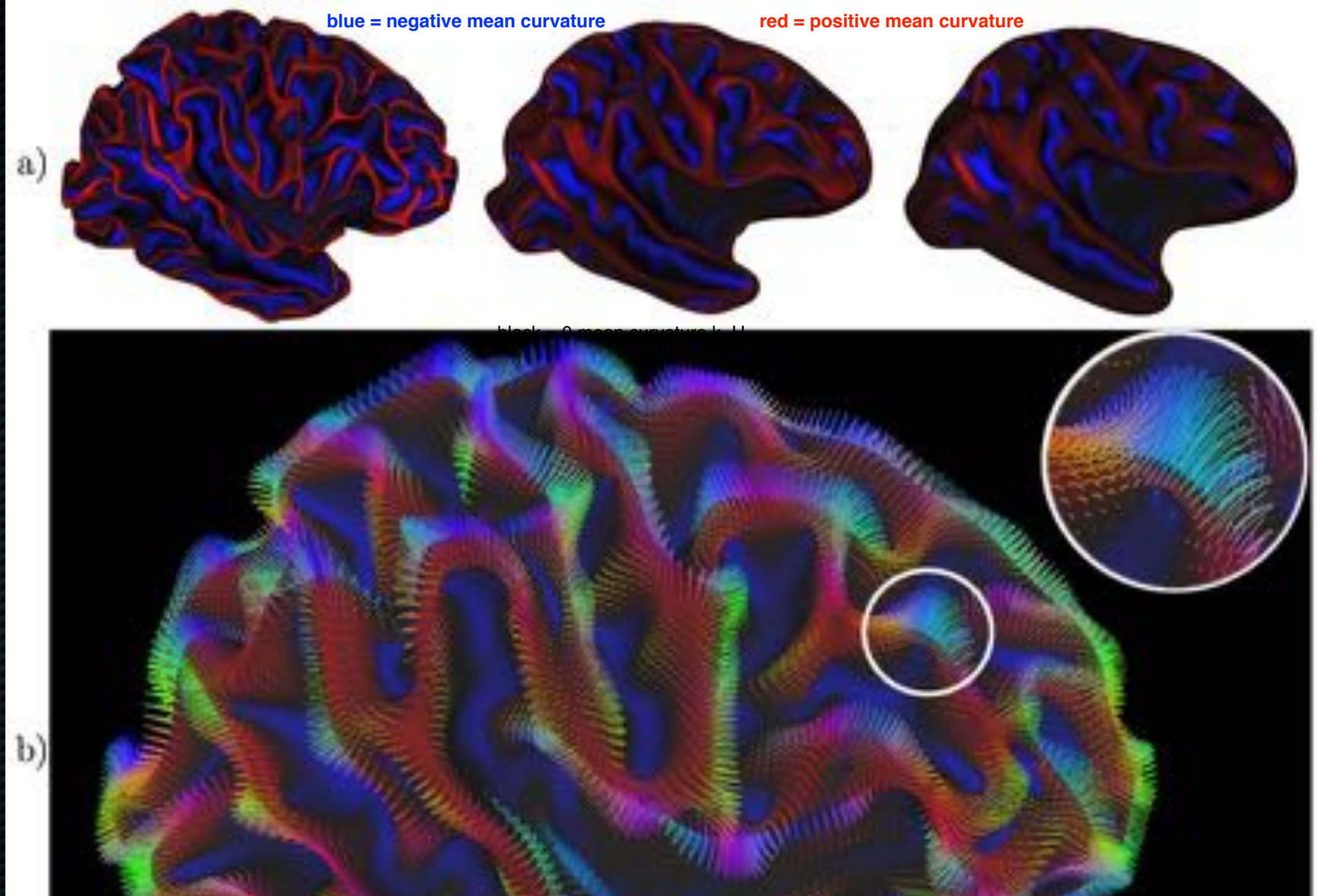
Position bias :

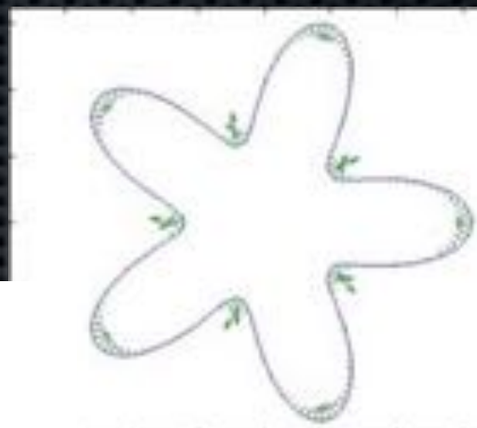
the gyral bias



1mm isotropic

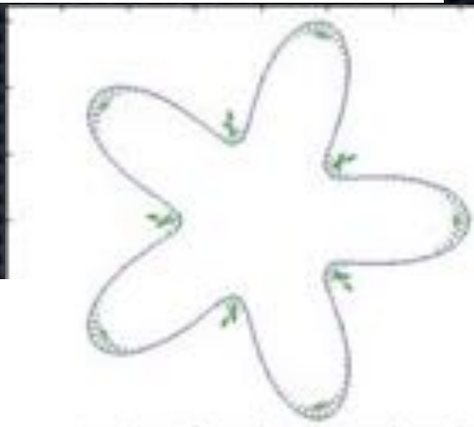
Mean-curvature flow

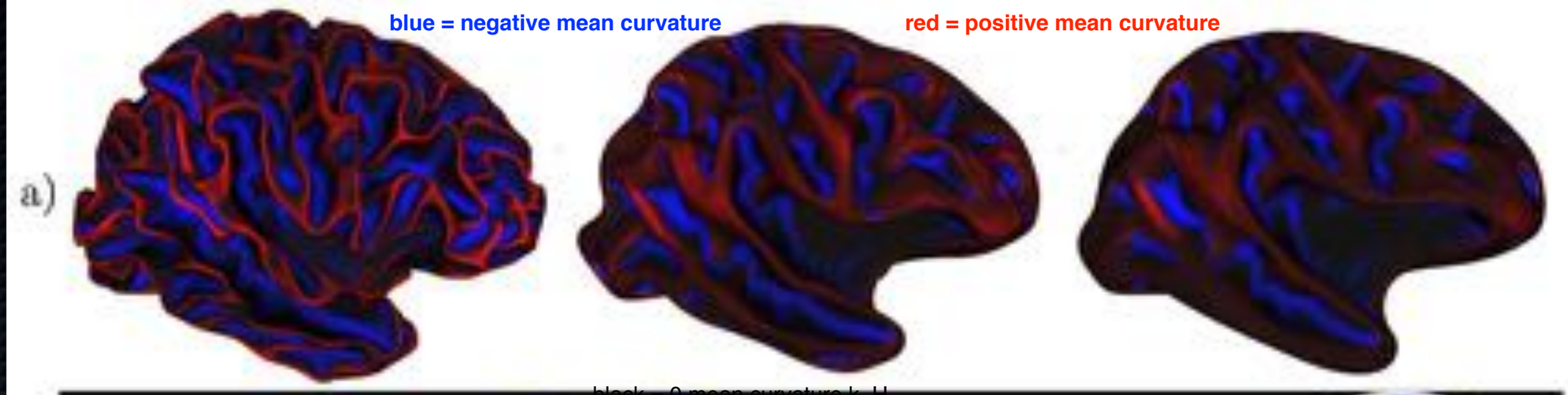


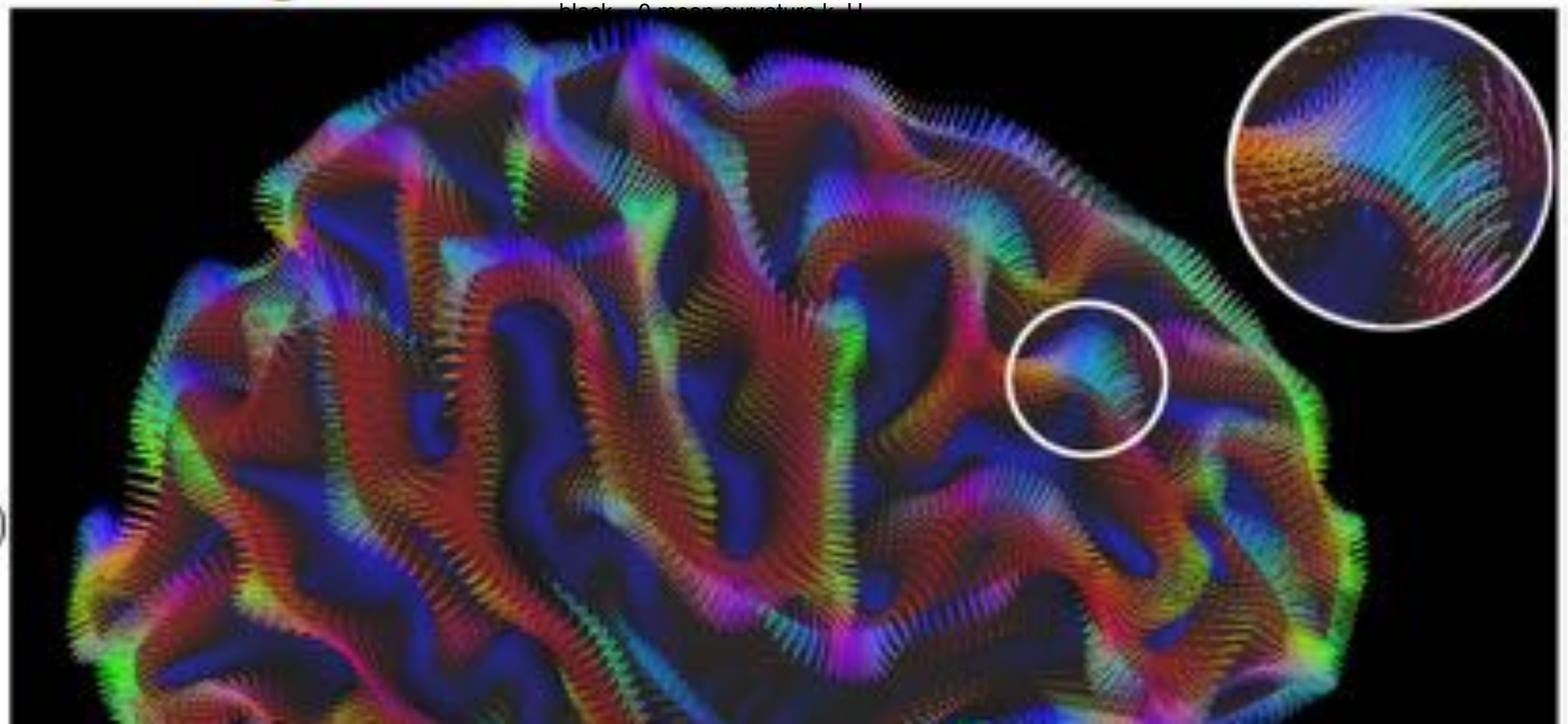


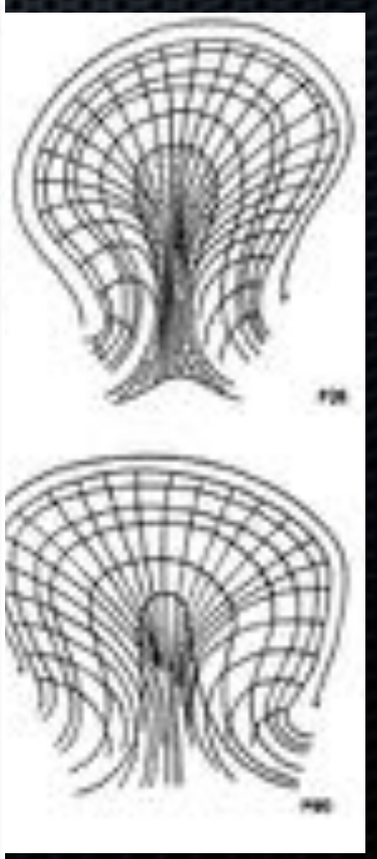
Mean-curvature flow

$$\frac{\partial}{\partial t}\mathcal{S} = -\lambda \cdot \kappa_H \cdot \mathbf{n}$$

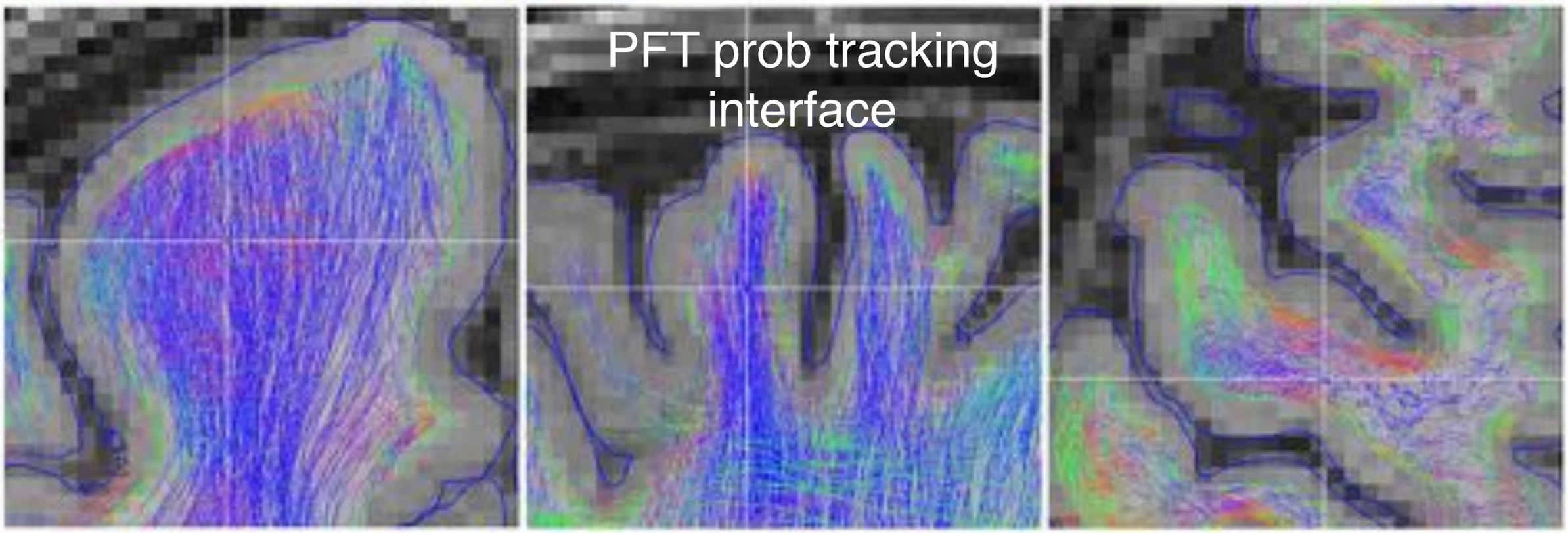


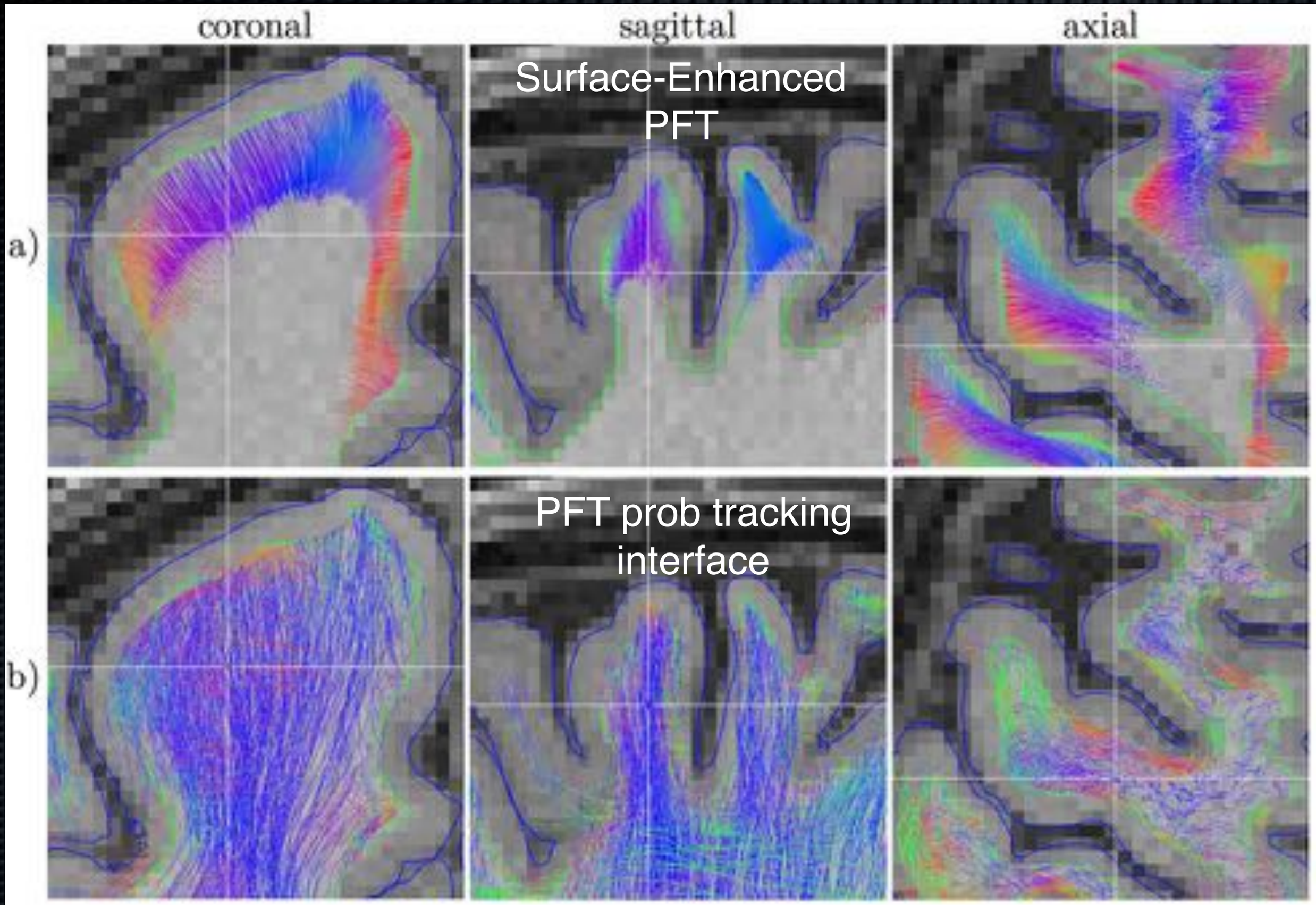


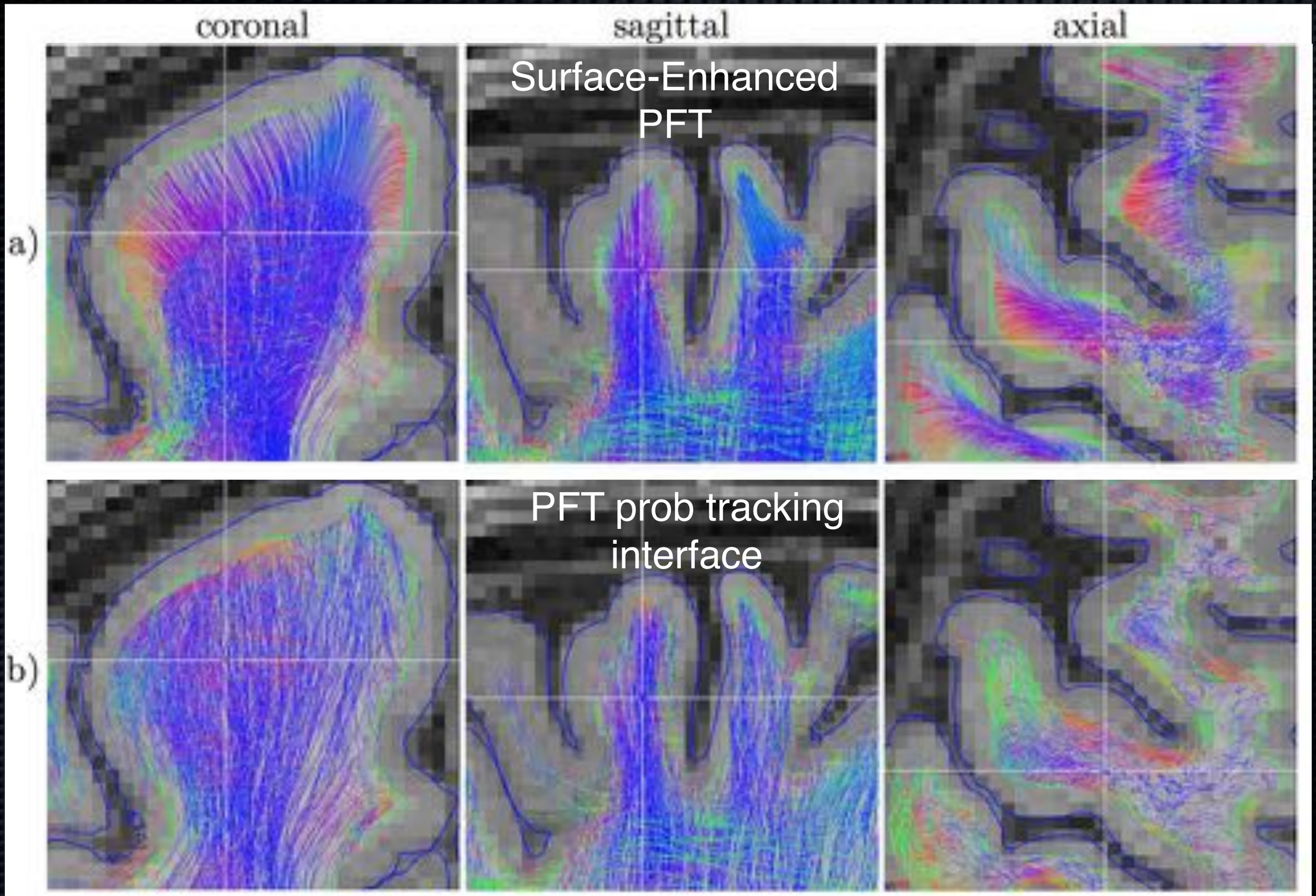




b)




coronal
sagittal
axial
a)
Surface-Enhanced
PFT
b)
PFT prob tracking
interface


coronal
sagittal
axial
a)
Surface-Enhanced PFT
b)
PFT prob tracking interface

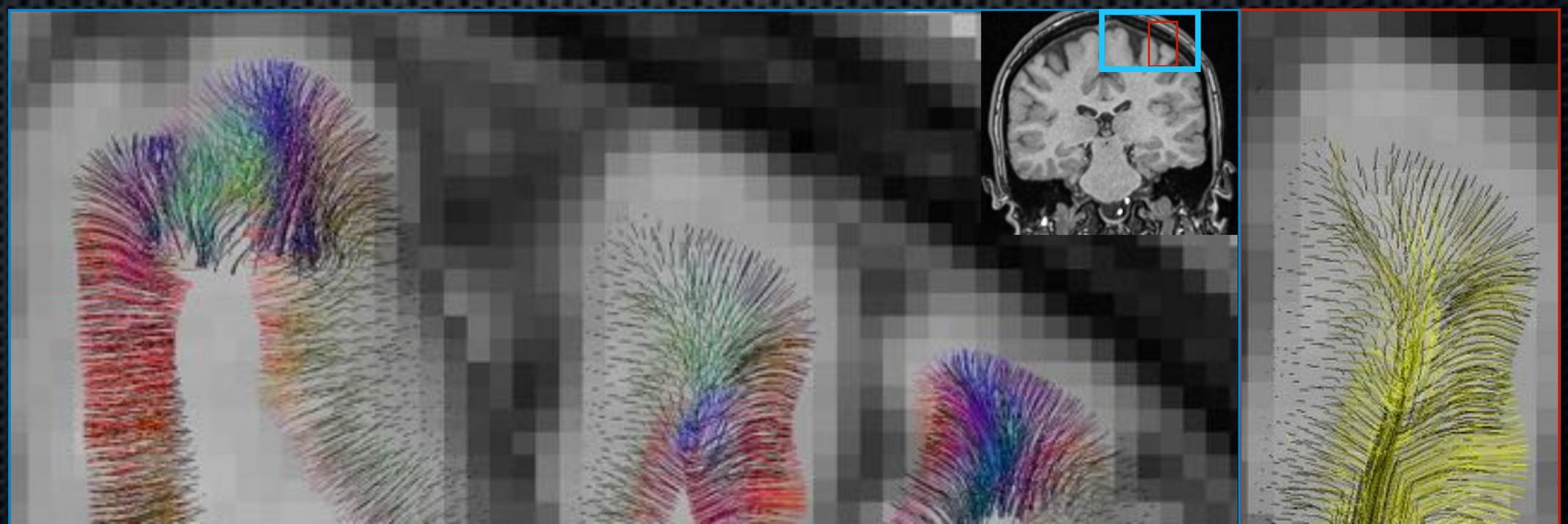
Surface-Enhanced Tractography

Etienne St-Onge[a], Alessandro Daducci[b], Gabriel Girard[a], Maxime Descoteaux[a]

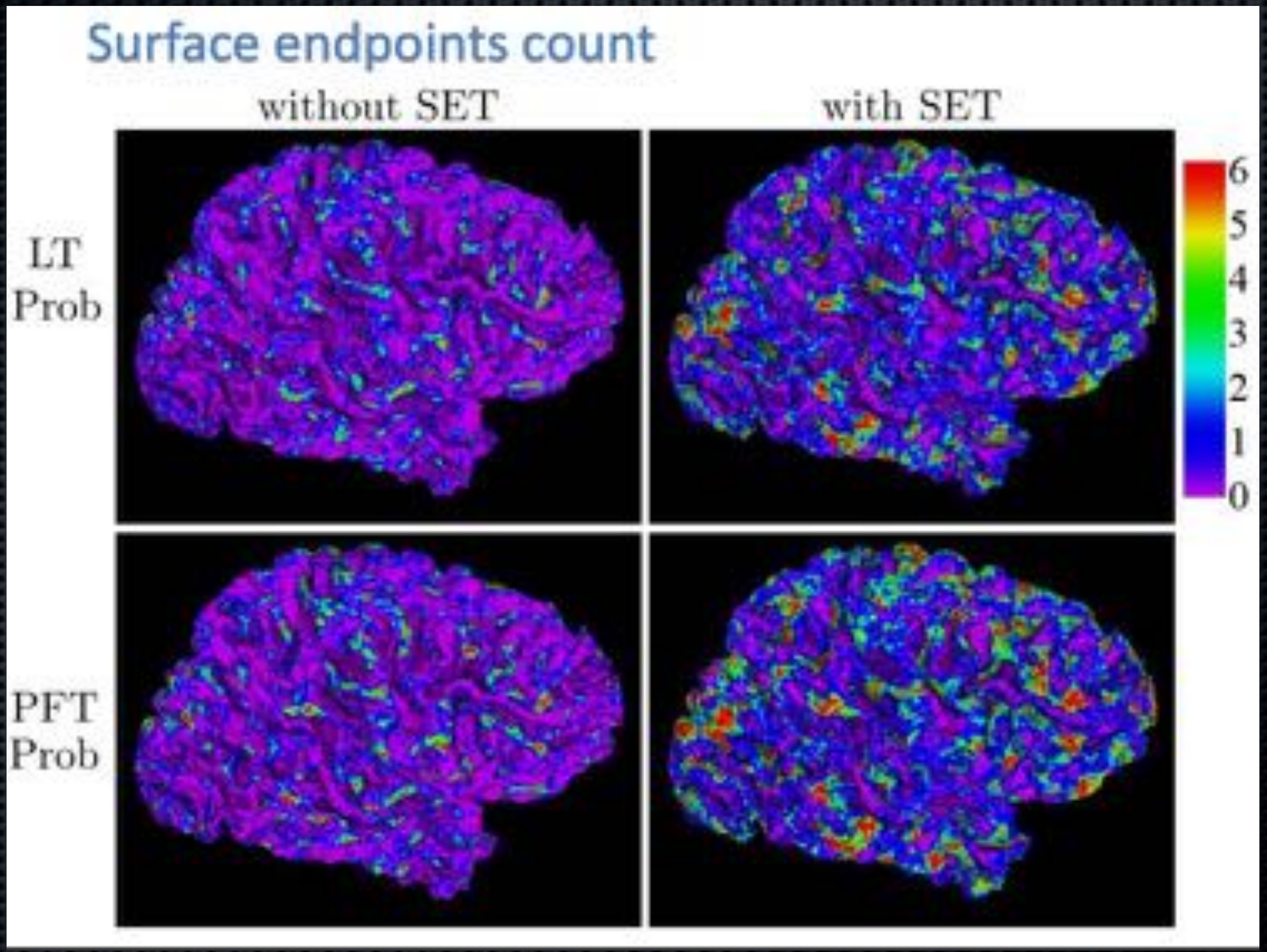
Reducing gyrial bias

[St-Onge et al ISMRM
NeuroImage
(under minor review)]

- More uniform cortical coverage by streamlines
- Improves test-retest of connectome (better reproducibility) increases the inter/intra ratio from 1.6 to 2.0
- Reduces number of small ‘broken’ streamlines, better reconstruction of longe-range connections



Open challenge (40% of empty cortex)



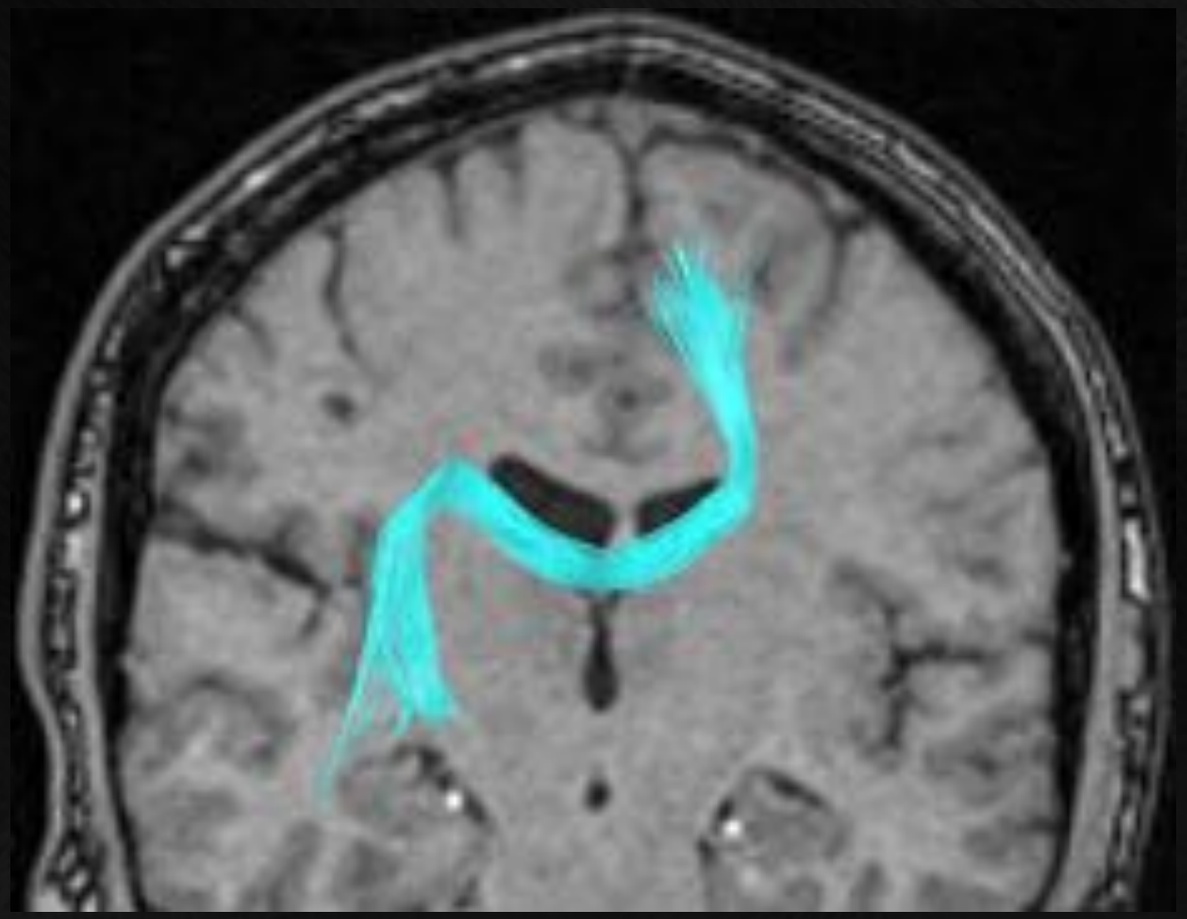
[St-Onge et al ISMRM 18]

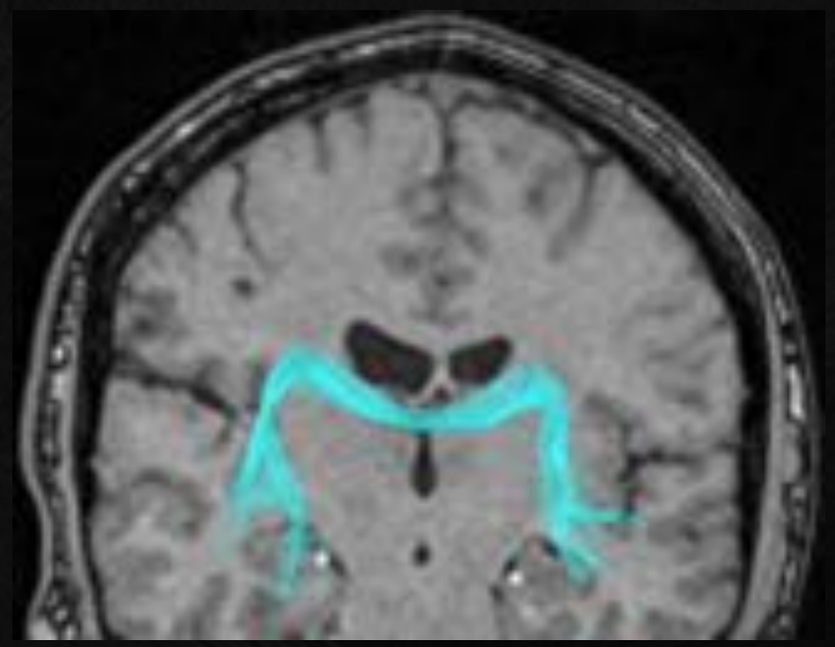
Tractography challenges

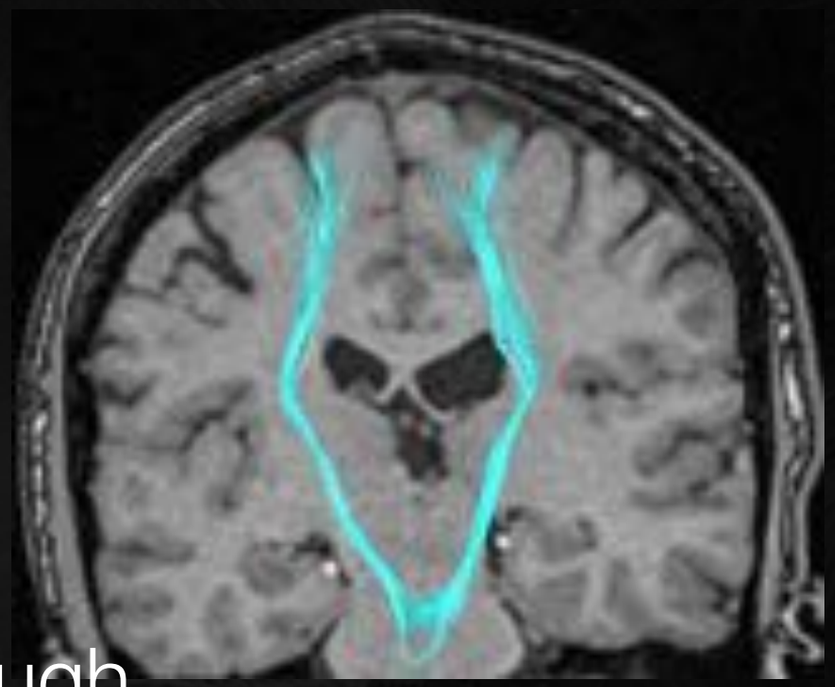
- **No connections**
- **Tractography biases**
  - Length bias
  - Size bias
  - Shape bias
  - Position bias (gyral bias, partial volume areas)
- **Invalid connections**

- invalid connections
- (false positives)

Dense Invalid Connections





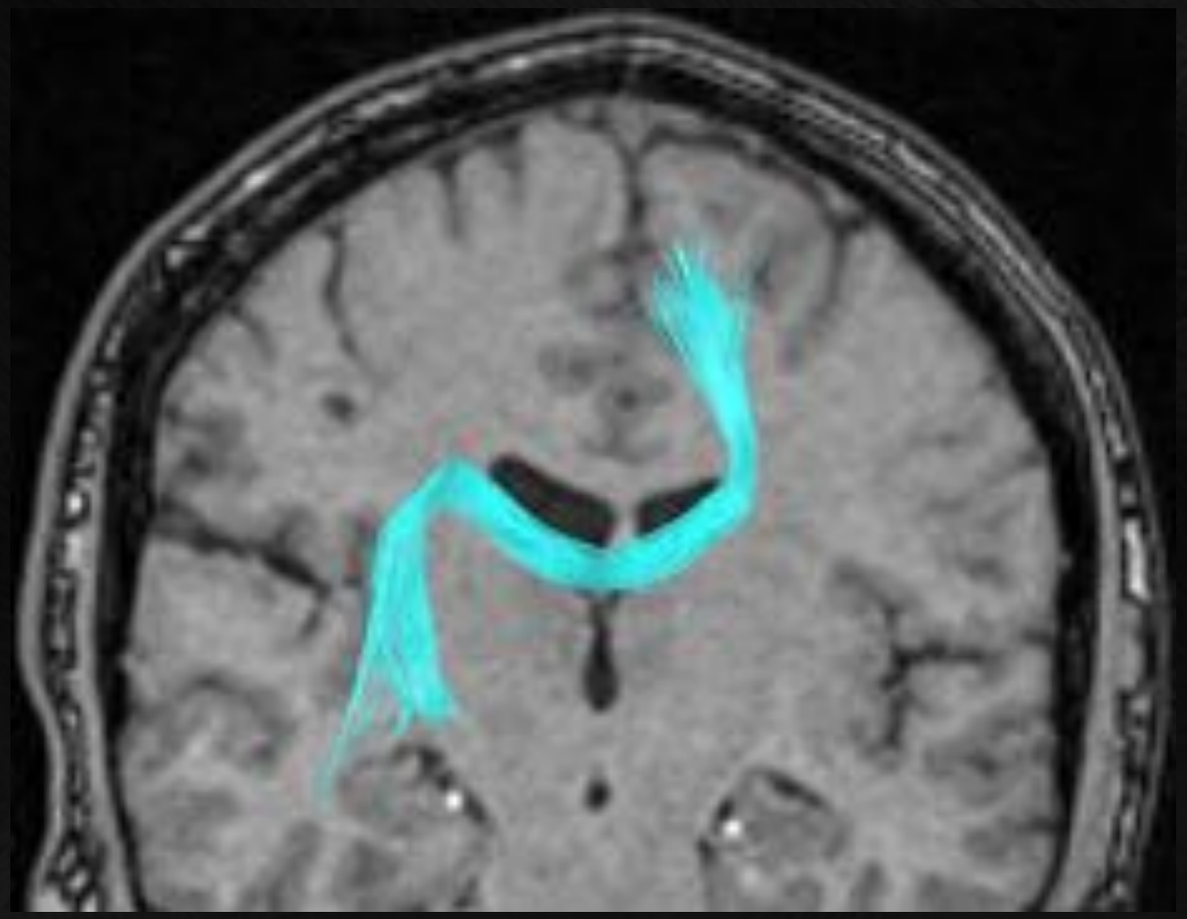


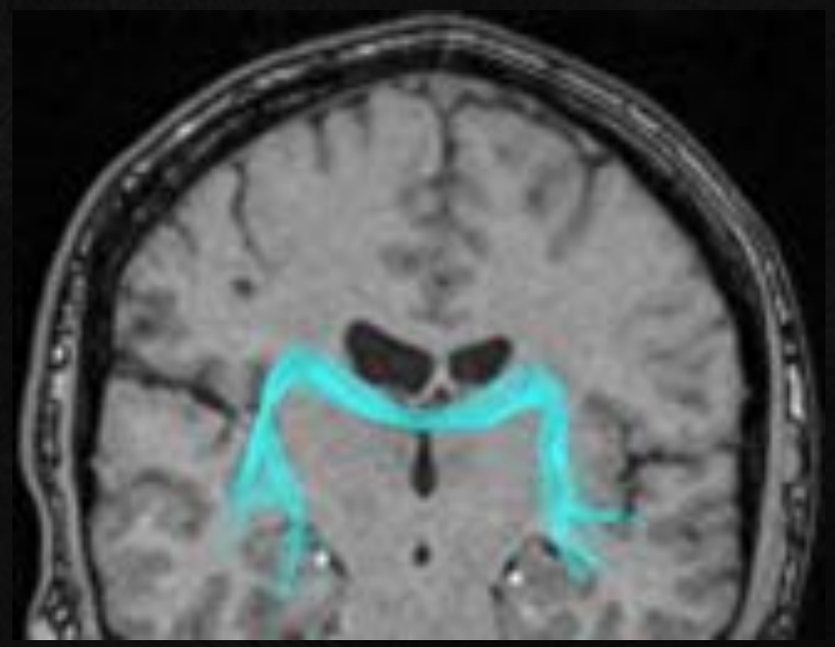
- Connecting invalid cortical or subcortical regions
- Connecting valid regions but through a wrong path

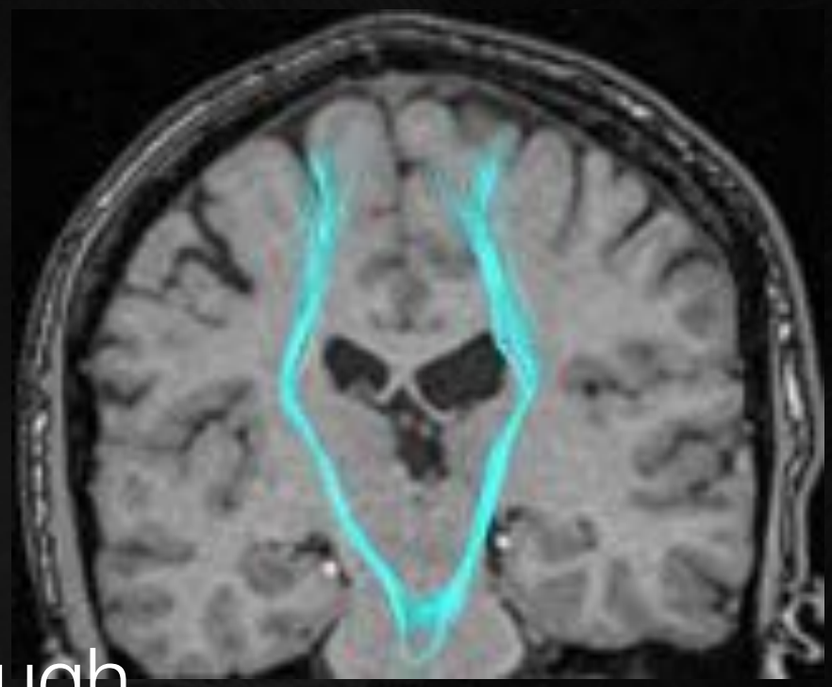
[Cote, Girard et al., MIA, 2013]

Dense Invalid Connections

- ?%







- Connecting invalid cortical or subcortical regions
- Connecting valid regions but through a wrong path

[Cote, Girard et al., MIA, 2013]

The false positive problem

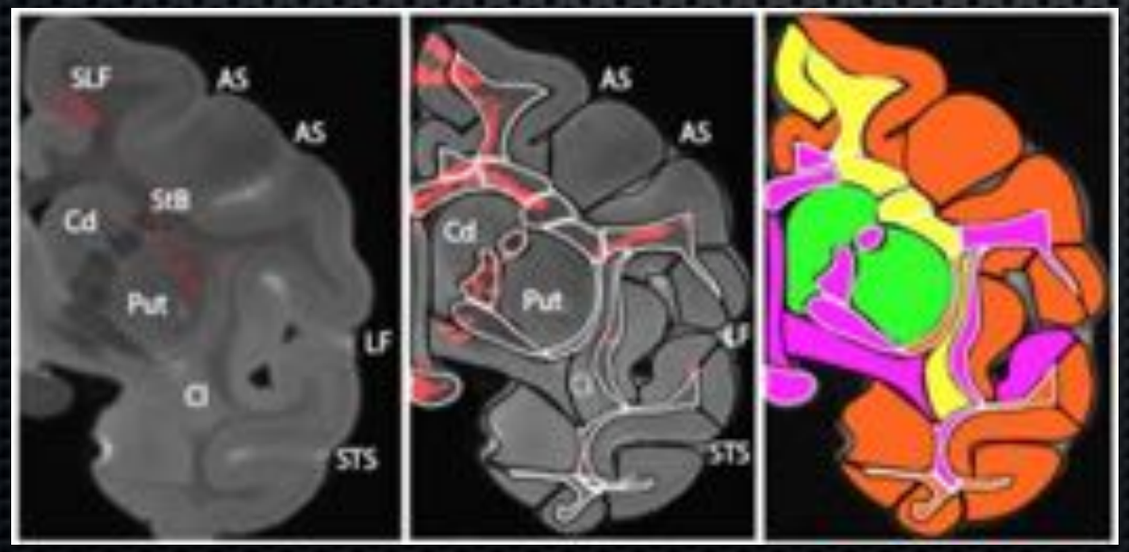
- Recent studies have shown that false positives are a major problem for tractography and connectomics

PNAS

Anatomical accuracy of brain connections derived from diffusion MRI tractography is inherently limited

Cibu Thomas[a,b,1], Frank Q. Ye[c,d], M. Okan Irfanoglu[a,b], Pooja Modi[a], Kadharbatcha S. Saleem[a], David A. Leopold[c,d], and Carlo Pierpaoli[a,b]

[a]Program on Pediatric Imaging and Tissue Sciences, Eunice Kennedy Shriver National Institute of Child Health and Human Development, Bethesda, MD, 20892; [b]Center for Neuroscience and Regenerative Medicine, Uniformed Services University of the Health Sciences, Bethesda, MD 20814; [c]Neurophysiology Imaging Facility, National Institute of Mental Health, National Institute of Neurological Disorders and Stroke, and National Eye Institute, Bethesda, MD 20892; [d]Section on Cognitive Neurophysiology and Imaging and [e]Section on Cognitive Neuroscience, Laboratory of Neuropsychology, National Institute of Mental Health, Bethesda, MD, 20892



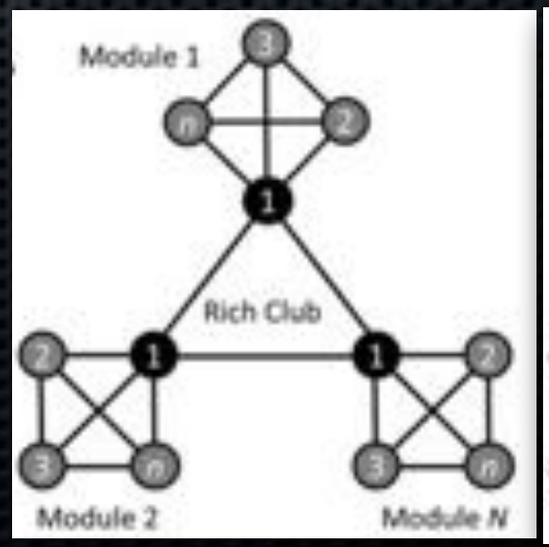
Contents lists available at ScienceDirect

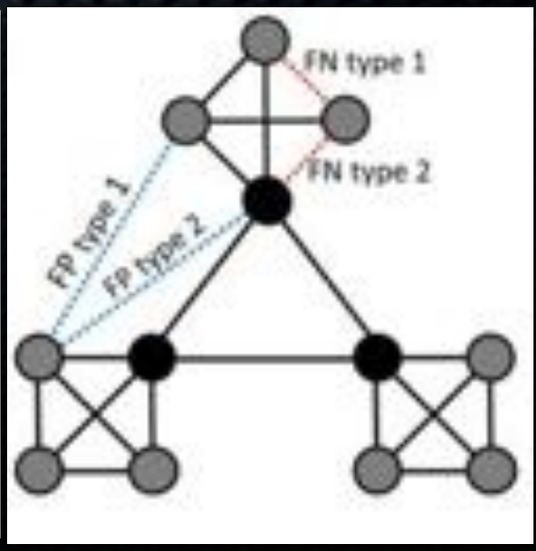
NeuroImage

journal homepage: www.elsevier.com/locate/ynimg

Connectome sensitivity or specificity: which is more important?

Andrew Zalesky [a,*], Alex Fornito [b], Luca Cocchi [c], Leonardo L. Gollo [c], Martijn P. van den Heuvel [d], Michael Breakspear [c,e]





How often do invalid bundles/connections occur?

Klaus H. Maier-Hein, Peter Neher, Jean-Christophe Houde, Marc-Alexandre Côté, Eleftherios Garyfallidis, Jidan Zhong, Maxime Chamberland, Fang-Cheng Yeh, Ying-Chia Lin, Qing Ji, Wilburn E. Reddick, John O. Glass, David Qixiang Chen, Yuanjing Feng, Chengfeng Gao, Ye Wu, Jieyan Ma, H Renjie, Qiang Li, Carl-Fredrik Westin, Samuel Deslauriers-Gauthier, J. Omar Ocegueda González, Michael Paquette, Samuel St-Jean, Gabriel Girard, François Rheault, Jasmeen Sidhu, Chantal M.W. Tax, Fenghua Guo, Hamed Y. Mesri, Szabolcs Dávid, Martijn Froeling, Anneriet M. Heemskerk, Alexander Leemans, Arnaud Boré, Basile Pinsard, Christophe Bedetti, Matthieu Desrosiers, Simona Brambati, Julien Doyon, Alessia Sarica, Roberta Vasta, Antonio Cerasa, Aido Quattrone, Jason Yeatman, Ali R. Khan, Wes Hodges, Simon Alexander, David Romascano, Muhamed Barakovic, Anna Auría, Oscar Esteban, Alia Lemkaddem, Jean-Philippe Thiran, H. Ertan Cetingul, Benjamin L. Odry, Boris Mailhe, Mariappan S. Nadar, Fabrizio Pizzagalli, Gautam Prasad, Julio E. Villalon-Reina, Justin Galvis, Paul M. Thompson, Francisco De Santiago Requejo, Pedro Luque Laguna, Luis Miguel Lacerda, Rachel Barrett, Flavio Dell'Acqua, Laurent Petit, Emmanuel Caruyer, Alessandro Daducci, Tim B. Dyrby Tim Holland-Letz, Bram Stieltjes, **Maxime Descoteaux**

http://biorxiv.org/content/early/2016/11/07/084137.article-metrics

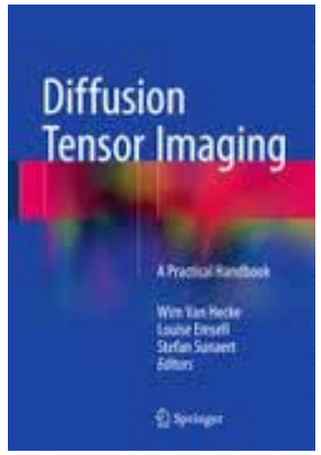
nature COMMUNICATIONS

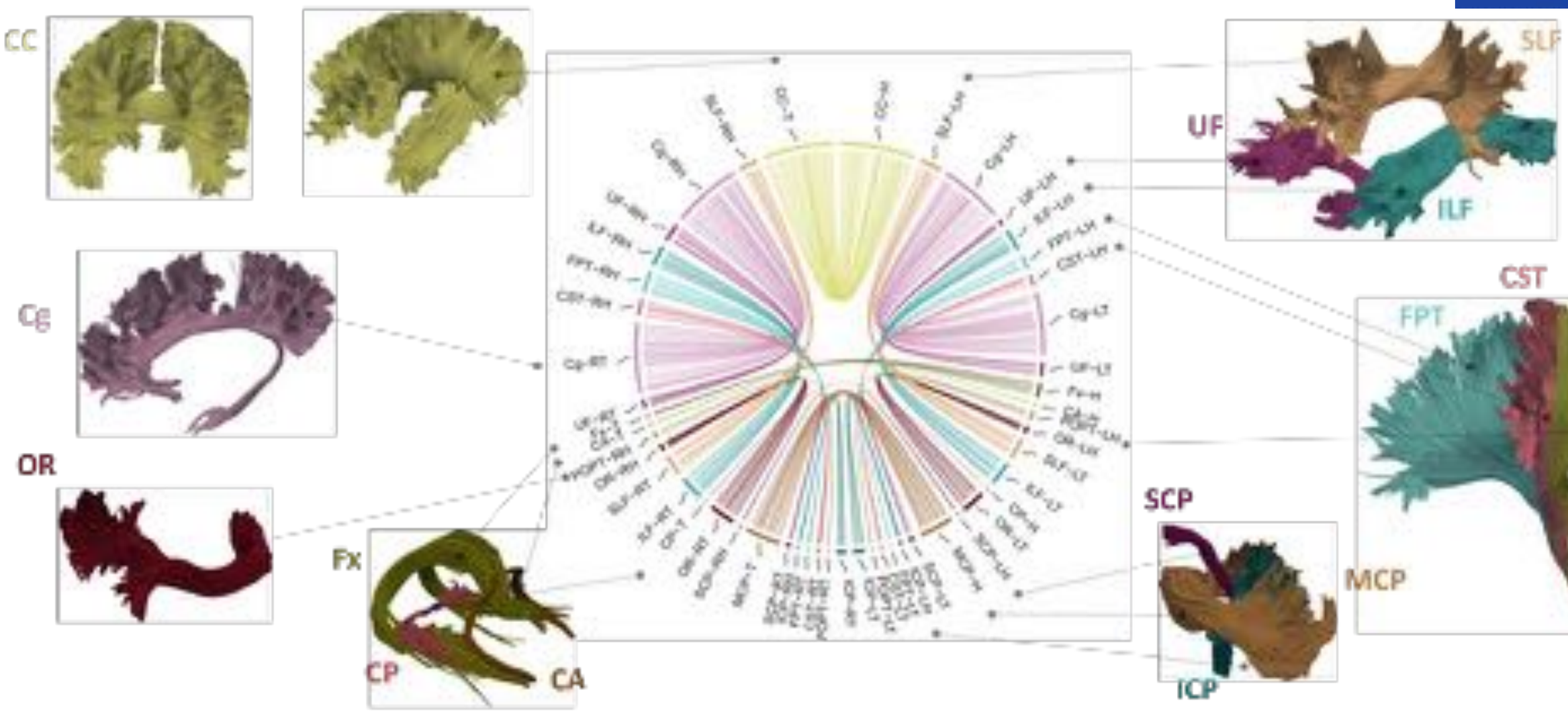
DOI: 10.1038/s41467-017-01285-x OPEN

The challenge of mapping the human connectome based on diffusion tractography

Klaus H. Maier-Hein, Peter Neher, Jean-Christophe Houde, Marc-Alexandre Côté, Eleftherios Garyfallidis, Jidan Zhong, Maxime Chamberland, Fang-Cheng Yeh, Ying-Chia Lin, Qing Ji, Wilburn E. Reddick, John O. Glass, David Qixiang Chen, Yuanjing Feng, Chengfeng Gao, Ye Wu, Jieyan Ma, H Renjie, Qiang Li, Carl-Fredrik Westin, Samuel Deslauriers-Gauthier, J. Omar Ocegueda González, Michael Paquette, Samuel St-Jean, Gabriel Girard, François Rheault, Jasmeen Sidhu, Chantal M.W. Tax, Fenghua Guo, Hamed Y. Mesri, Szabolcs Dávid, Martijn Froeling, Anneriet M. Heemskerk, Alexander Leemans, Arnaud Boré, Basile Pinsard, Christophe Bedetti, Matthieu Desrosiers, Simona Brambati, Julien Doyon, Alessia Sarica, Roberta Vasta, Antonio Cerasa, Aido Quattrone, Jason Yeatman, Ali R. Khan, Wes Hodges, Simon Alexander, David Romascano, Muhamed Barakovic, Anna Auría, Oscar Esteban, Alia Lemkaddem, Jean-Philippe Thiran, H. Ertan Cetingul, Benjamin L. Odry, Boris Mailhe, Mariappan S. Nadar, Fabrizio Pizzagalli, Gautam Prasad, Julio E. Villalon-Reina, Justin Galvis, Paul M. Thompson, Francisco De Santiago Requejo, Pedro Luque Laguna, Luis Miguel Lacerda, Rachel Barrett, Flavio Dell'Acqua, Laurent Petit, Emmanuel Caruyer, Alessandro Daducci, Tim B. Dyrby Tim Holland-Letz, Bram Stieltjes, **Maxime Descoteaux**

- Includes 25 well-known ground truth bundles
- Exact ground truth connectivity (terminations)
- Covers ~70% of the white matter





ISMRM 2015 Tractography challenge data

FiberFox: Neher, Laun, Stieltjes, Maier-Hein. MRM (2014)

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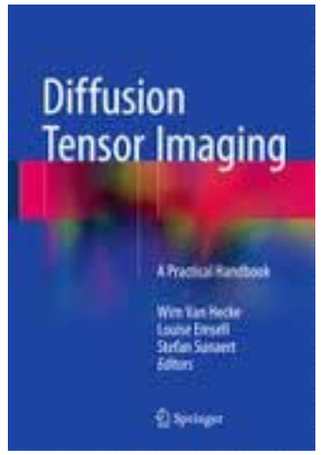
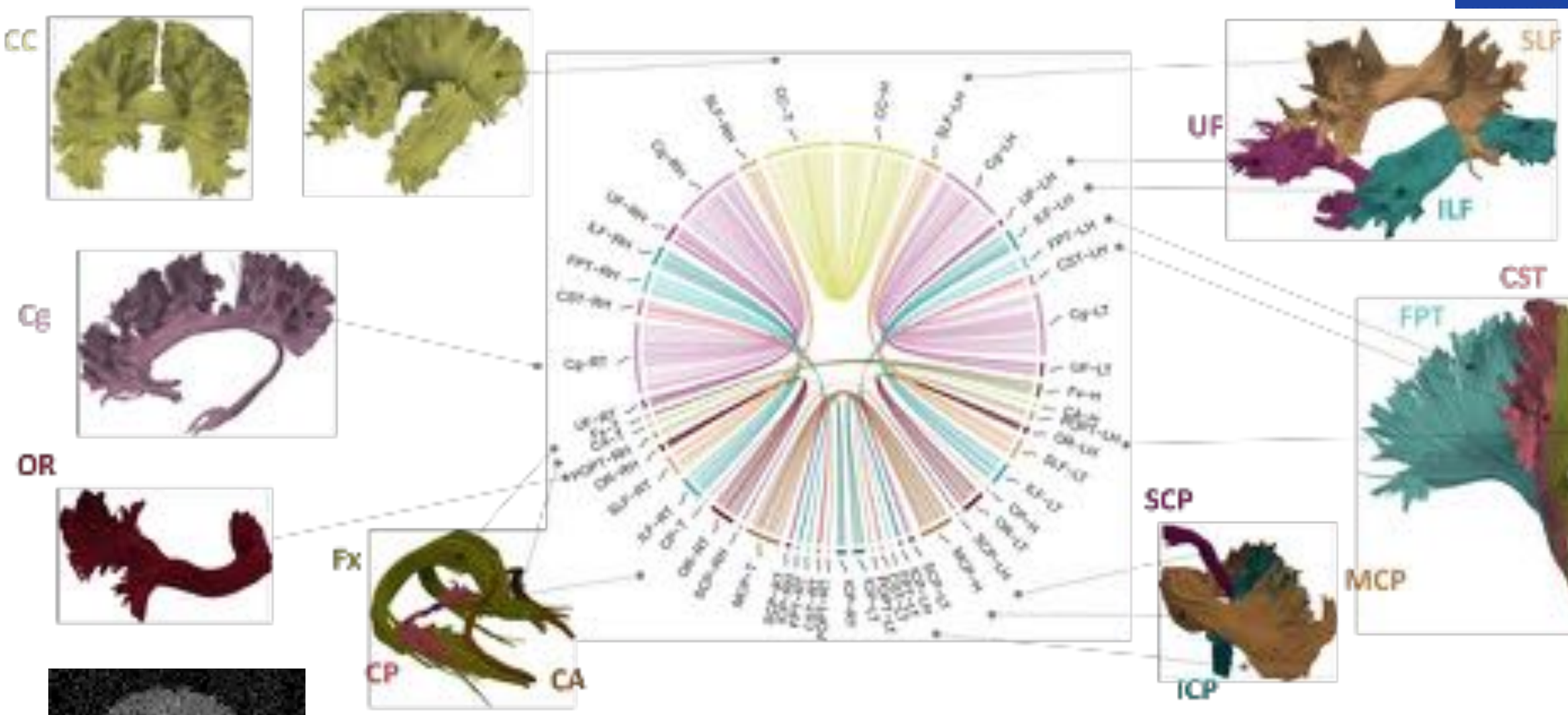




ISMRM 2015 Tractography challenge data

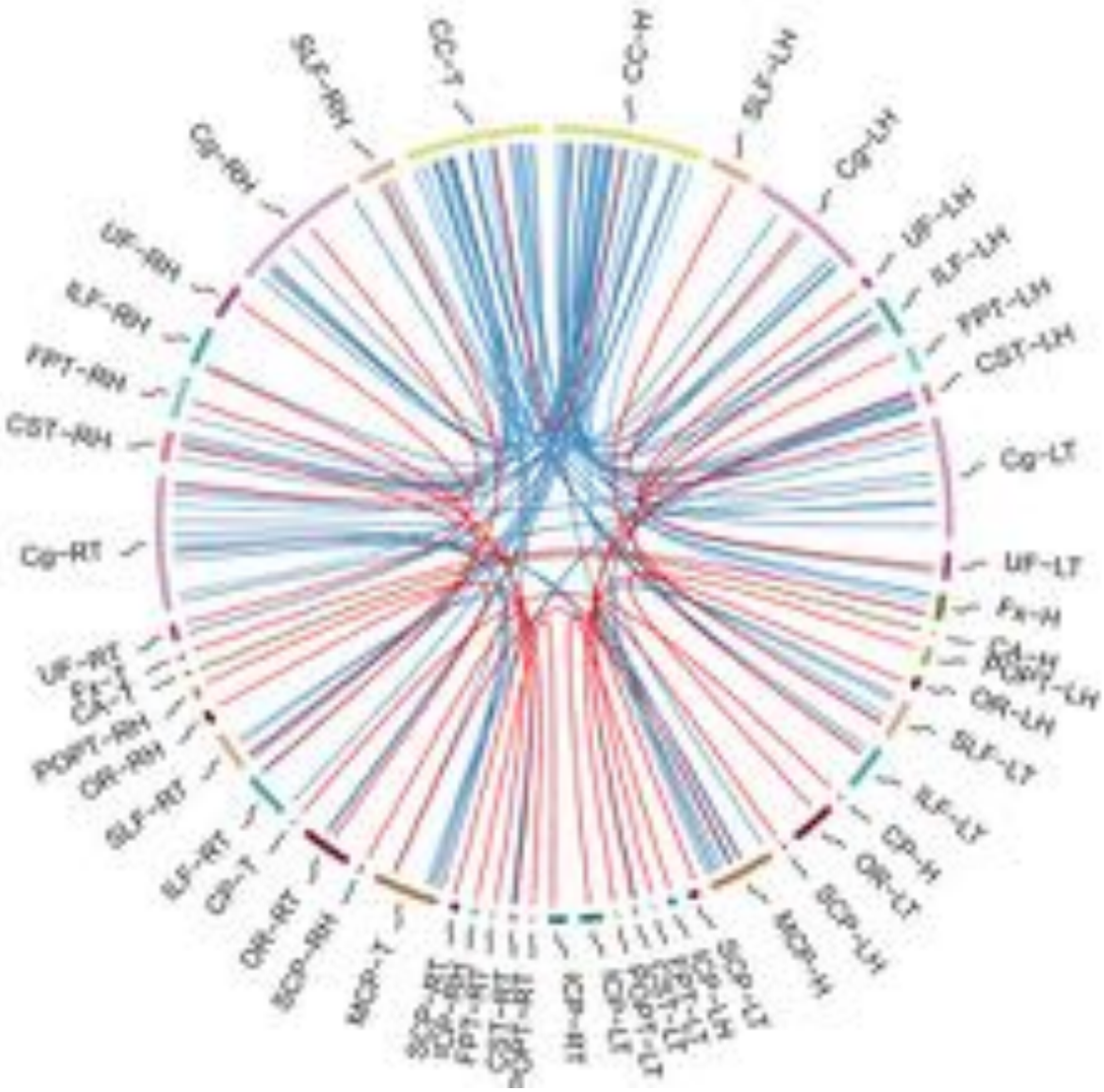
FiberFox: Neher, Laun, Stieltjes, Maier-Hein. MRM (2014)

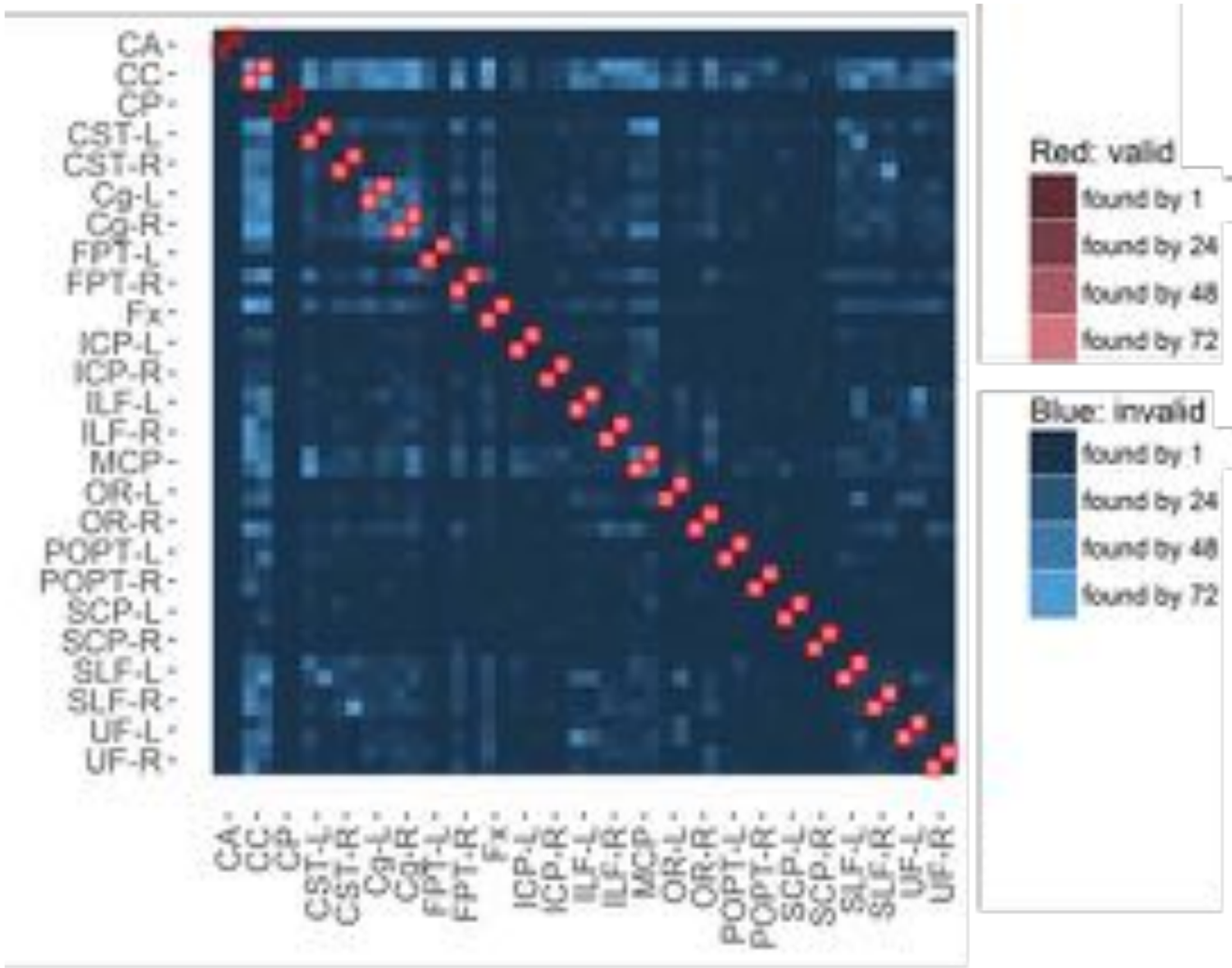
Evaluation with the T*ractometer*
(comparison with ground truth)

[Tractometer: Côté et al Descoteaux. Medical Image Analysis (2013)]

http://www.tractometer.org/ismrm_2015_challenge/

Overview of frequently occurring valid (red) & invalid (blue) bundles.

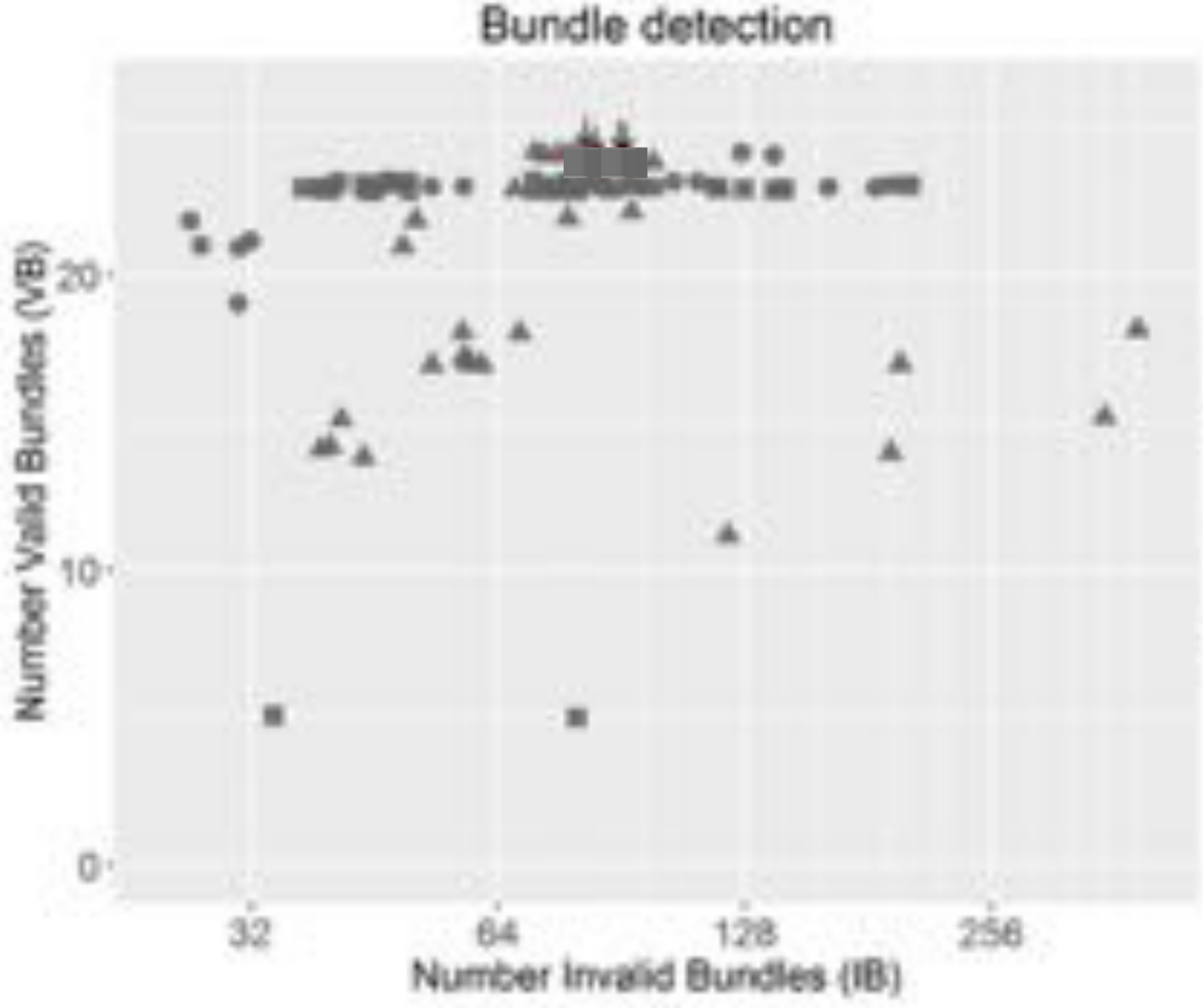




✓ Invalid bundles detected by more than half of the submissions

[Maier-Hein et al, NatureComm 2017]

The tractography algorithms found most existing valid bundles, but ...



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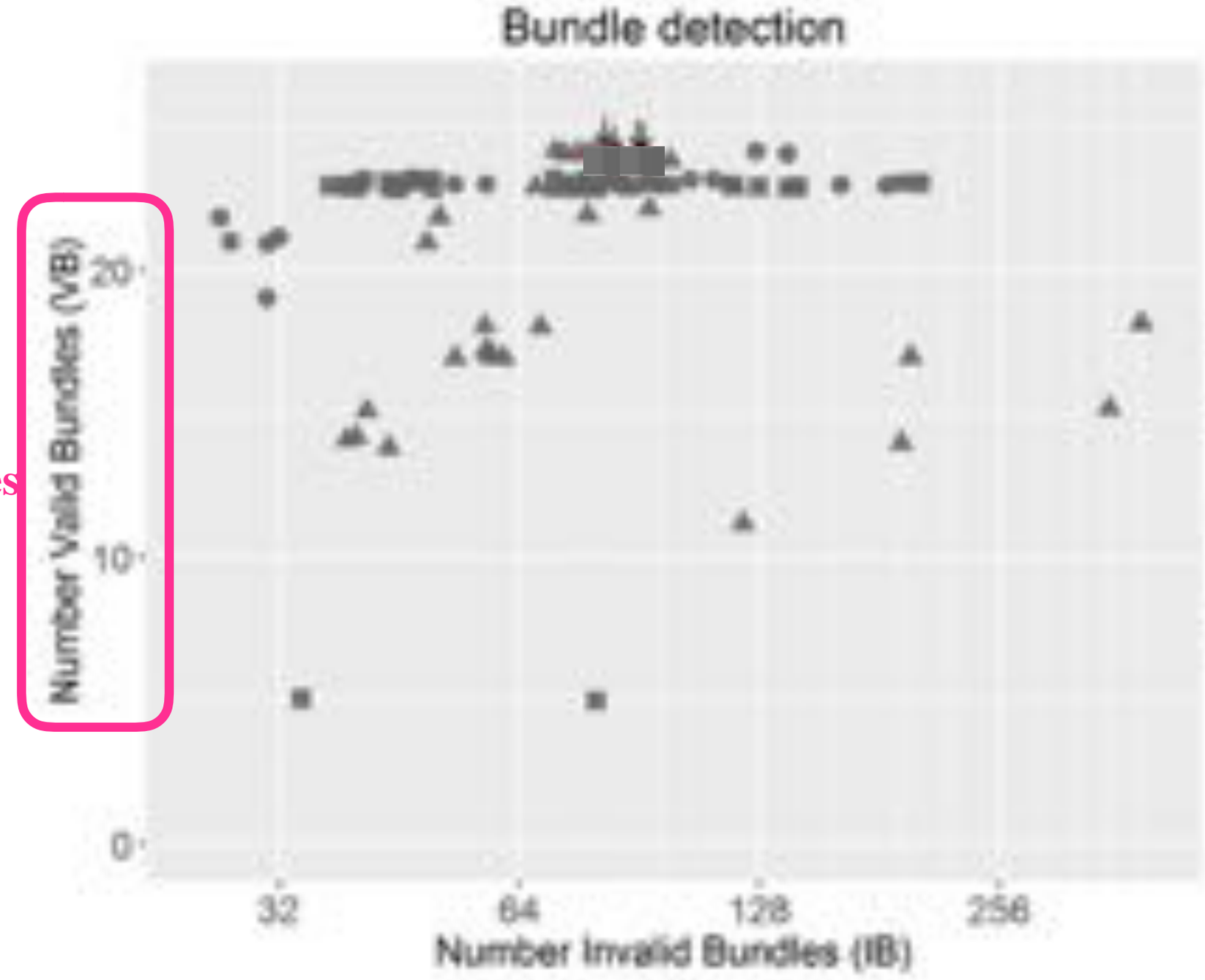

Average 23/25 valid bundles

http://www.tractometer.org/ismrm_2015_challenge/

[Maier-Hein et al, NatureComm 2017]

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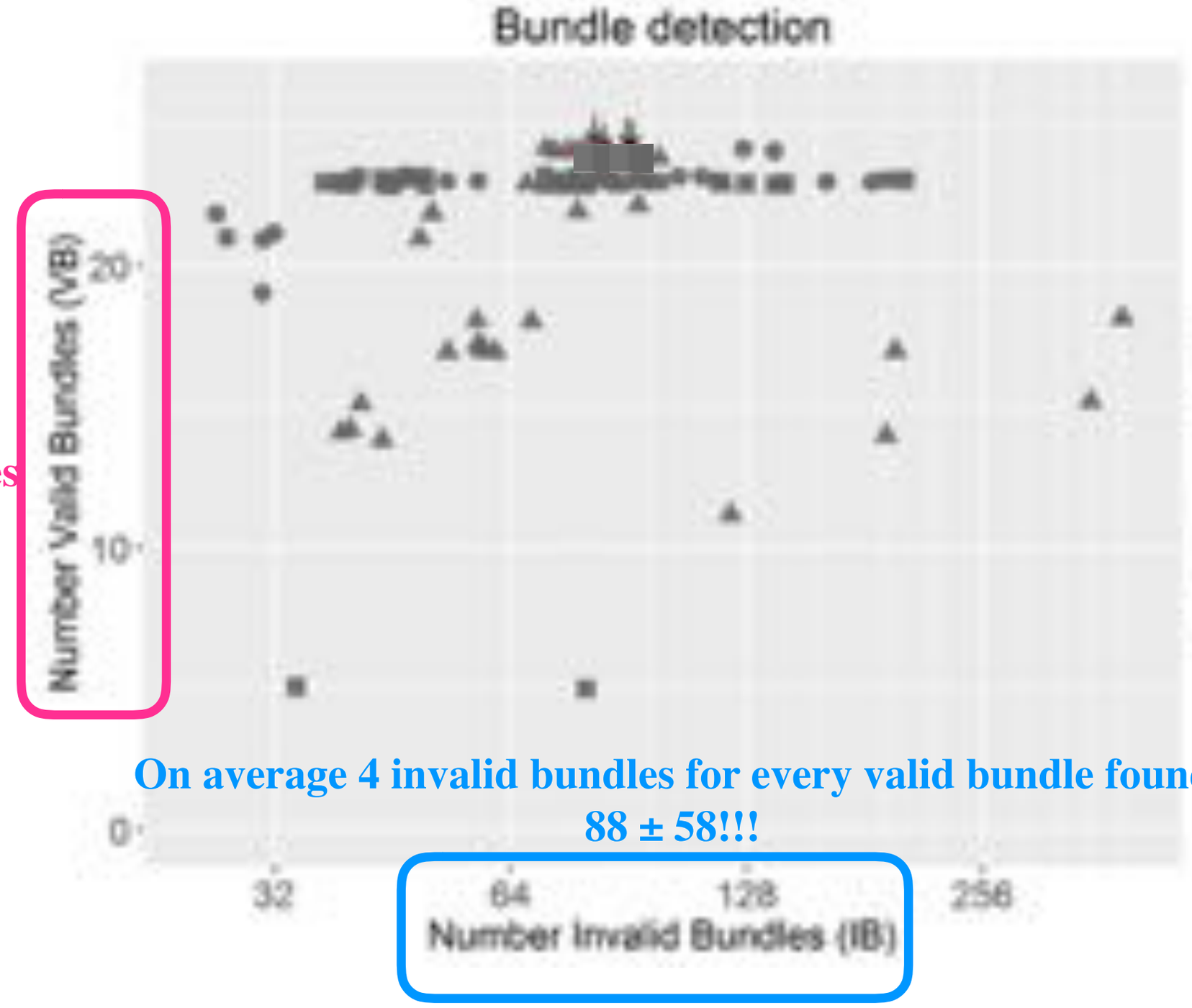


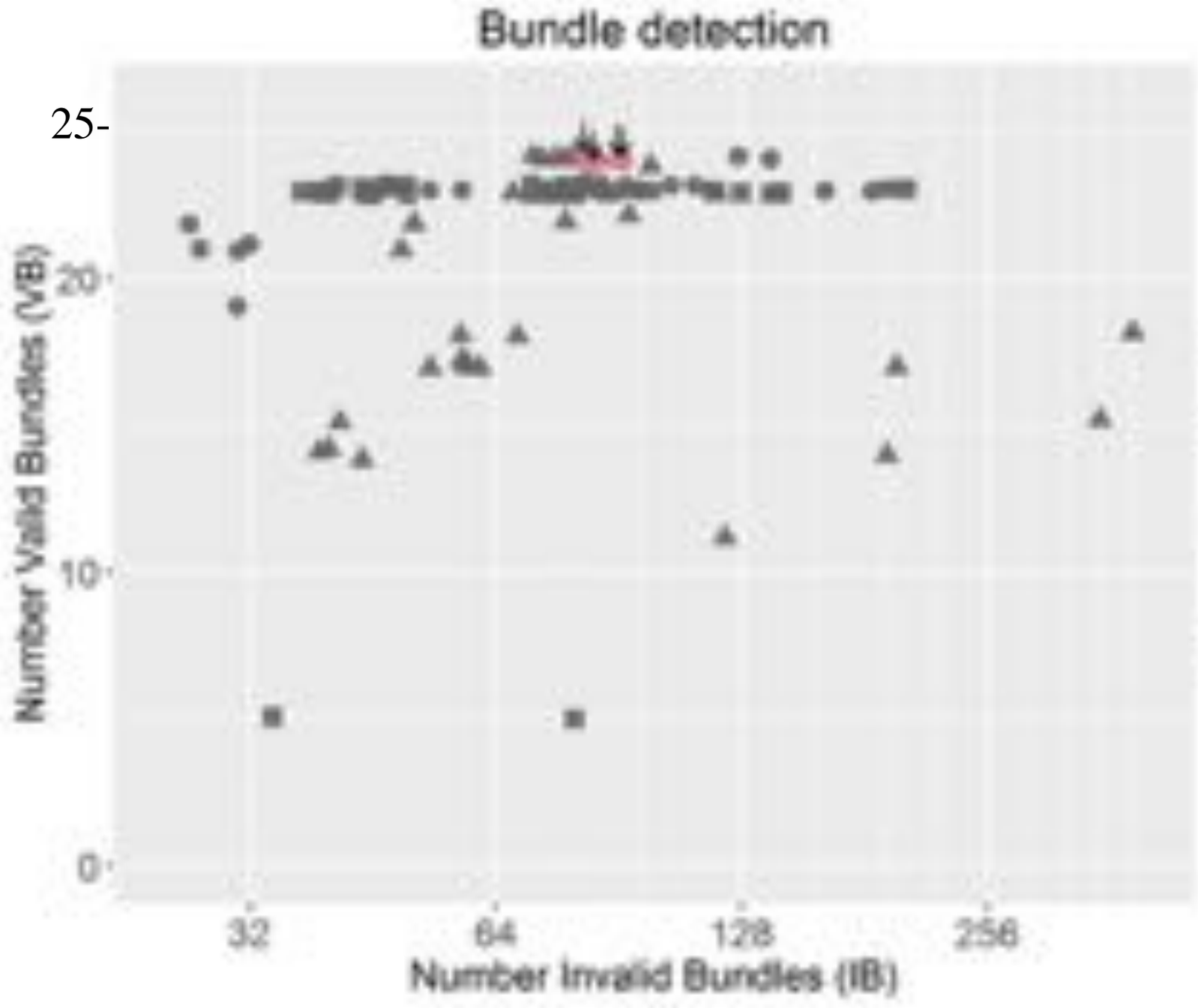
Average 23/25 valid bundles

On average 4 invalid bundles for every valid bundle found
88 ± 58!!!

http://www.tractometer.org/ismrm_2015_challenge/

[Maier-Hein et al, NatureComm 2017]

Tracking on ground truth directions helps on some measures but not for false positives



http://www.tractometer.org/ismrm_2015_challenge/

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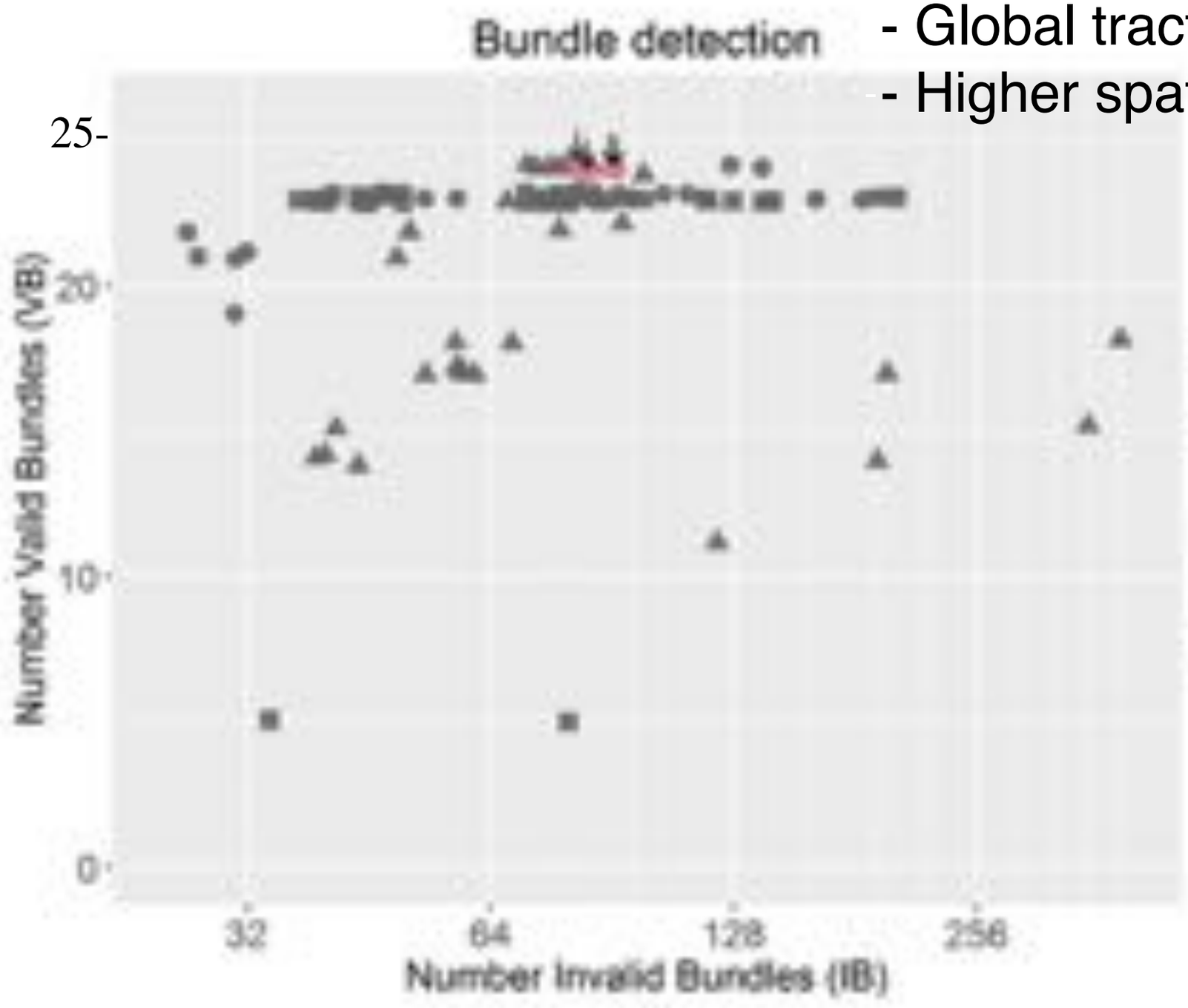


- Global tractography
- Higher spatial resolution

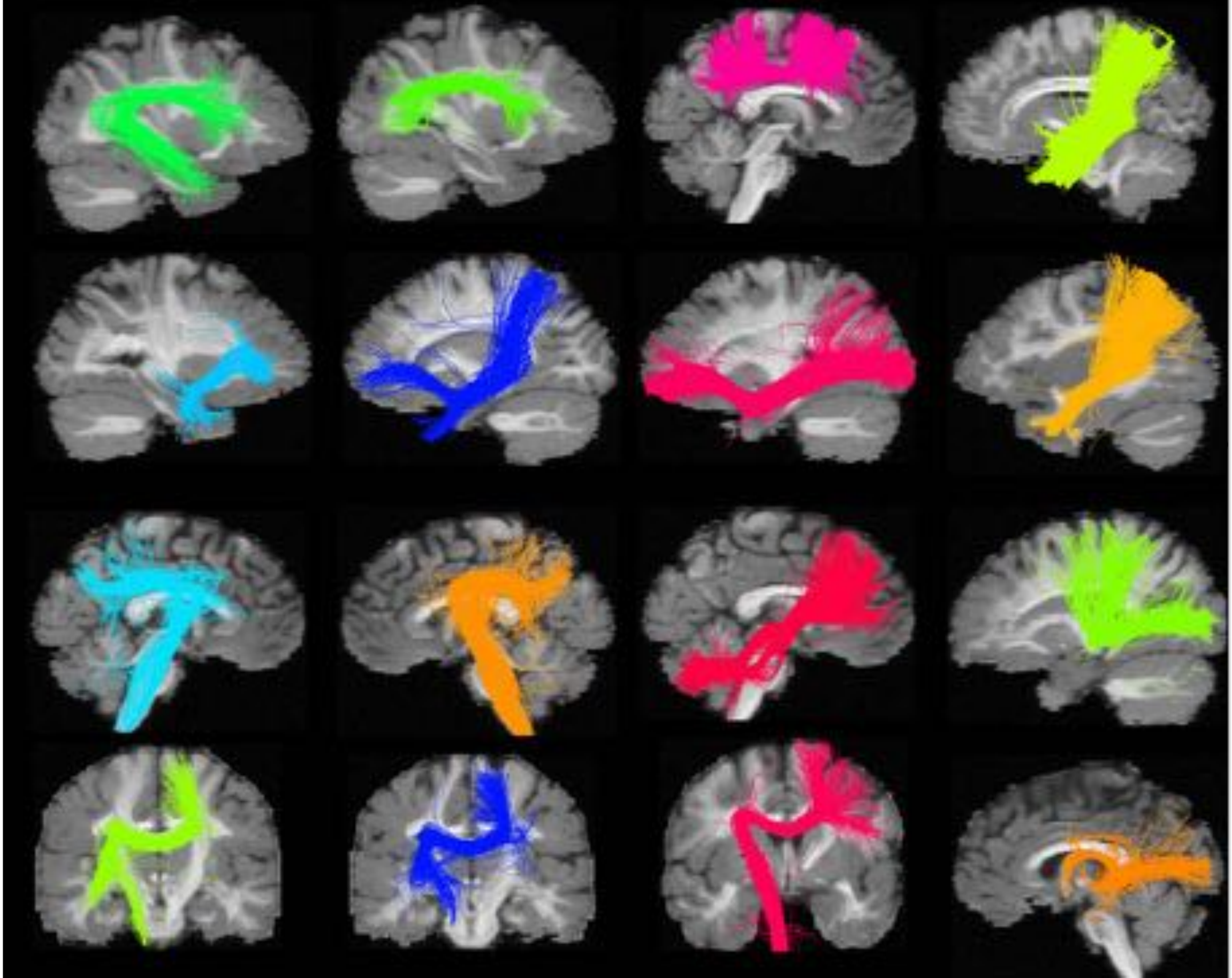
neither

http://www.tractometer.org/ismrm_2015_challenge/

[Maier-Hein et al, NatureComm 2017]

What do false positives look like?

Examples of **invalid bundles** from **HARDI probabilistic**

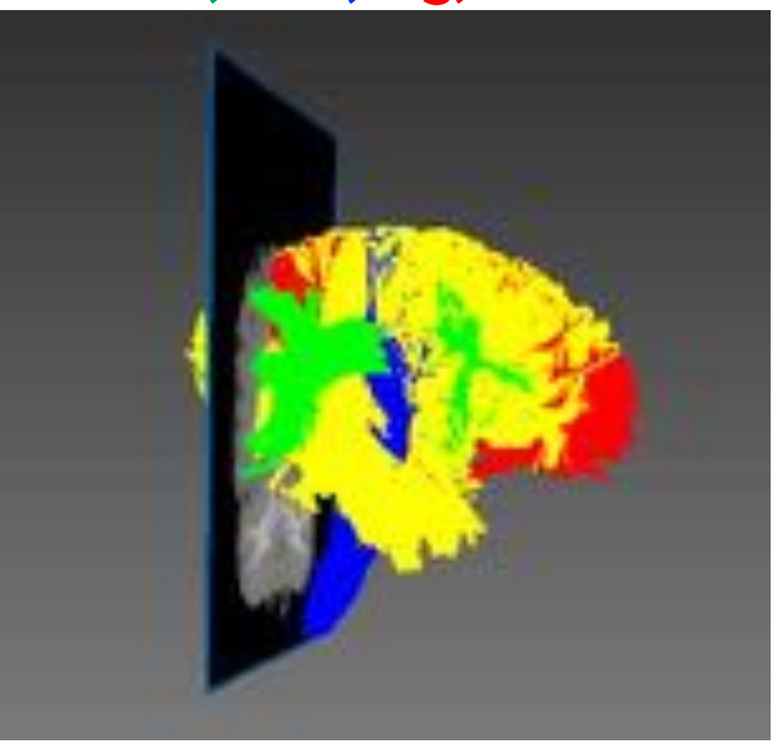


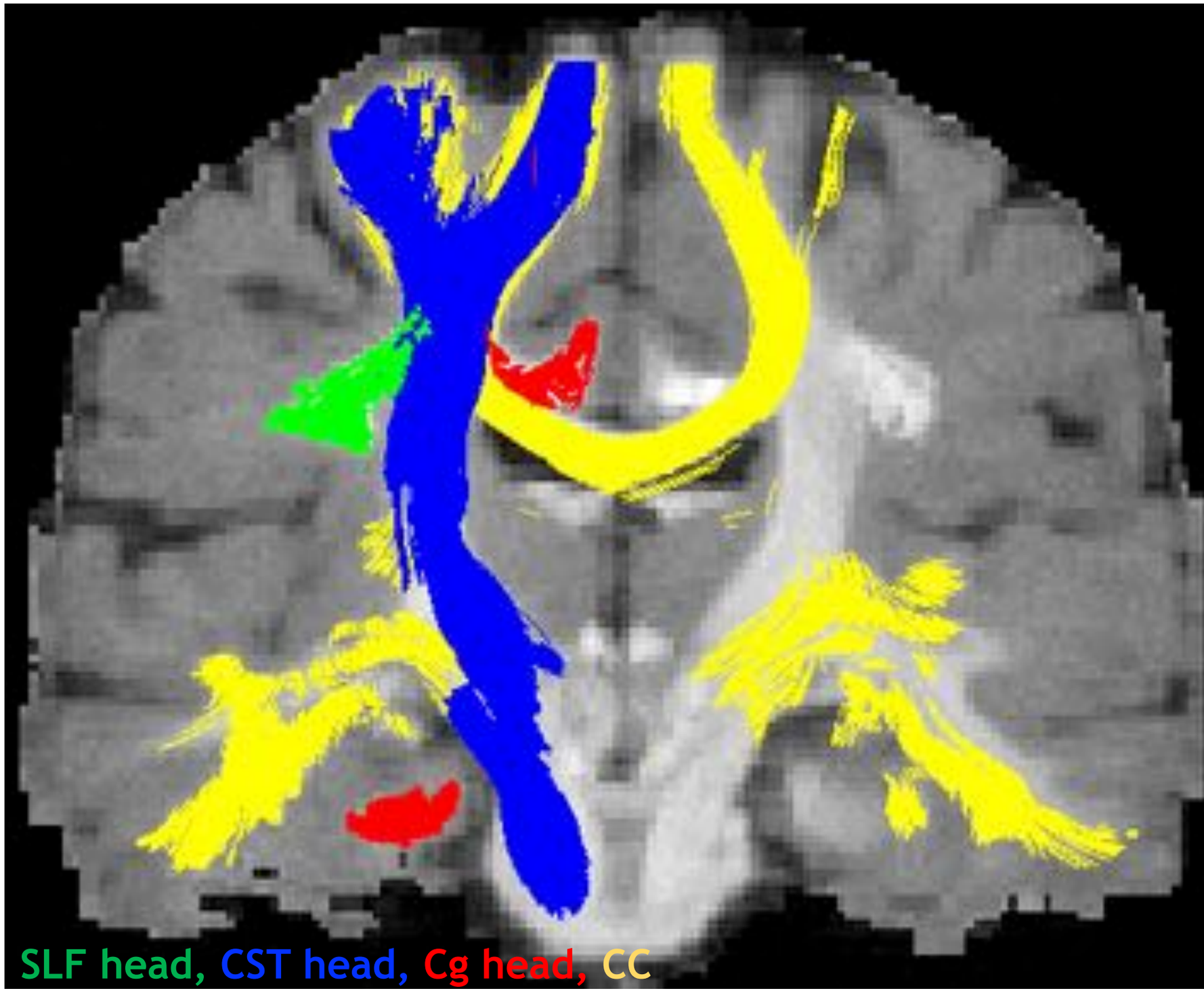
Examples of **invalid bundles** from **HARDI probabilistic**

Dense & thick
in locations *not*
in the data

What’s happening?

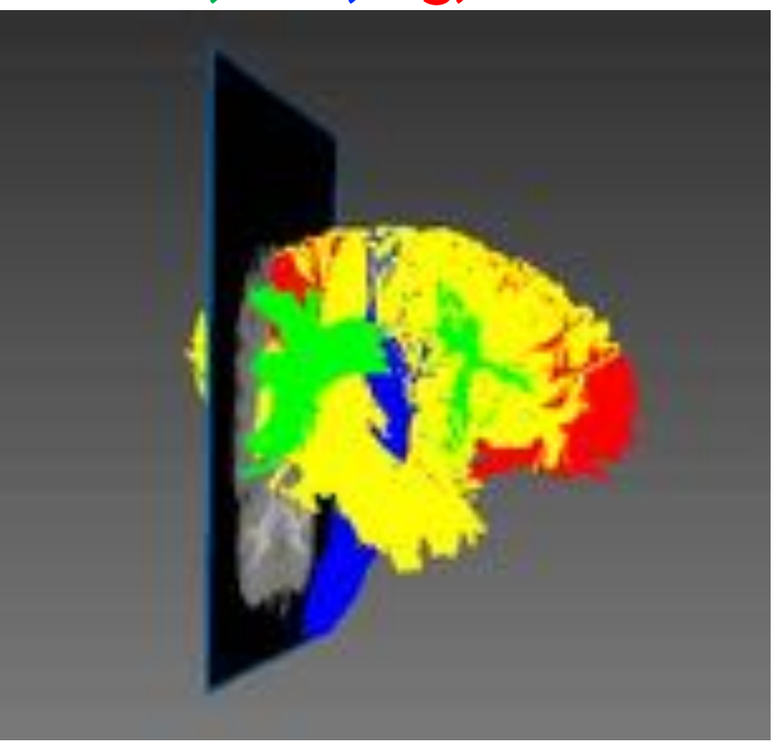
SLF, CST, Cg, CC

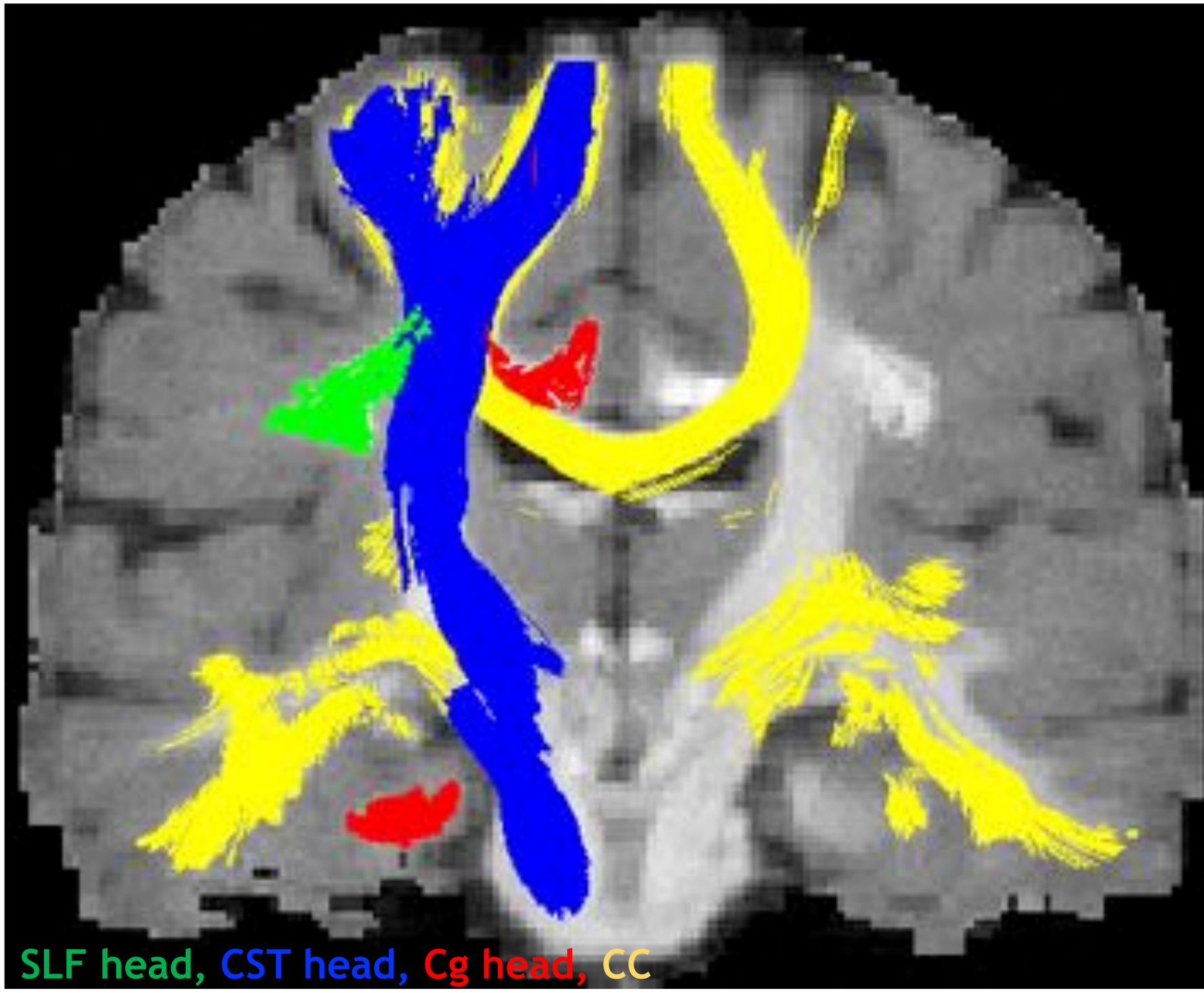




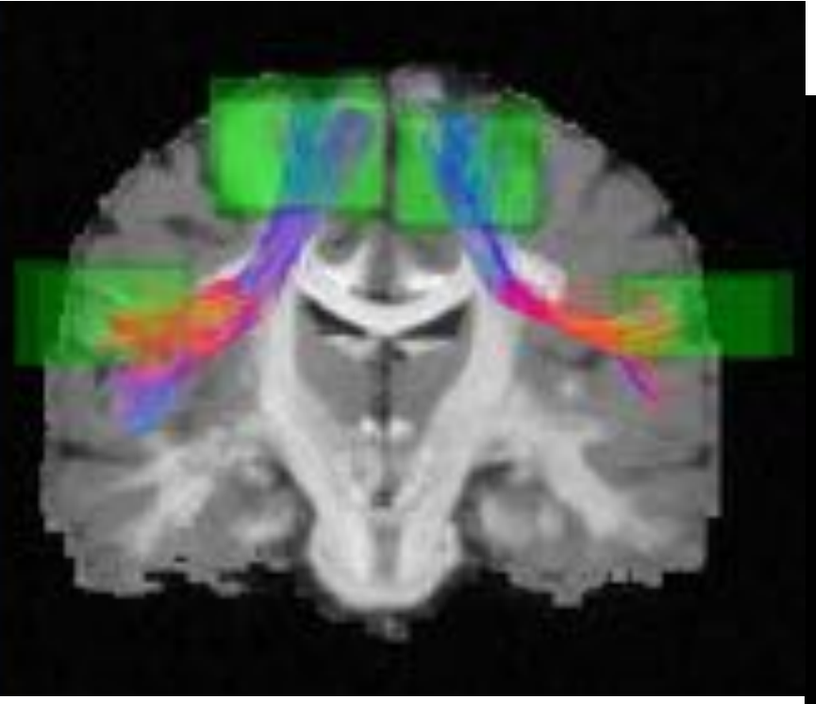
[Maier-Hein et al, NatureComm 2017]

SLF, CST, Cg, CC

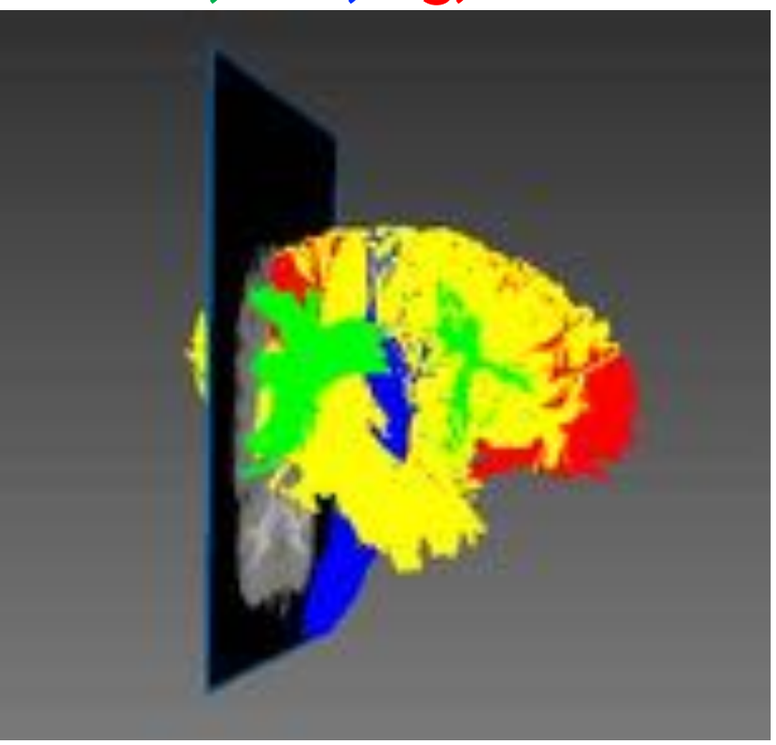


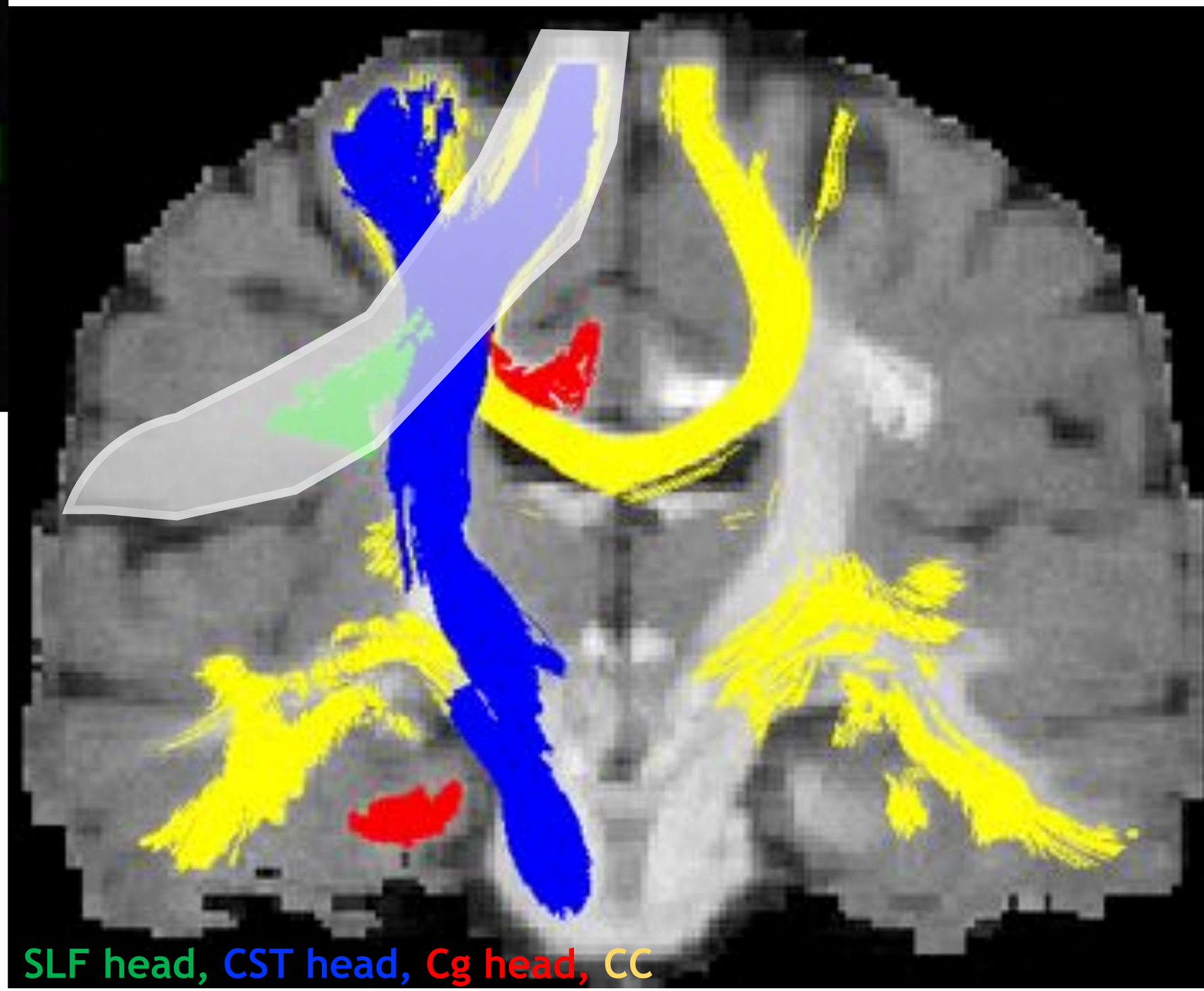


[Maier-Hein et al, NatureComm 2017]



SLF, CST, Cg, CC



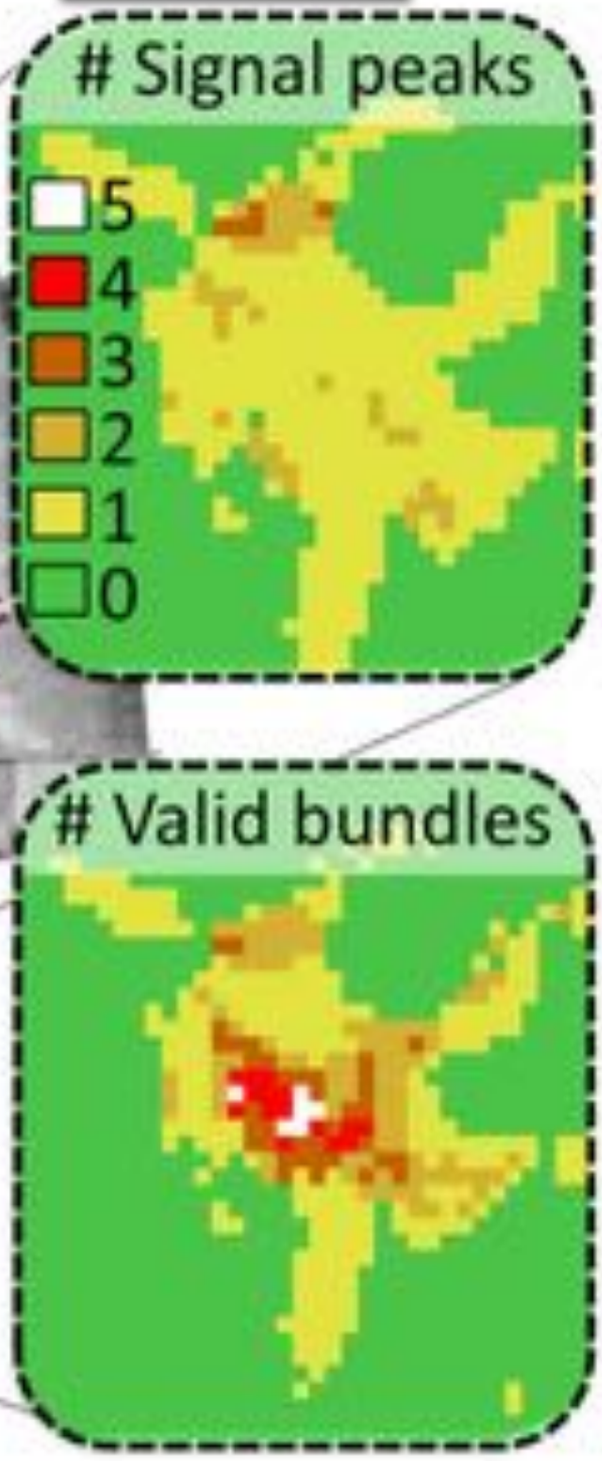


Easy to track
un-existent bundles!

[Maier-Hein et al, NatureComm 2017]

a. Valid bundles through bottleneck

bottlenecks

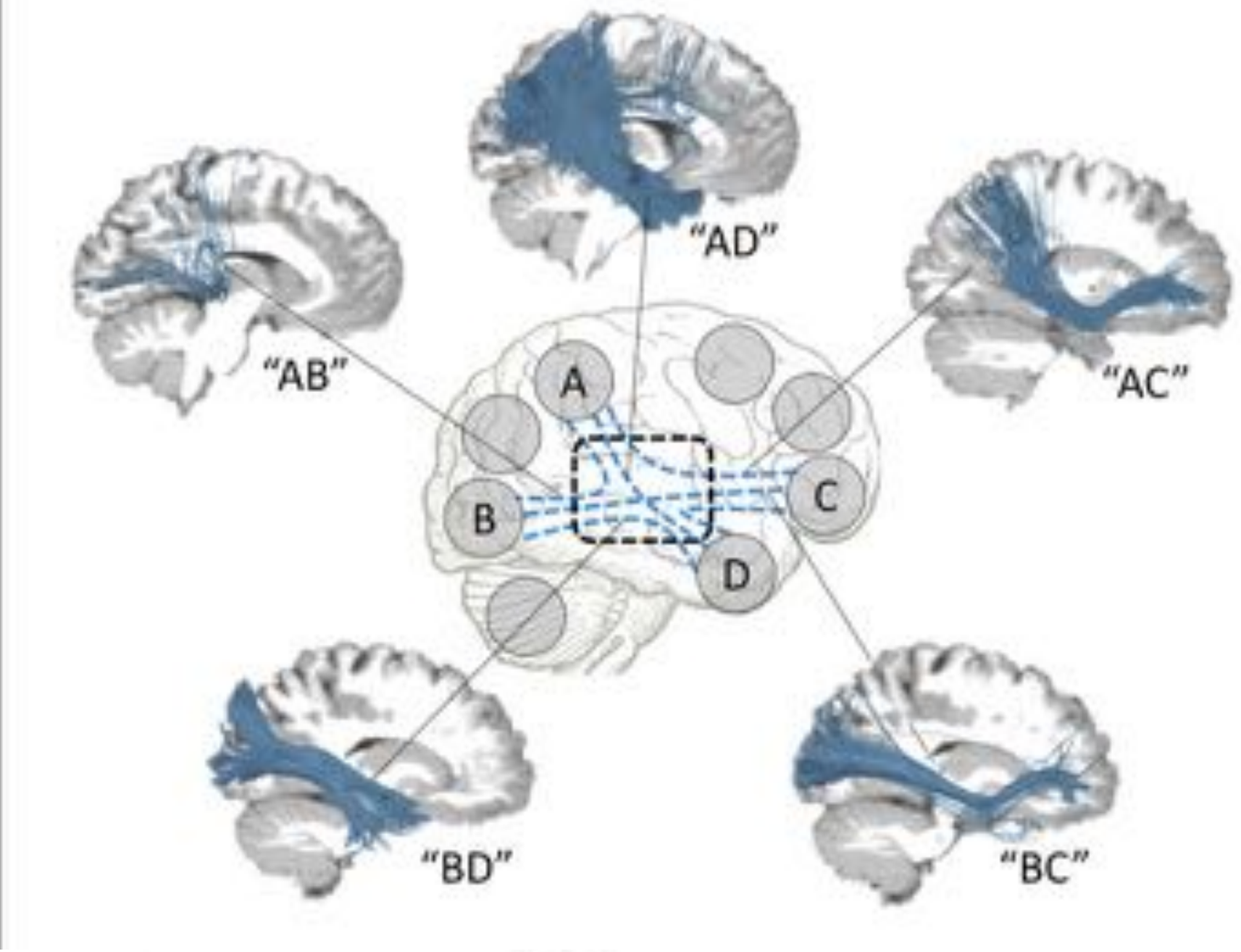


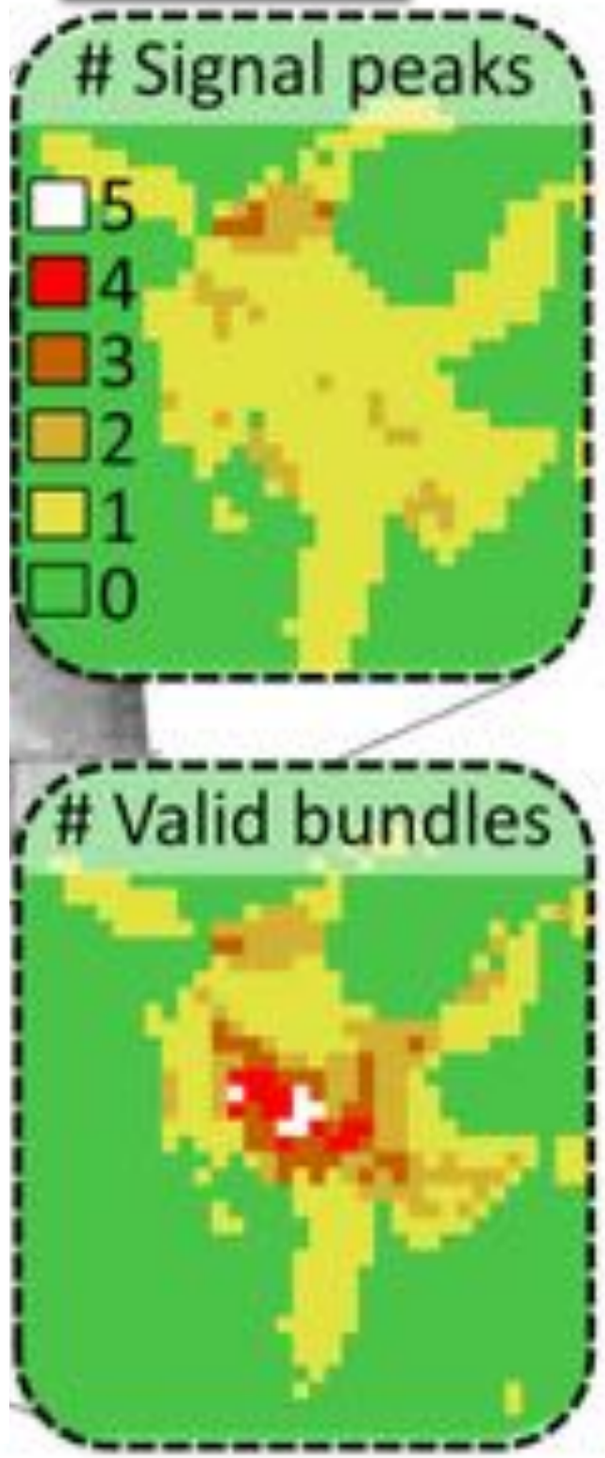
[Maier-Hein et al, NatureComm 2017]

a. Valid bundles through bottleneck

bottlenecks

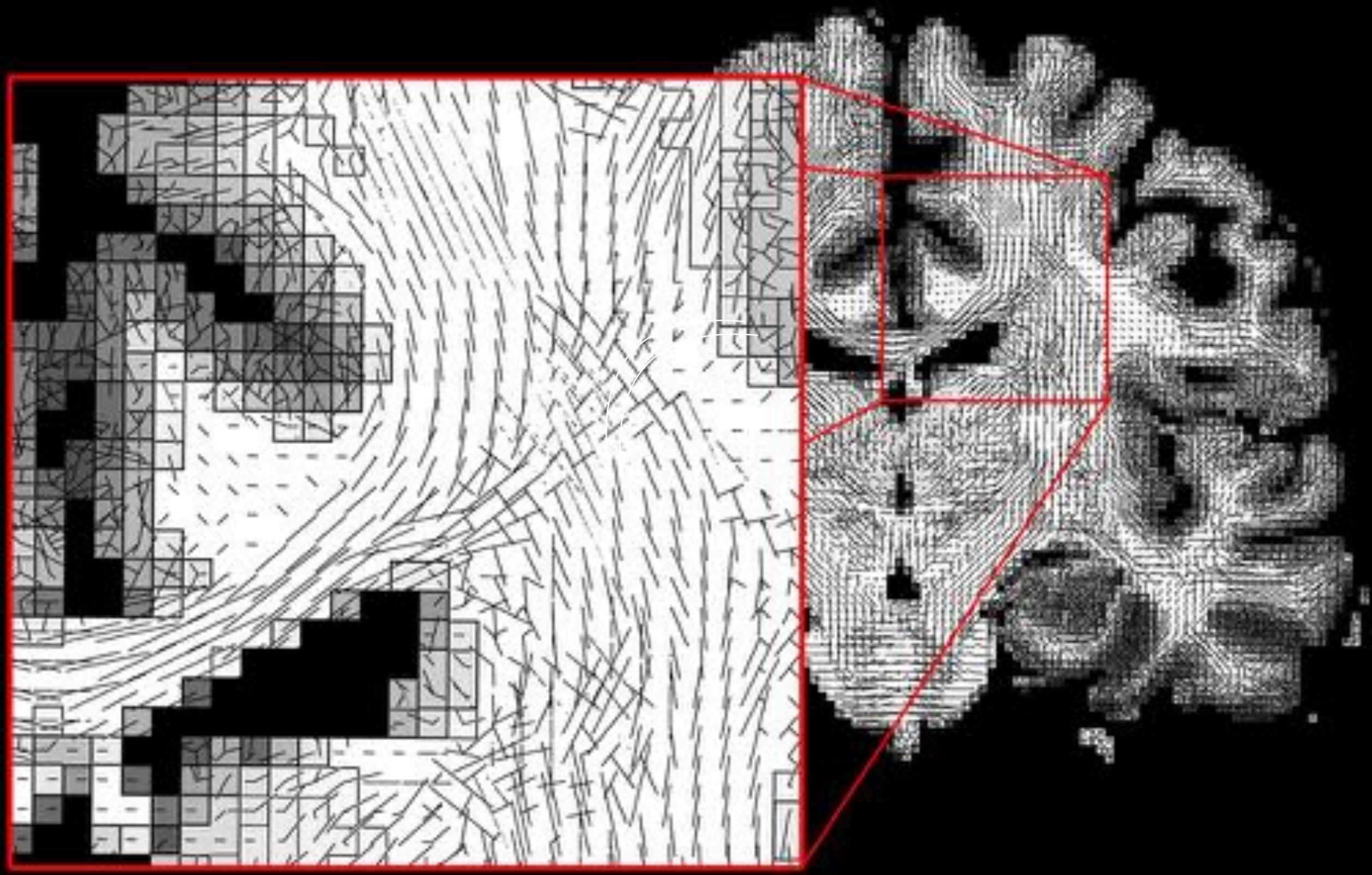
c. Invalid bundles through bottleneck (selection)



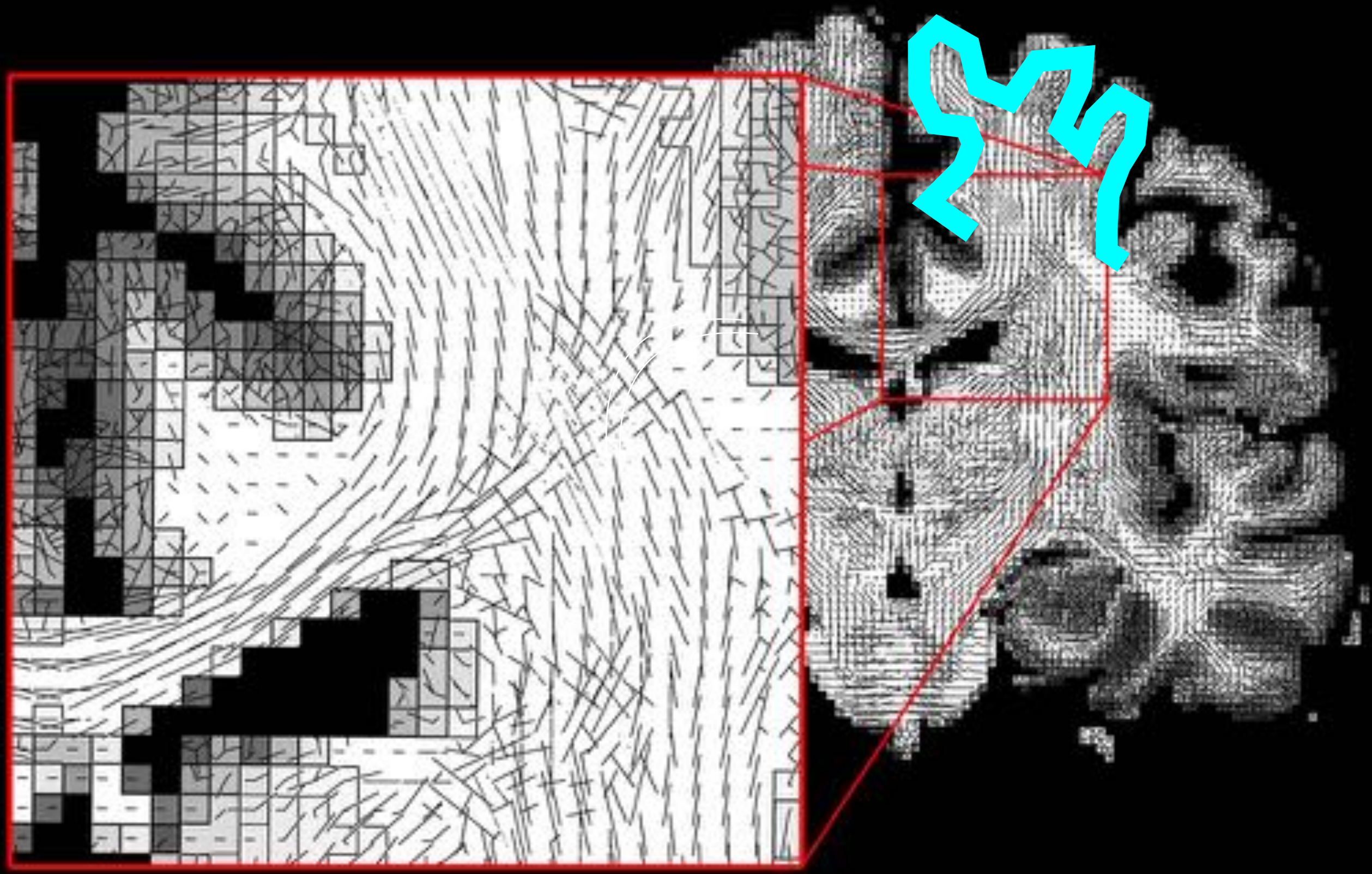


[Maier-Hein et al, NatureComm 2017]

Local orientations are not enough!



Local orientations are not enough!



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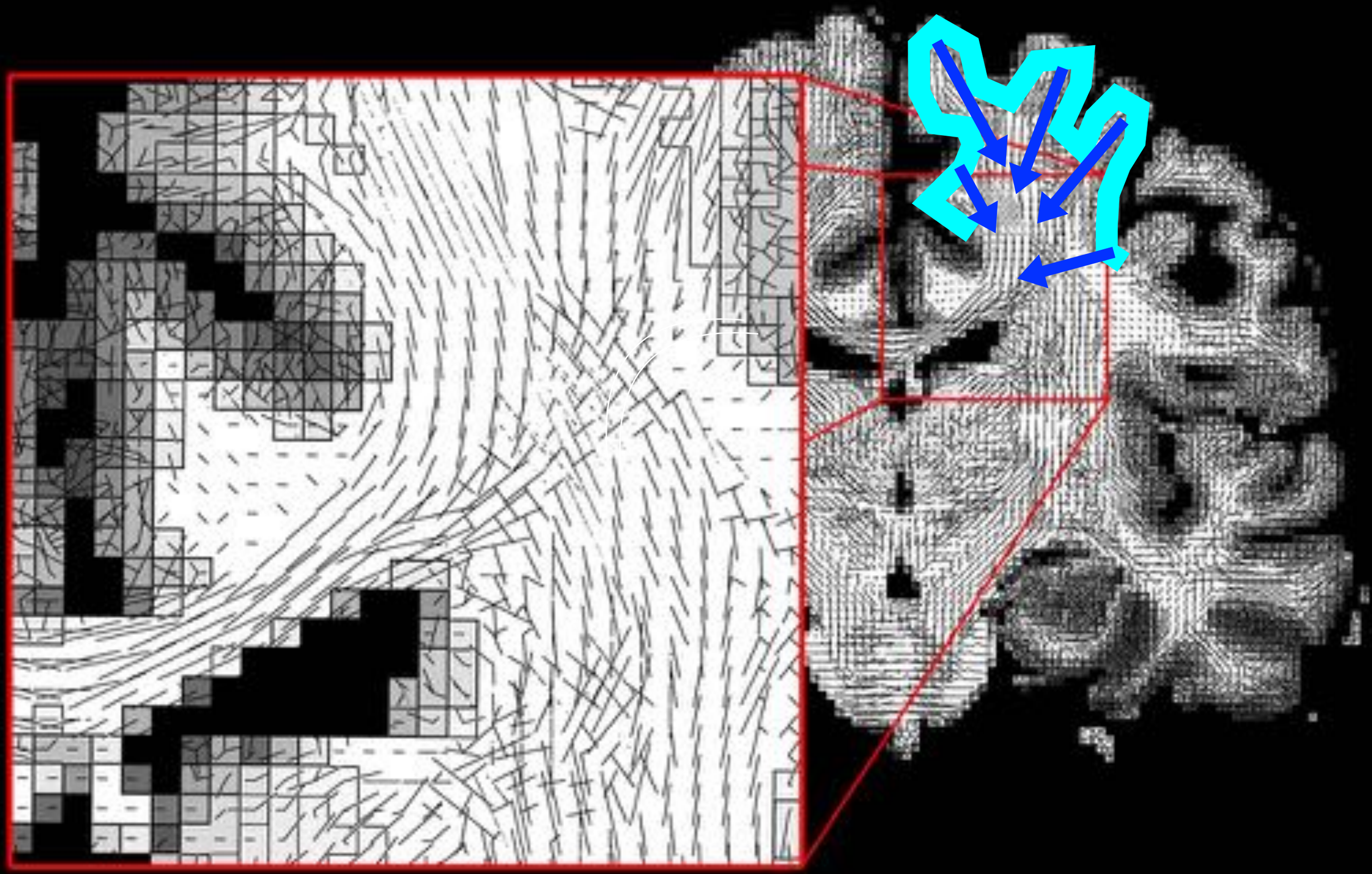

- Advanced streamline-weighting/filtering to **reduce invalid connections**

Advanced streamline filtering techniques

- SIFT1, SIFT2, LIFE, COMMIT
  [Smith et al 2014-2015, Pestilli et al 2014, Daducci et al 2014]

- Remove streamlines that
  do not explain the diffusion MRI data
  (or assign a low weight to streamlines not explaining data)

Advanced streamline filtering techniques

- SIFT1, SIFT2, LIFE, COMMIT
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Advanced streamline filtering techniques

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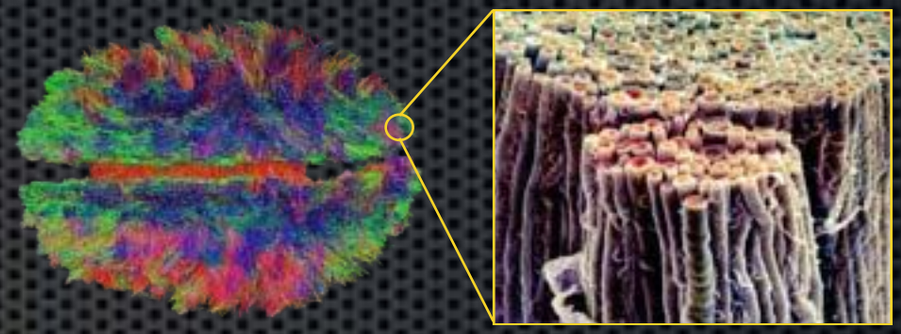
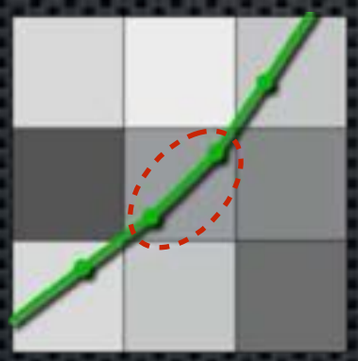
- Remove streamlines that
  do not explain the diffusion MRI data
  (or assign a low weight to streamlines not explaining data)
- *Tractometer* reveals that they reduce invalid connections but *at the price of removing some valid connections*
- Global tractography shows similar trends

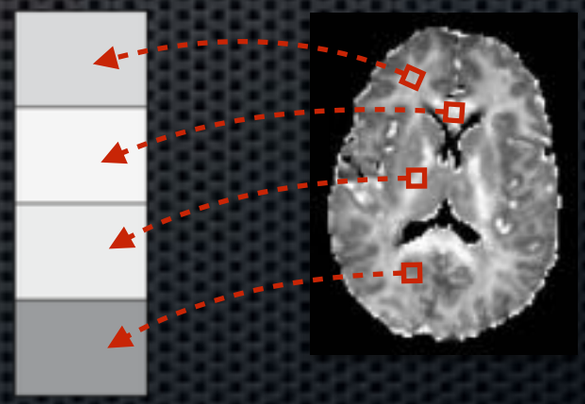
There is no space for everyone!



- Prior1: Streamlines are not just lines!
  - They have a volume
  - There must be a conservation of density in space



Streamlines have "volume" Every fiber contributes by its length



"Density" map Gives the total intra-axonal volume fraction in each voxel (NODDI)

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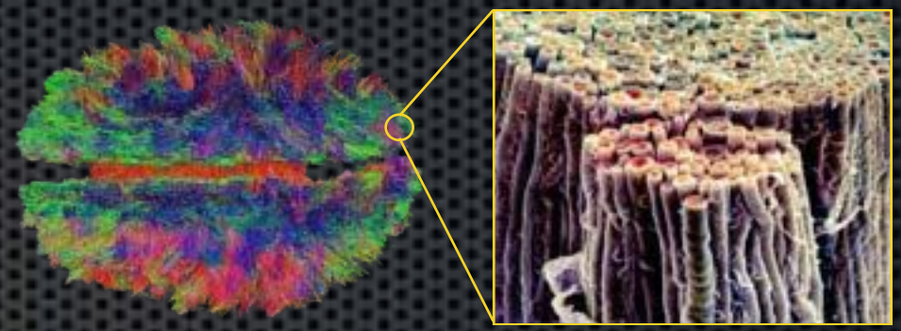

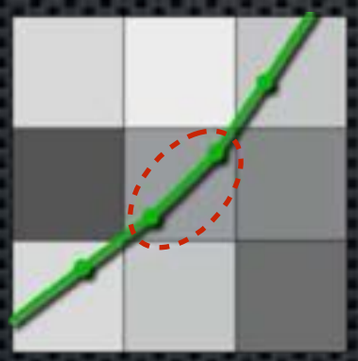

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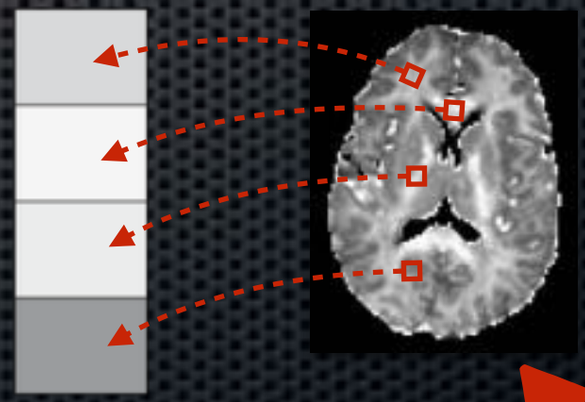


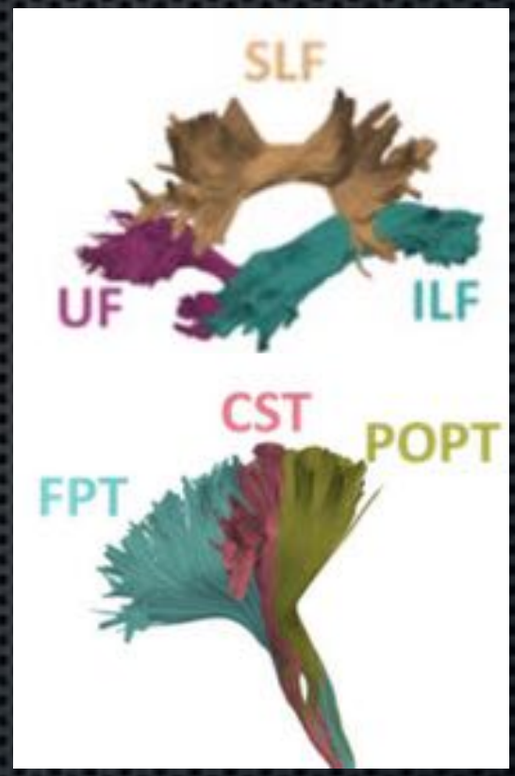
"Density" map
Gives the total intra-axonal volume fraction in each voxel (NODDI)

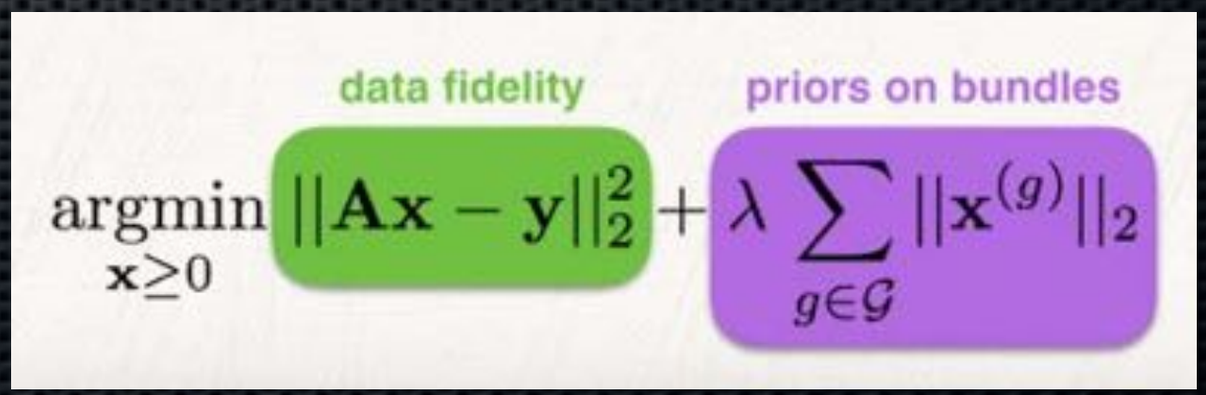
NOTE

This map might come from any modality,
e.g. myelin, T1, qMRI

There is no space for everyone!

- Prior 2: Fibers are organized in bundles
  - Streamlines are not independent





[Curtesy of A Daducci & Mateo Frigo MSc]

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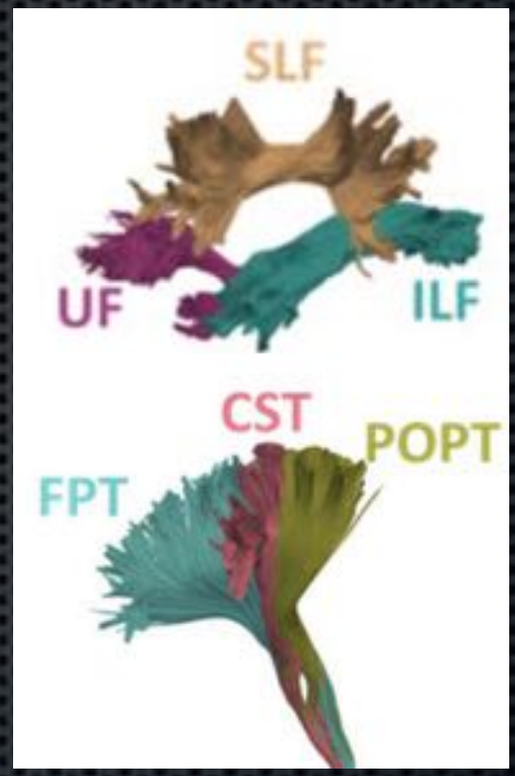
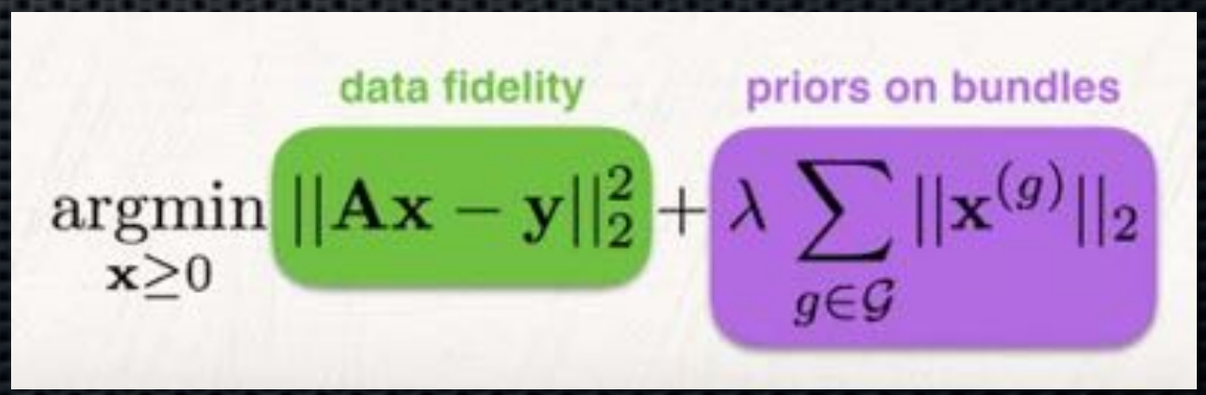


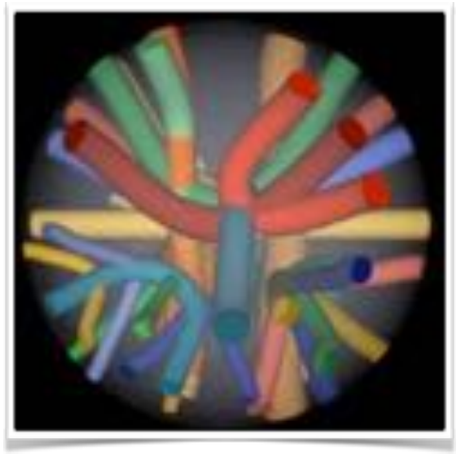
- COMMIT implementation with
  priors1 (conversation of density in space)
  priors2 (group sparsity)

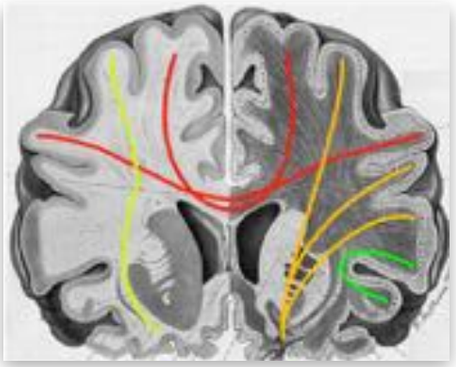


[Curtesy of A Daducci
& Mateo Frigo MSc]

False positives identification with COMMIT

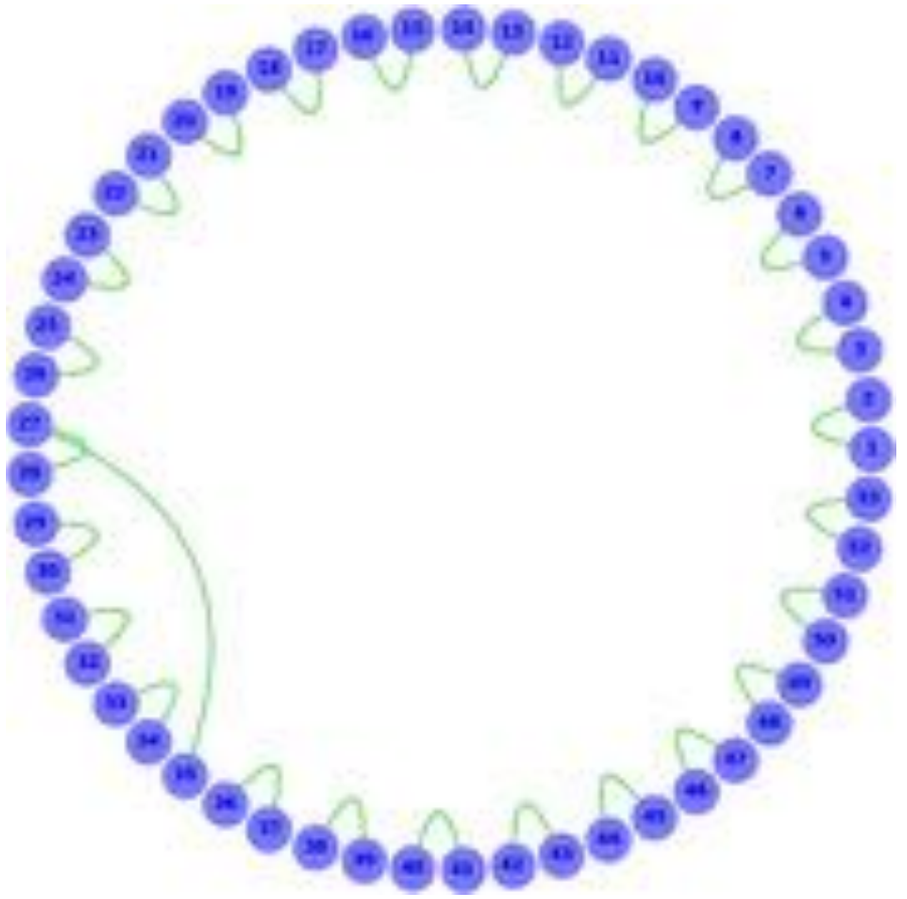
- Synthetic phantom [Caruyer et al. 2013]
  - **Geometry** mimicking a real brain
    - 27 bundles
    - Various configurations of *crossing*, *bending* and *fanning* fibers
    - *CSF* contamination
  - **Known ground-truth**





True Positives (**TP**)

False Positives (**FP**)

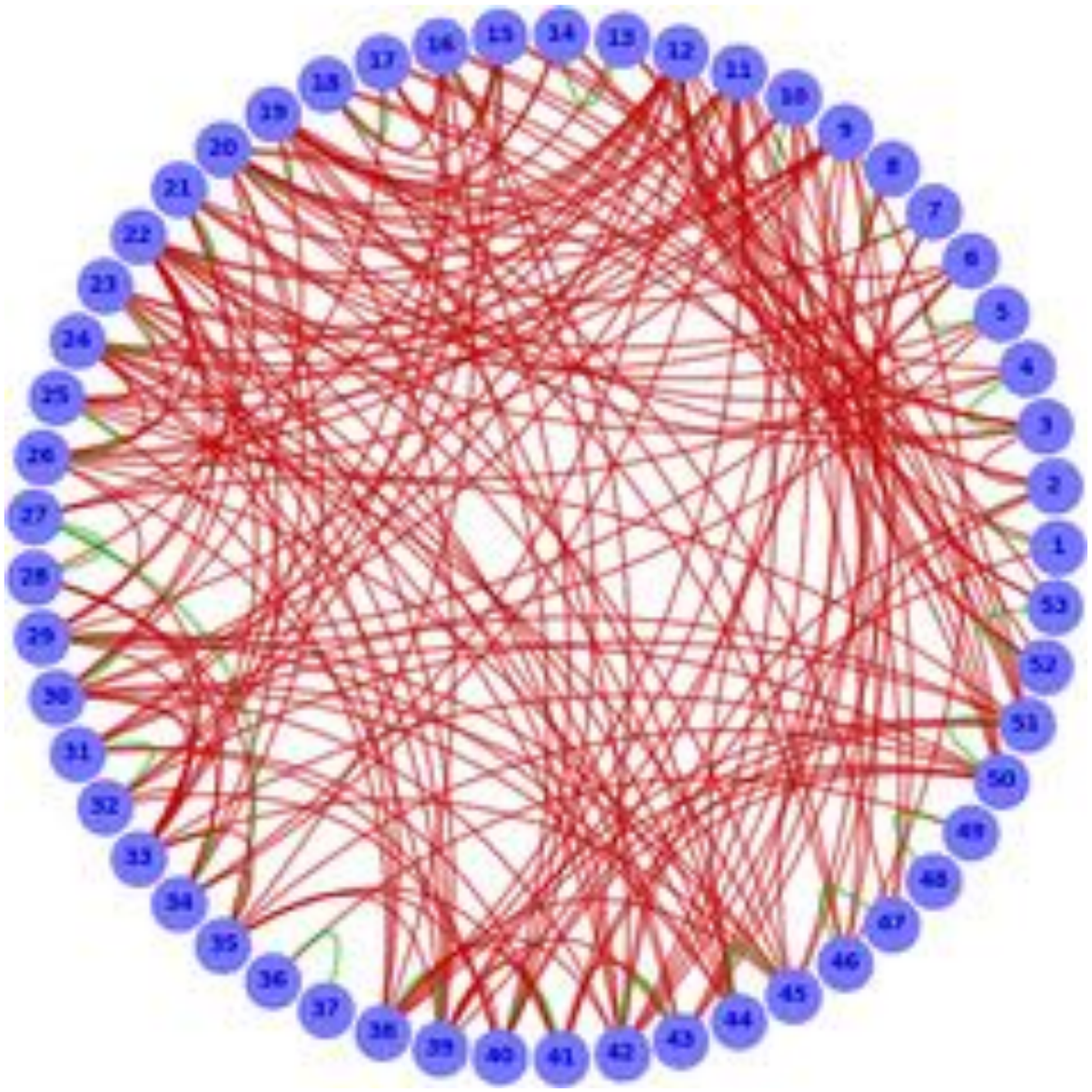


TP=27 (*sensitivity*=100%)

FP=0 (*specificity*=100%)

False positives identification with COMMIT v2

Streamline det tracking

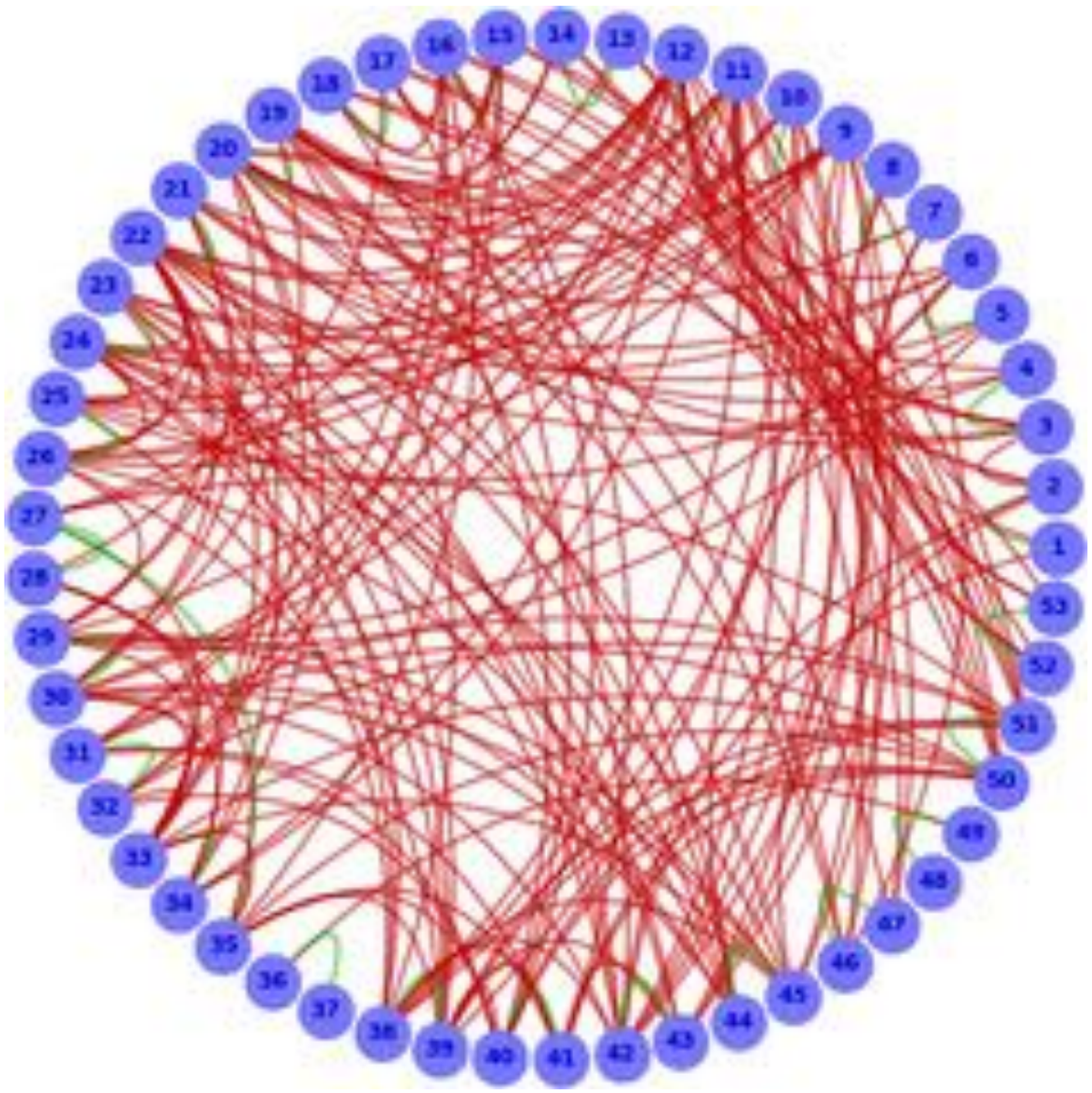


TP=27 (*sensitivity*=100%)

FP=**235** (*specificity*=**31.3%**)

False positives identification with COMMIT v2

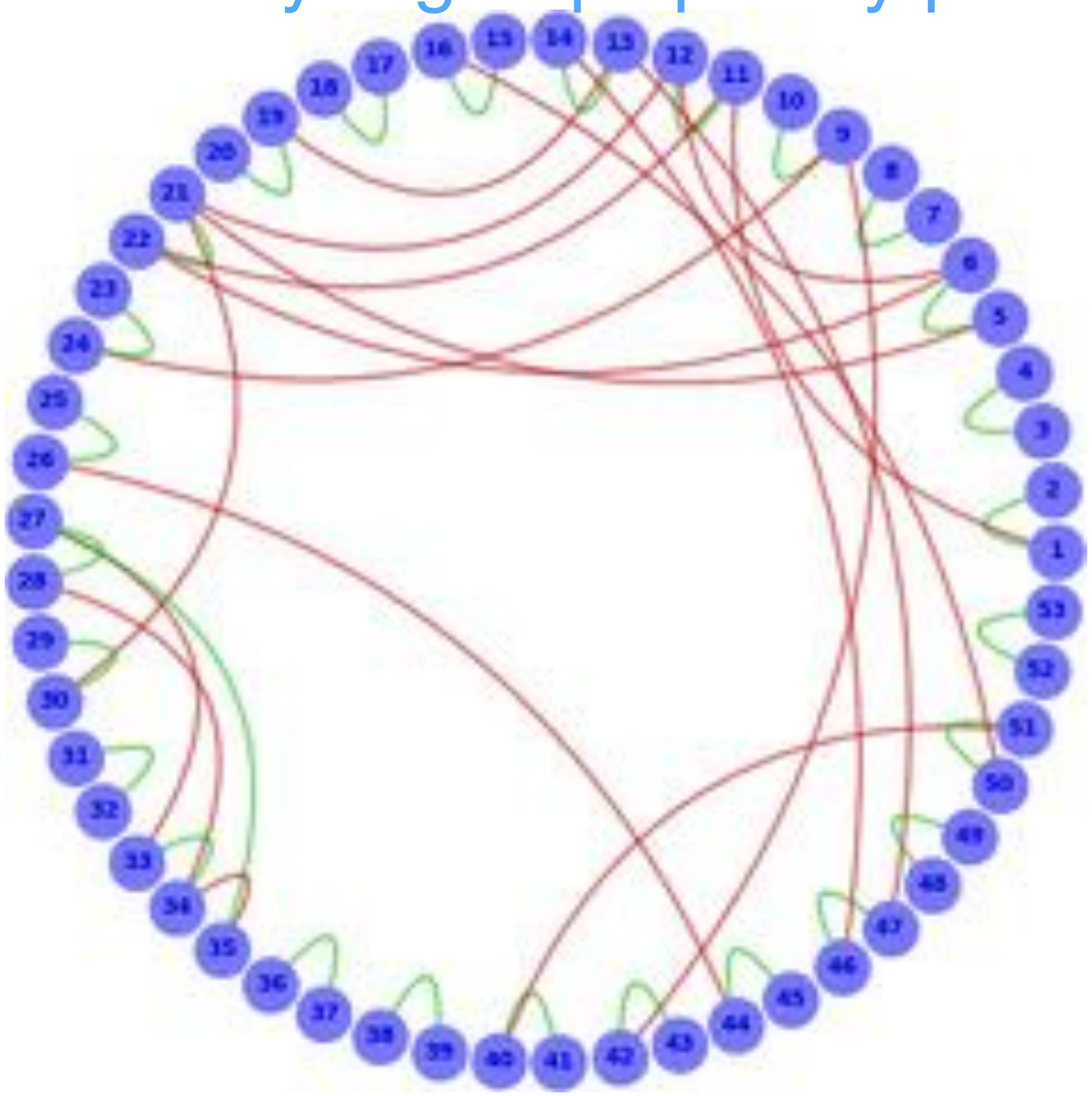
Streamline det tracking



TP=27 (*sensitivity*=100%)

FP=**235** (*specificity*=**31.3%**)

After COMMIT
density & group sparsity prior

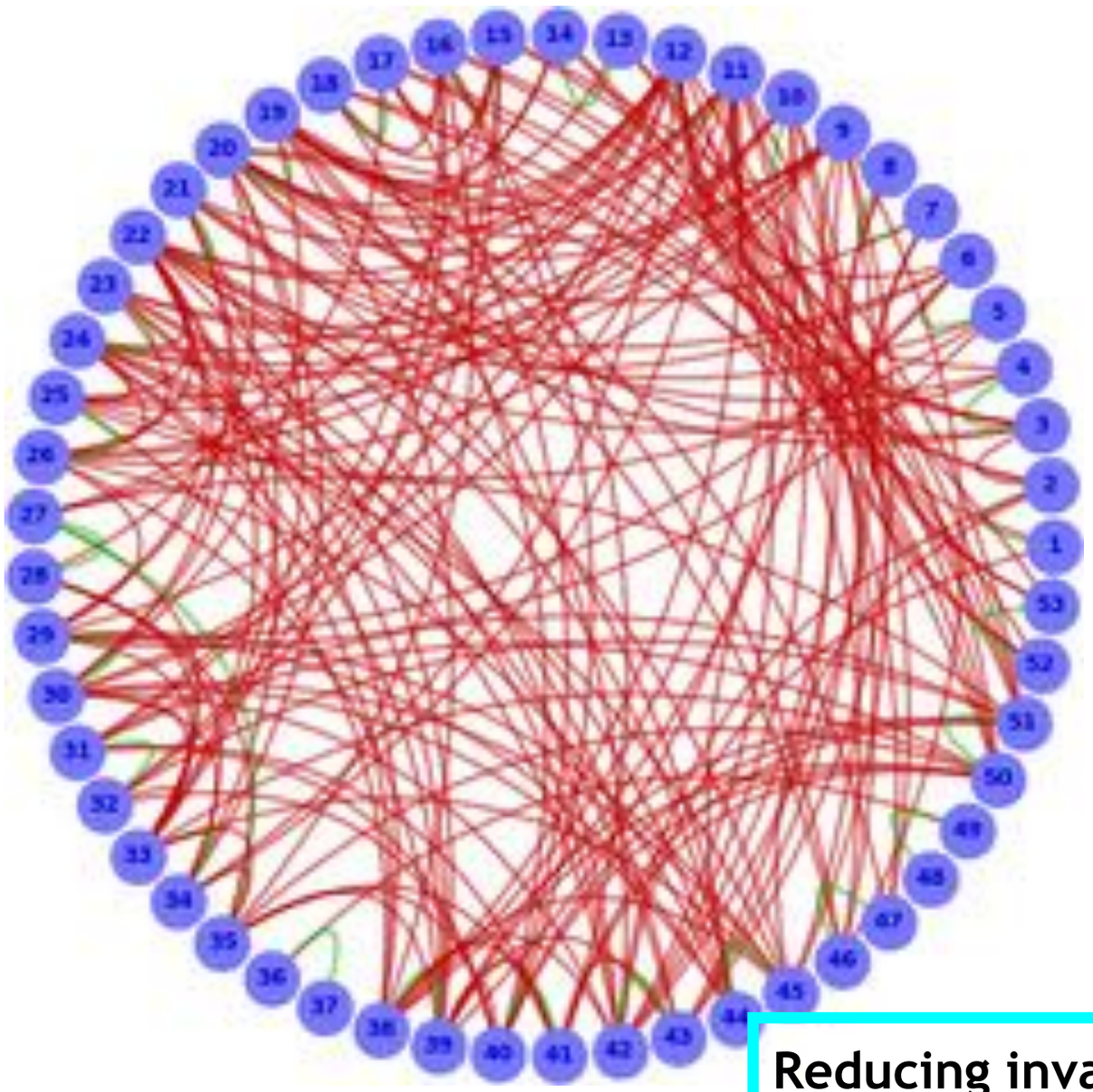


TP=27 (*sensitivity*=100%)

FP=**18** (*specificity*=**94.7%**)

False positives identification with COMMIT v2

Streamline det tracking



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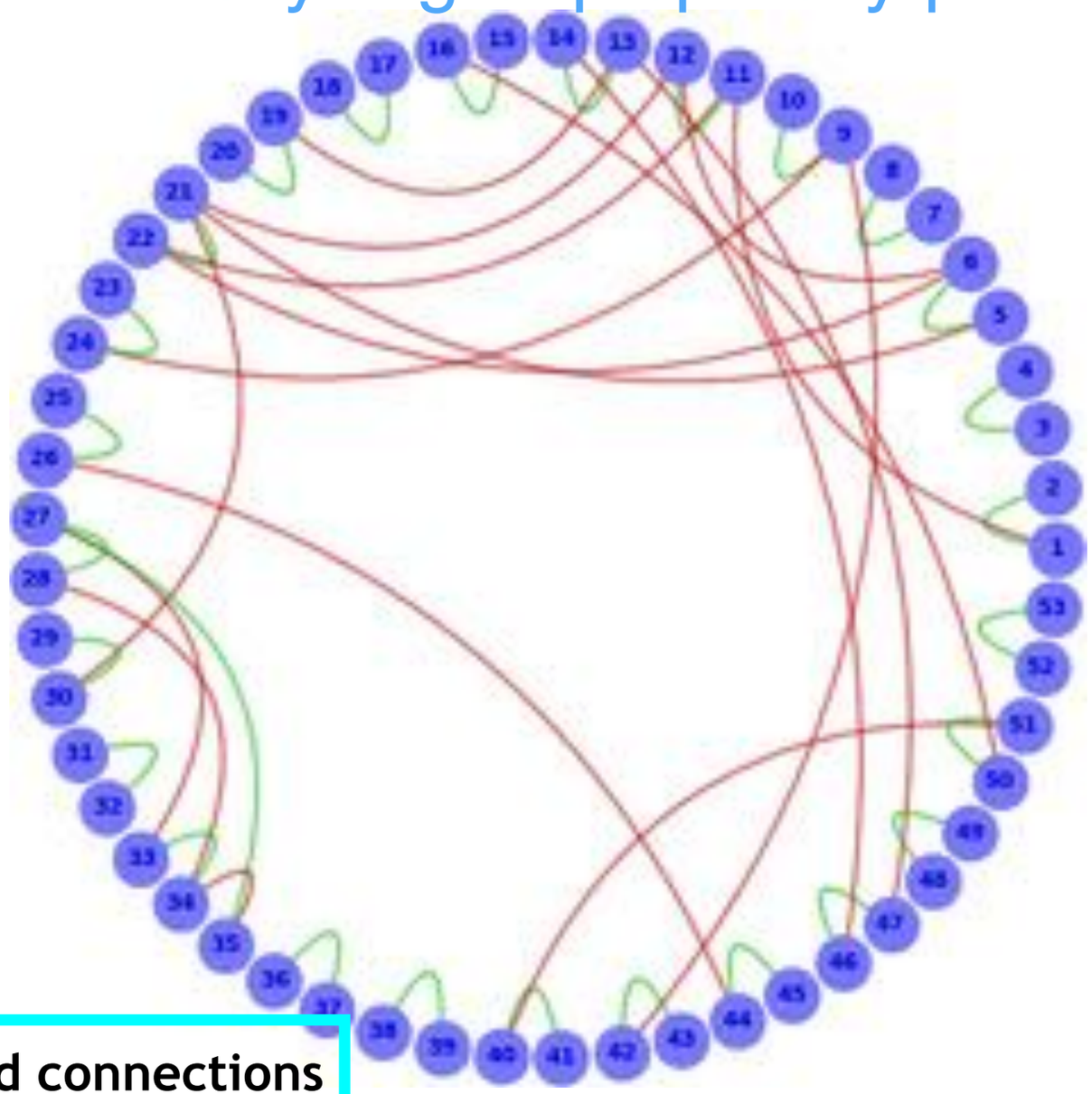


TP=27 (*sensitivity*=100%)

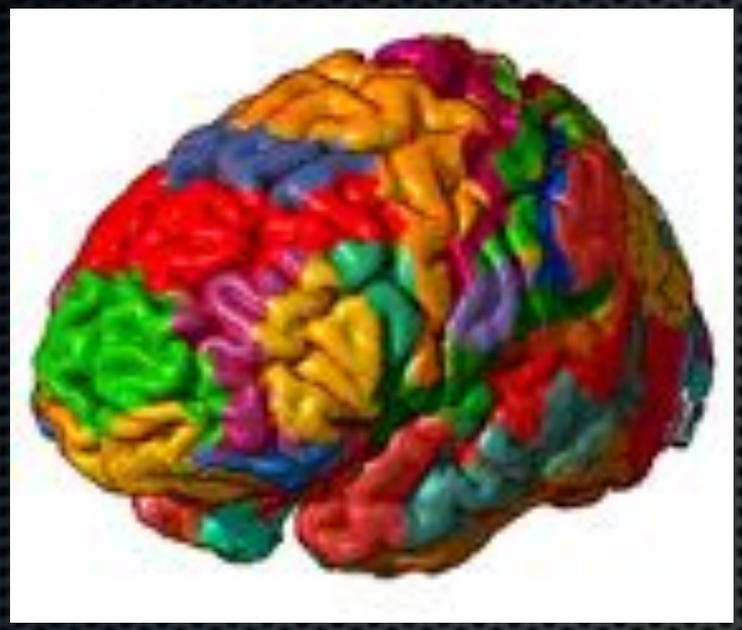
FP=**18** (*specificity*=**94.7%**)

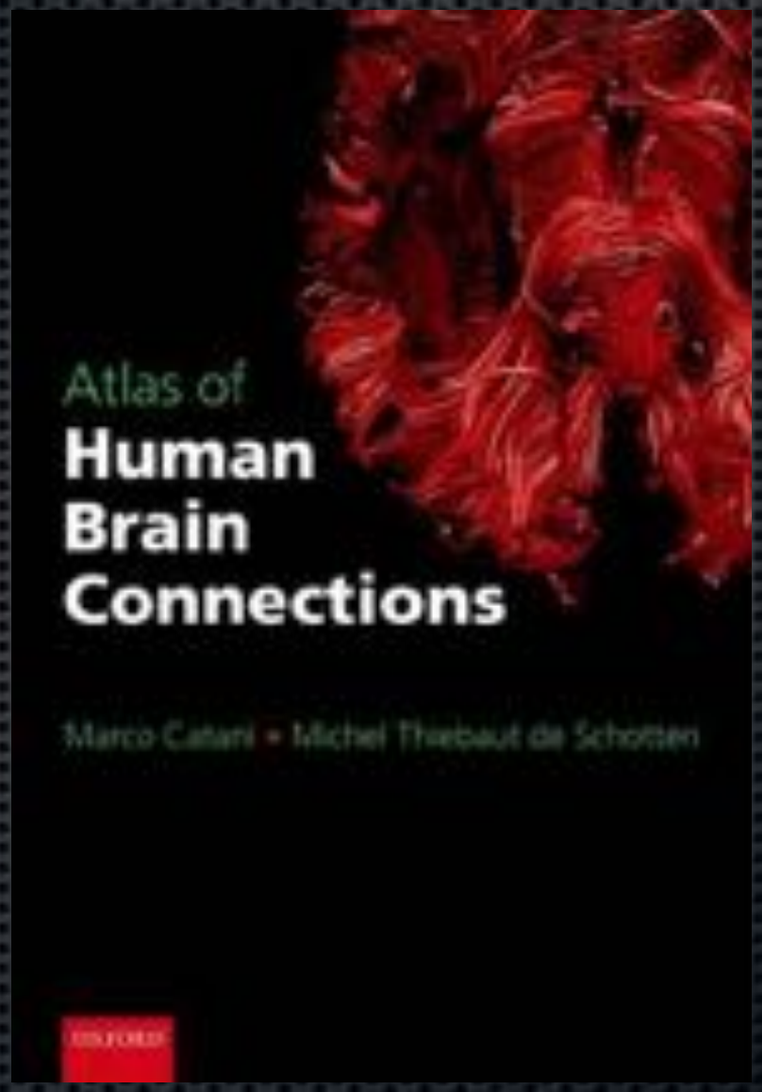
Reducing invalid connections

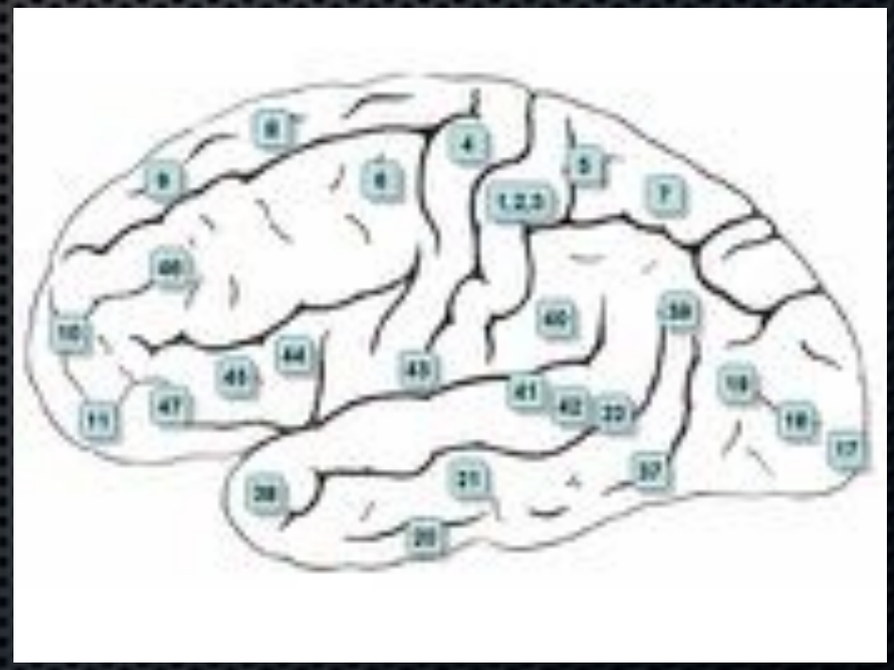
More *anatomical priors* to

reduce invalid connections

Tract selection with atlases, ROIs & anatomical knowledge







- Tractometer reveals that they reduce invalid connections but at the price of removing some valid connections

Position bias:
hard to track bundles

- Bundle-Specific Tractography (BST)
- Prior knowledge and bundle-specific parameters

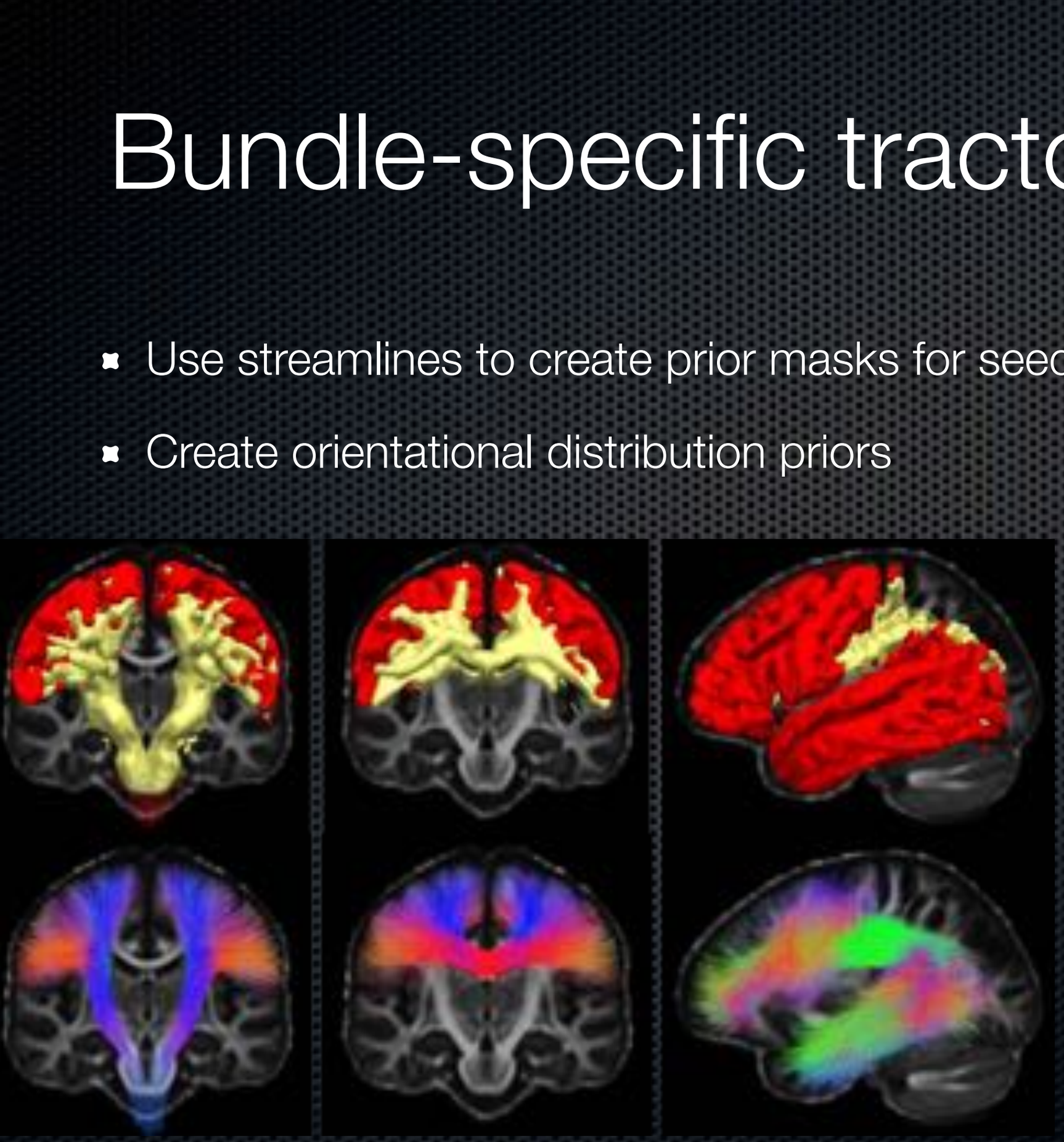
[Chamberland et al 2014]
[Chamberland et al HBM 2016]

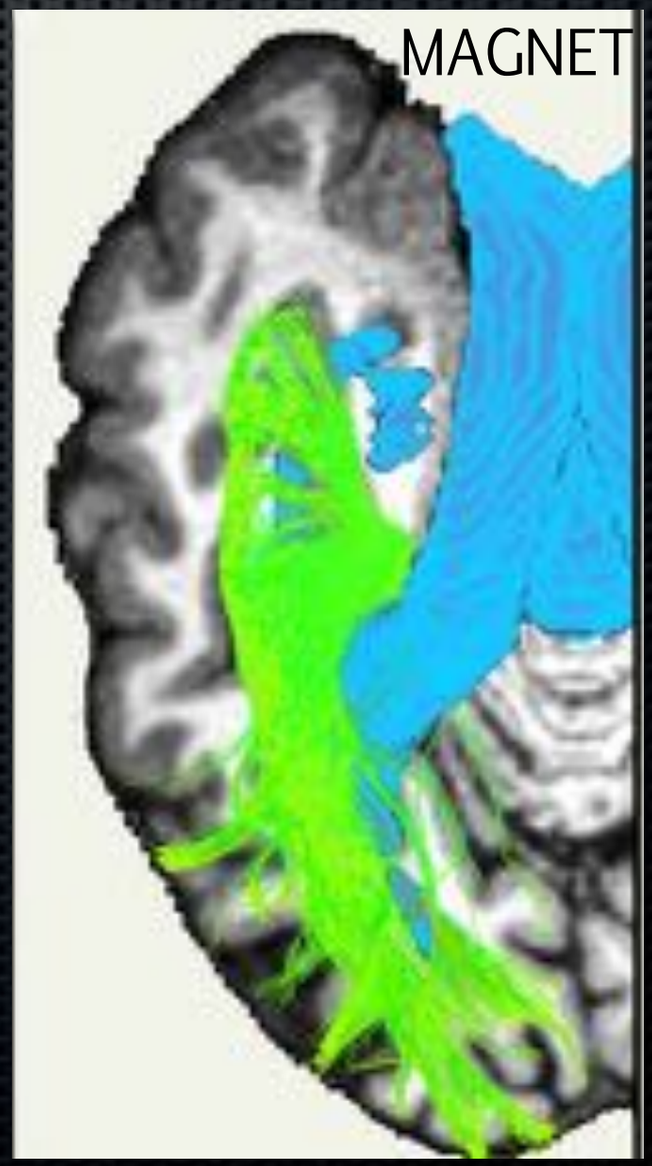
[Rheault et al CDMRI 2017]

Bundle-specific tractography

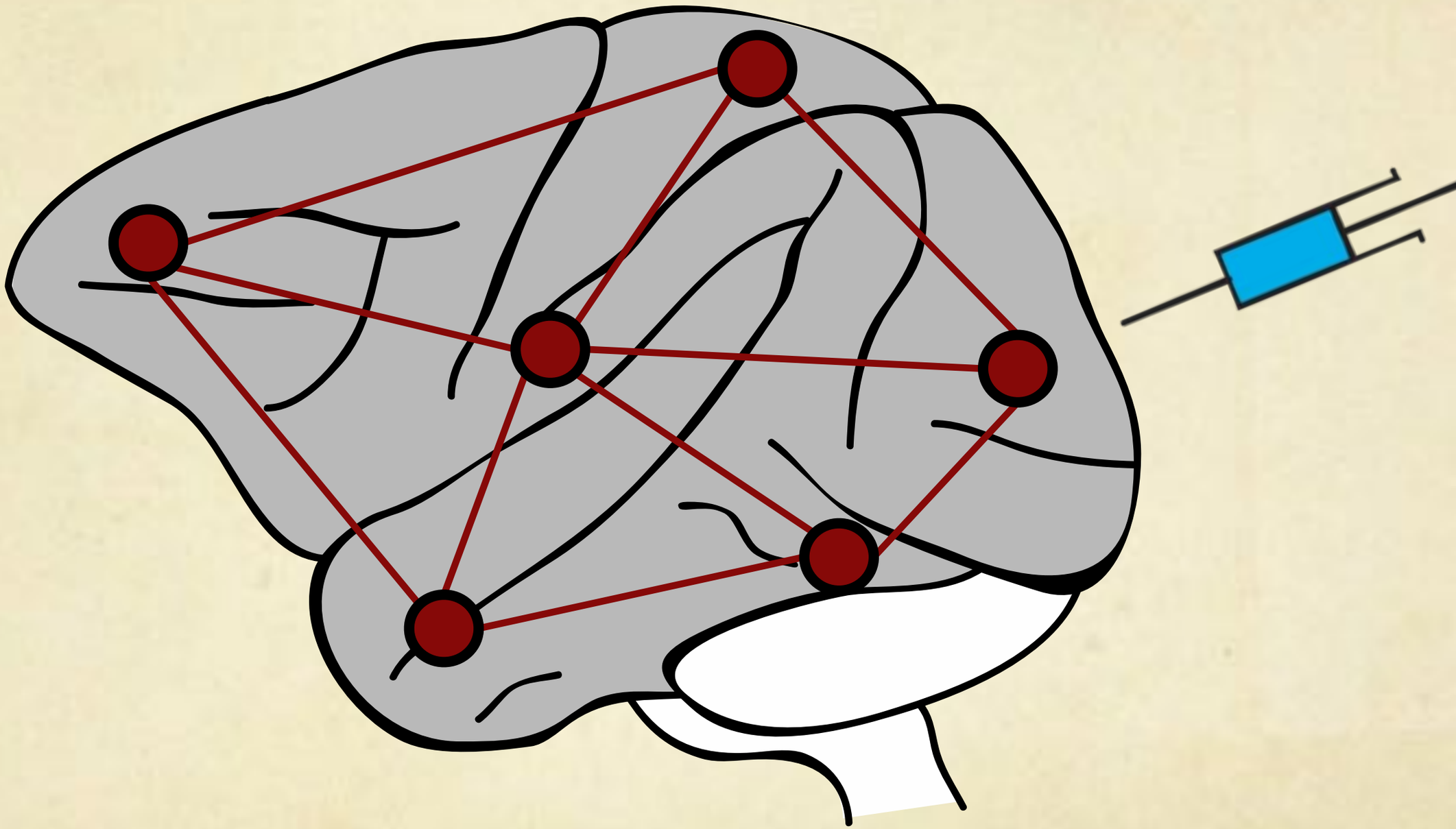
Reducing position bias

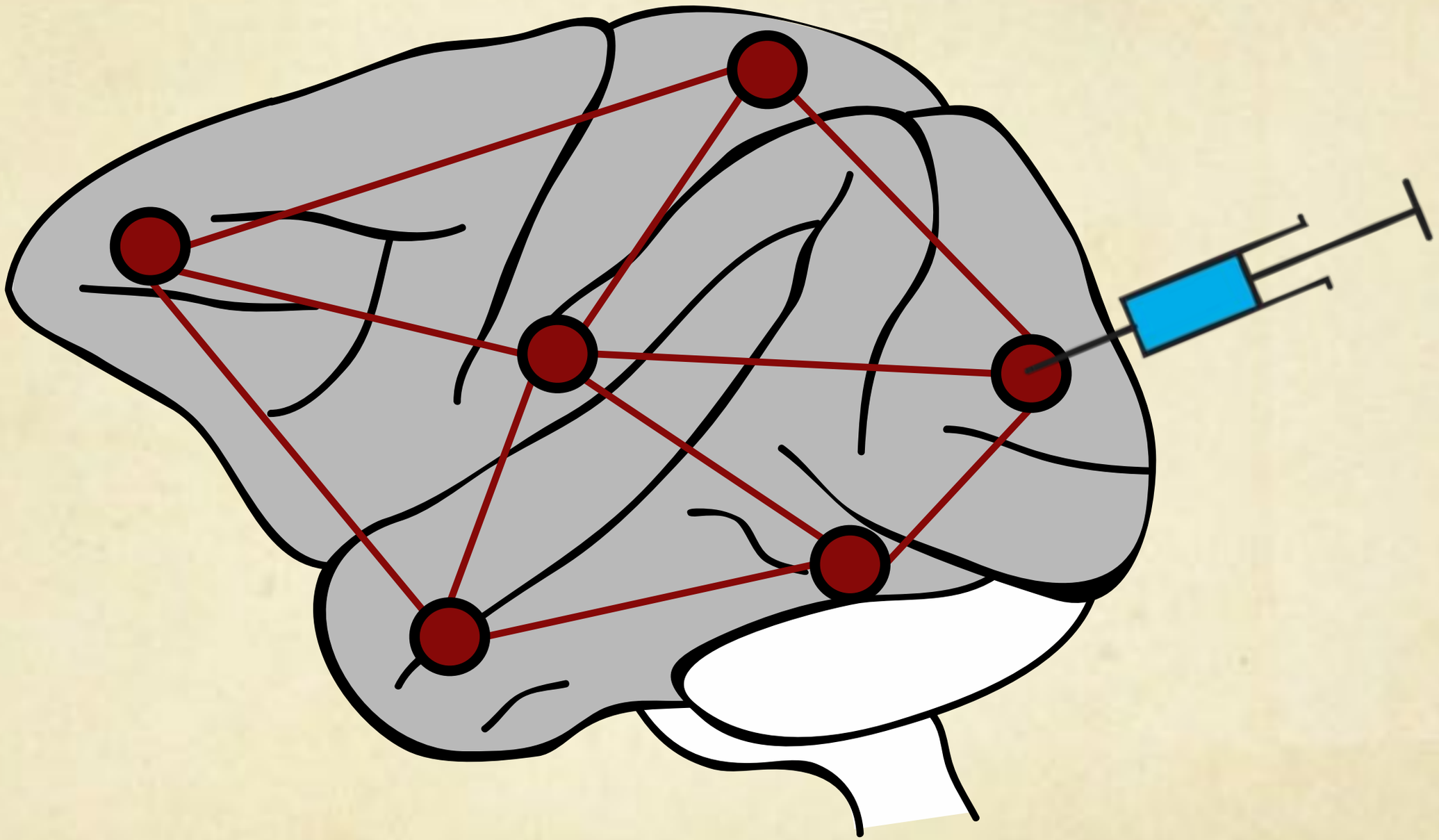
- Use streamlines to create prior masks for seeding / masking
- Create orientational distribution priors

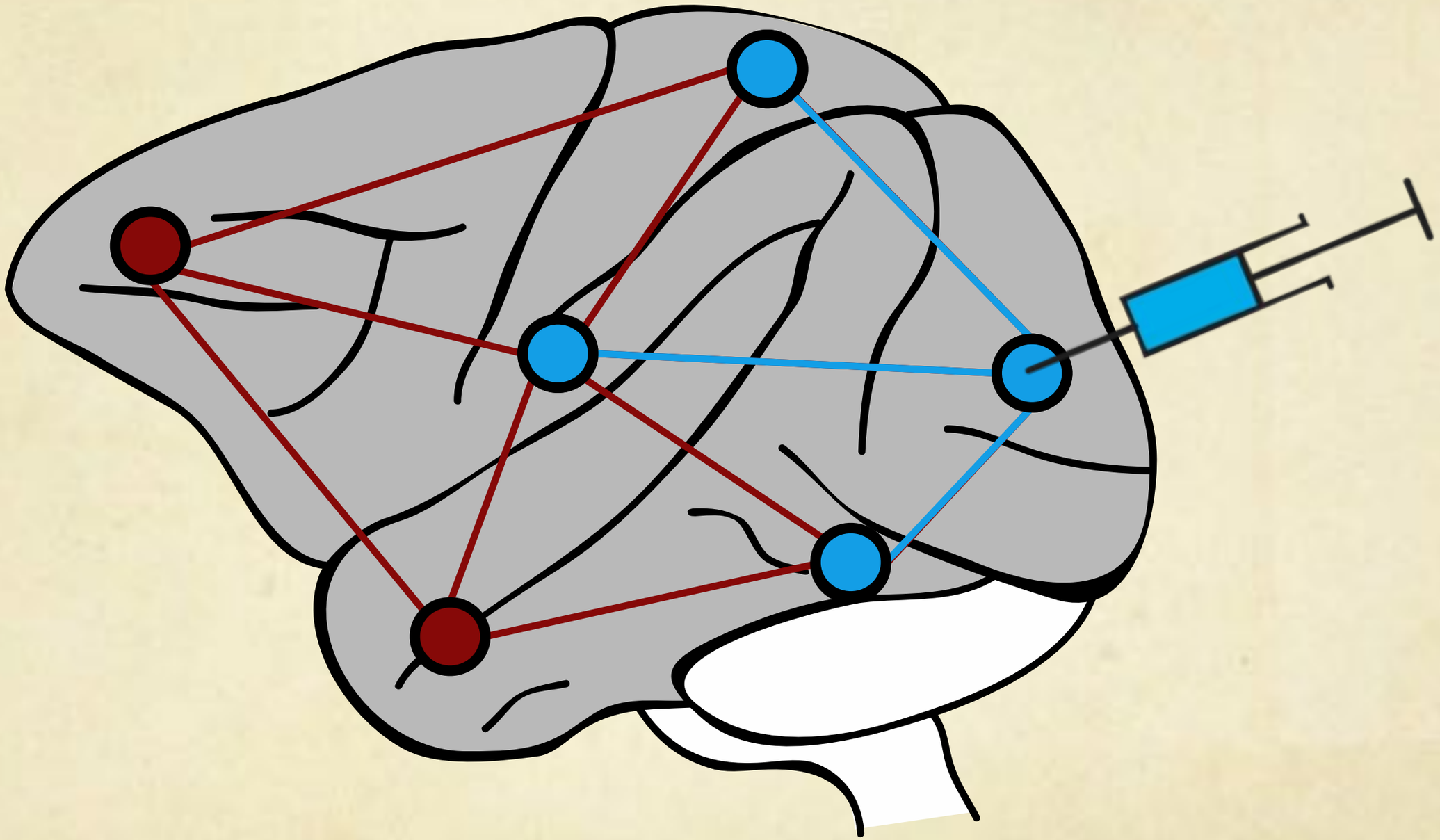


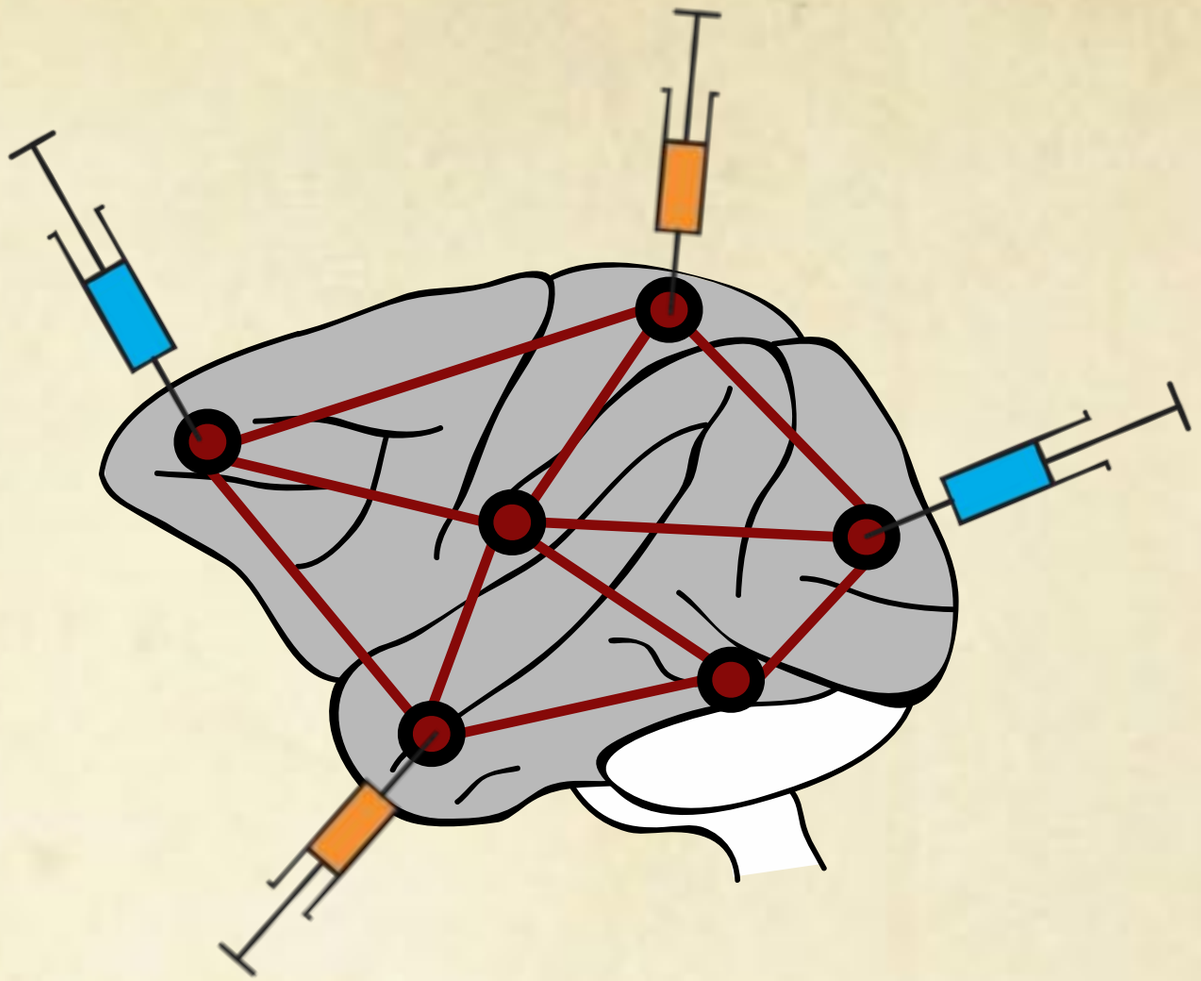


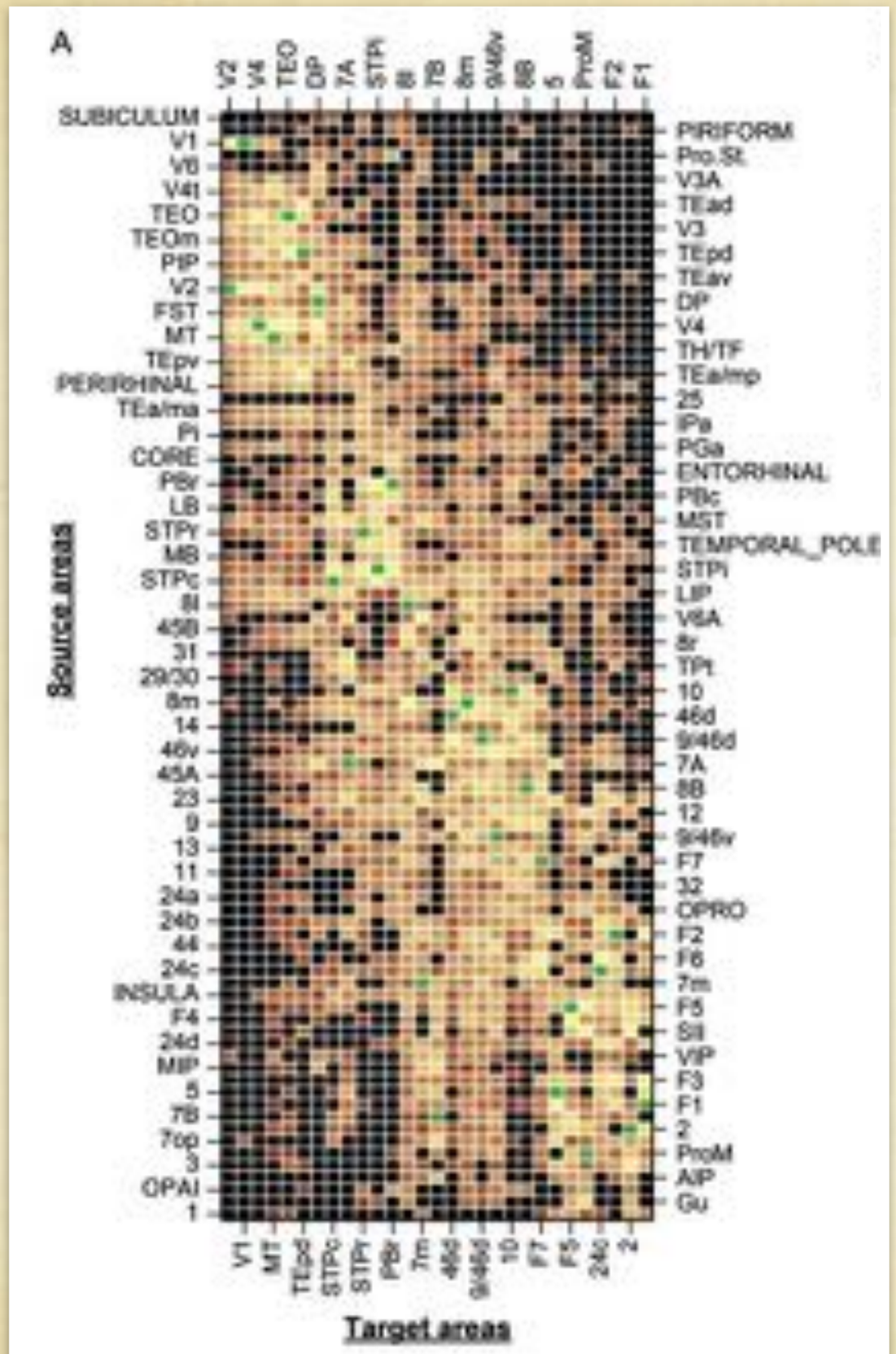
The validation challenge!



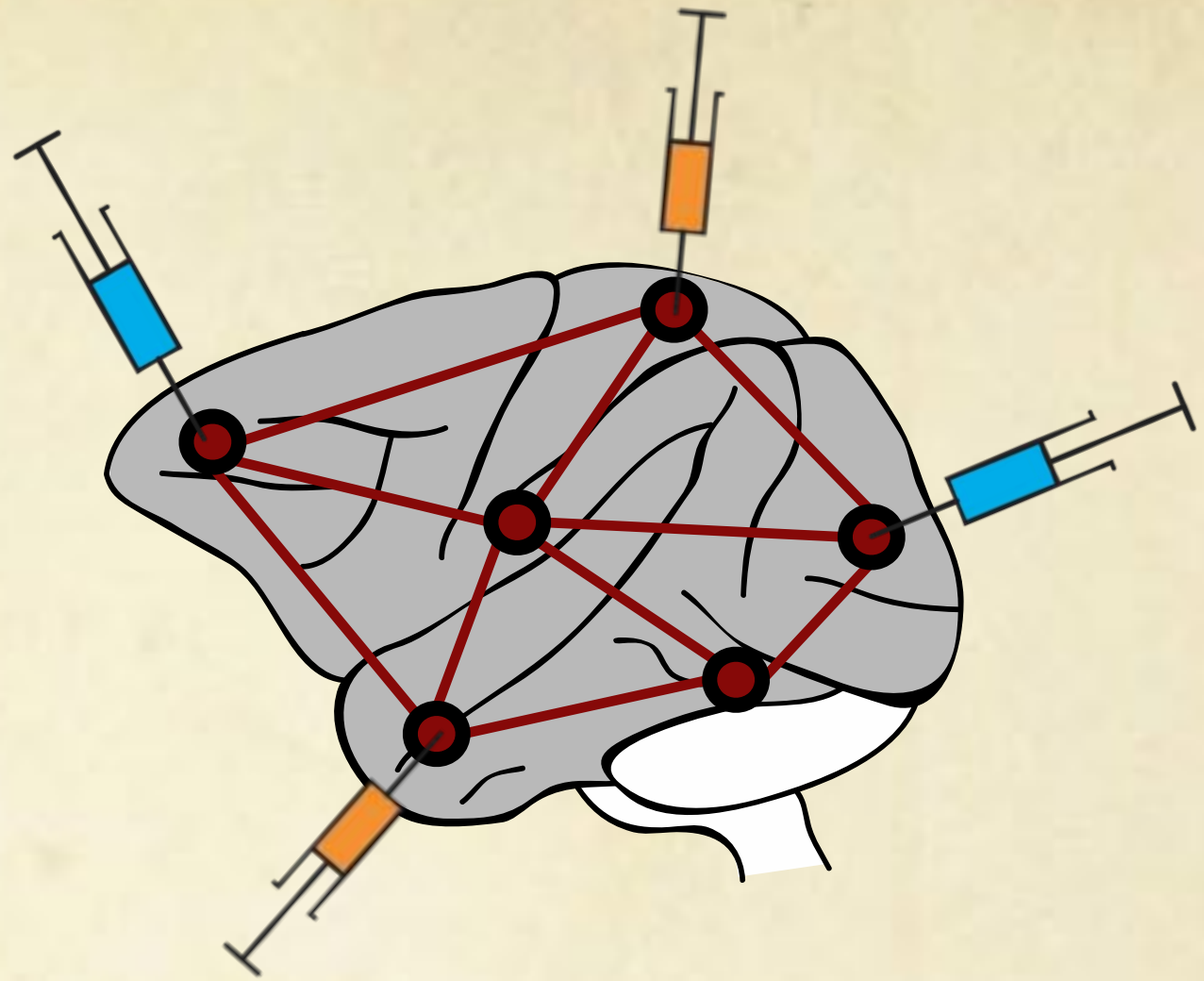


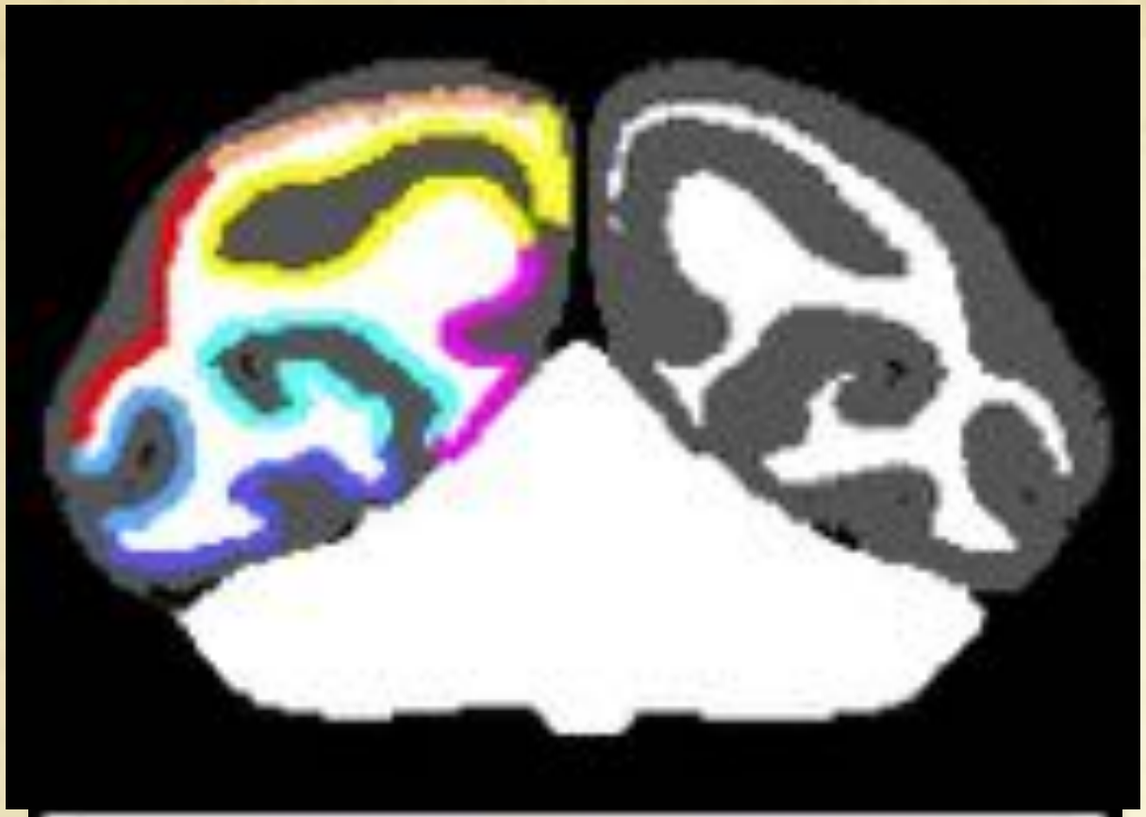


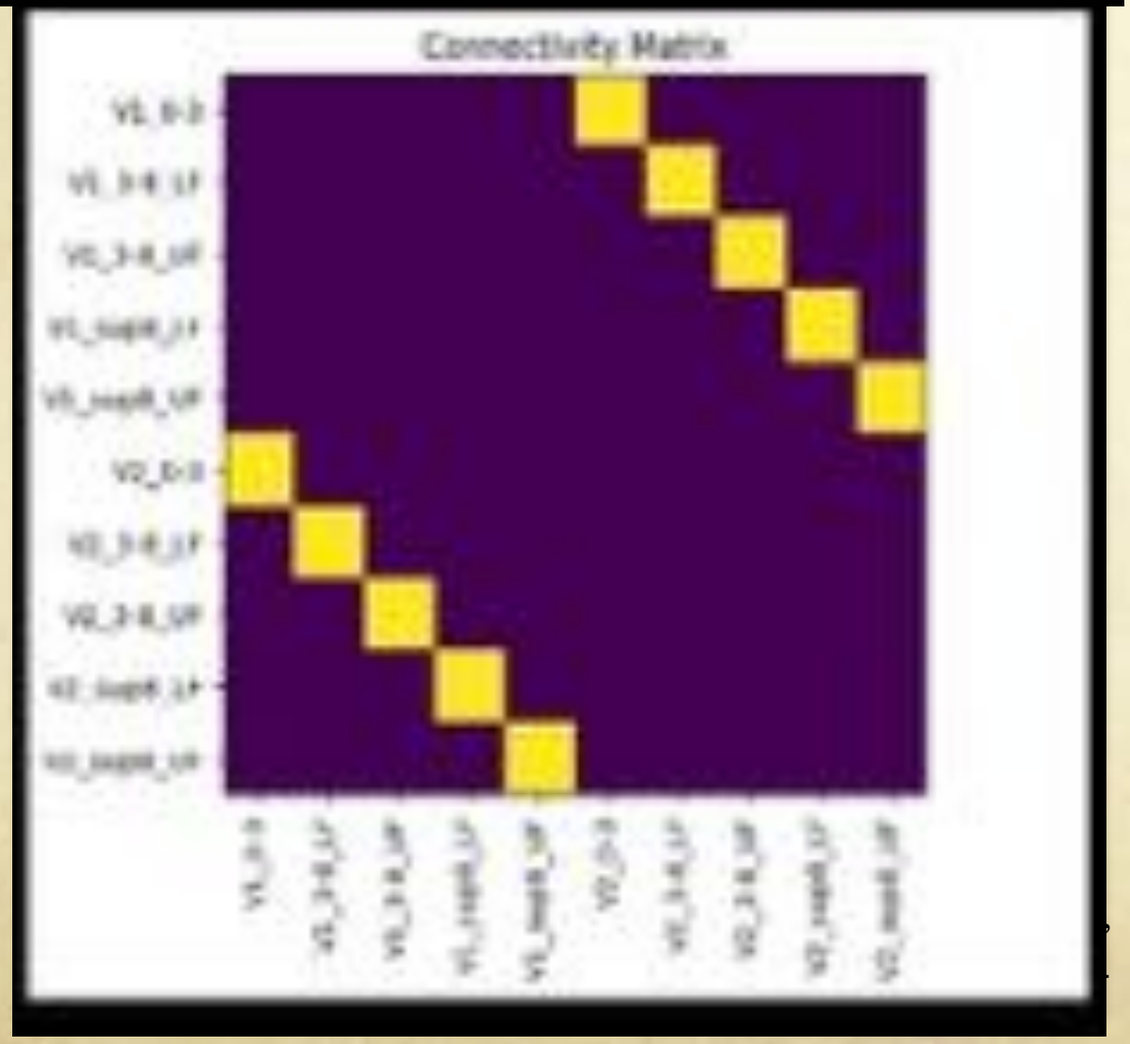


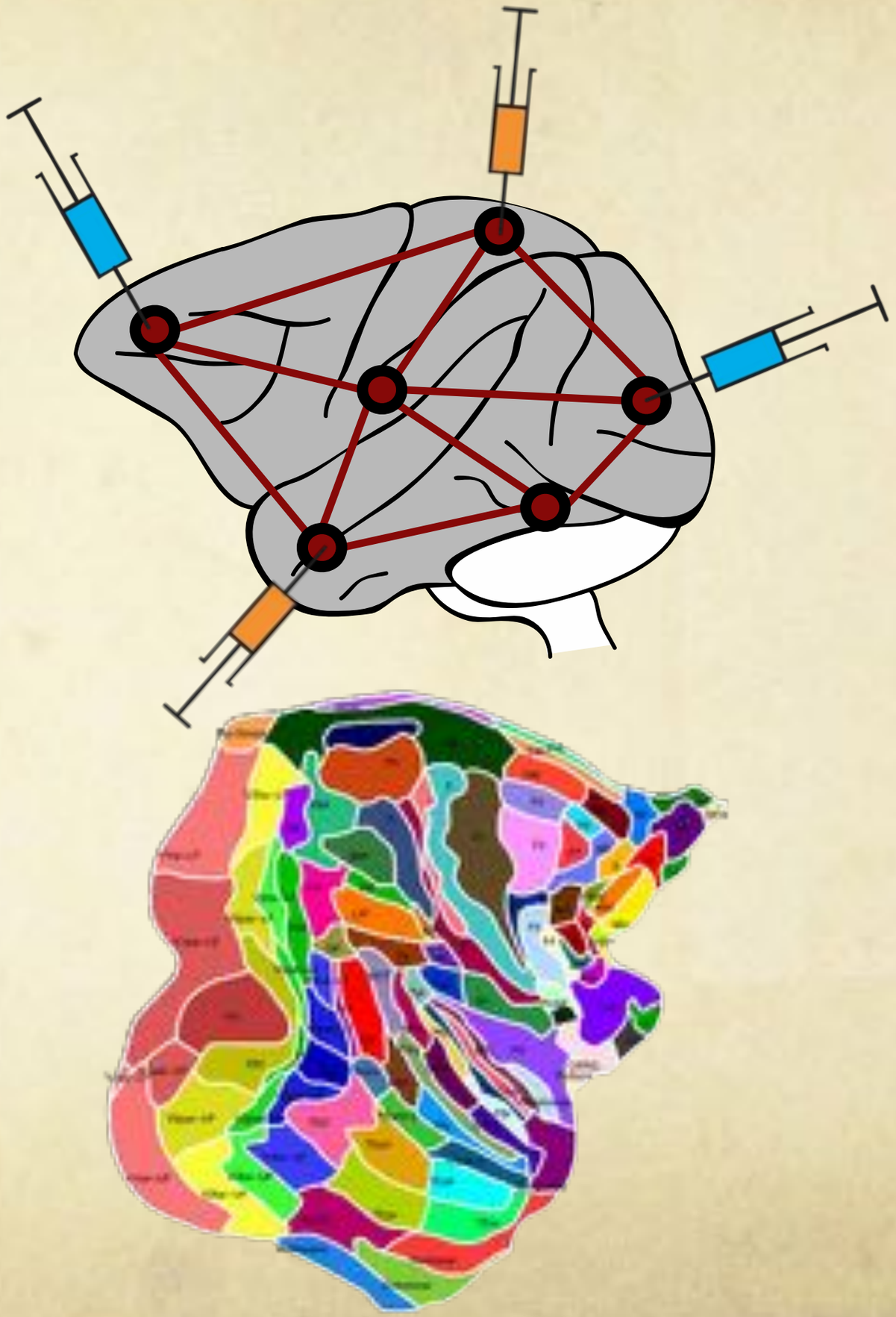


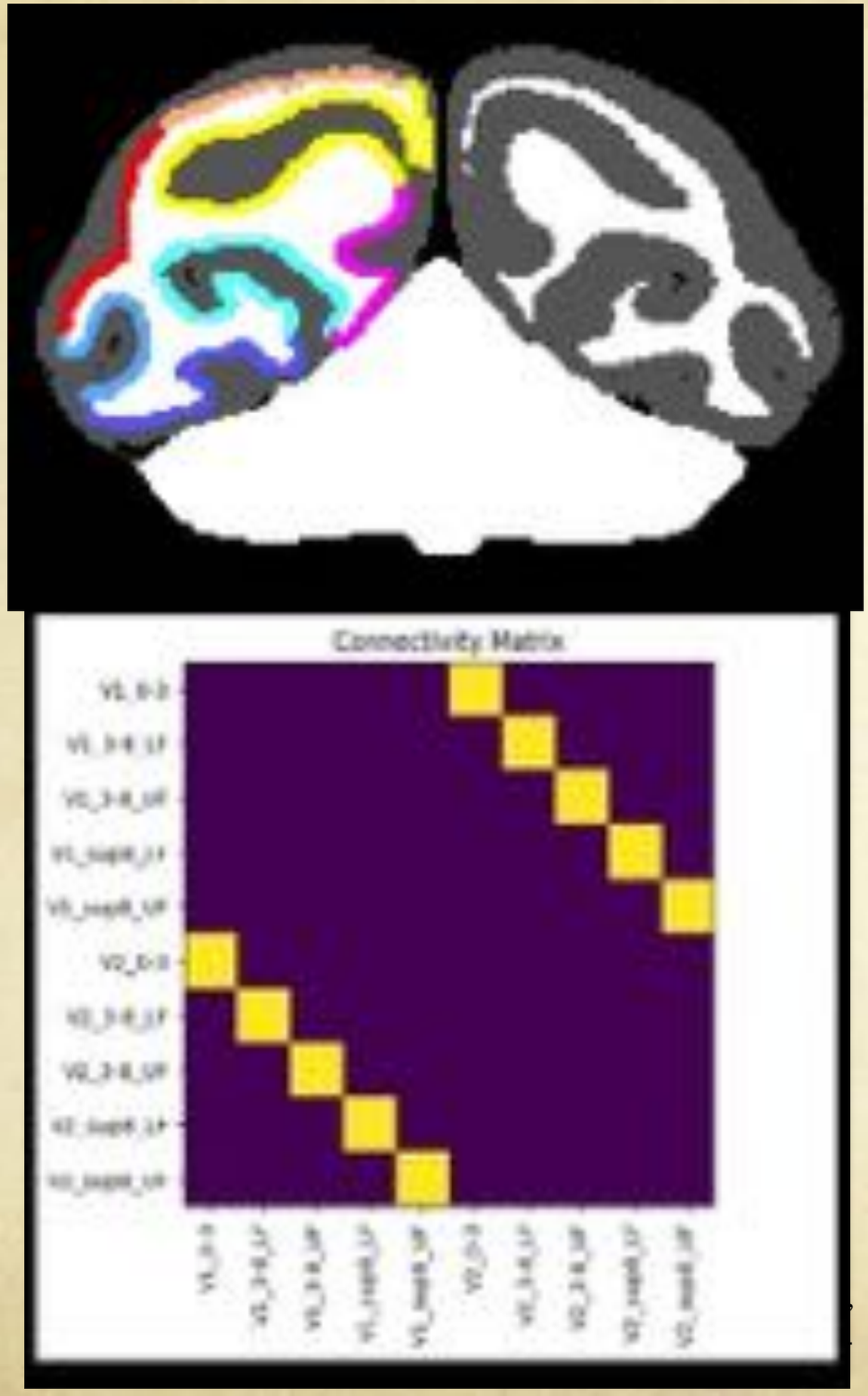
Markov, Ercsey-Ravasz,
Ribeiro Gomes, Lamy, **Magrou** et al., 2014






Connectivity Matrix





High resolution (300 um)
High angular (192 dirs)
Multi b-value (4 b's)

b=0

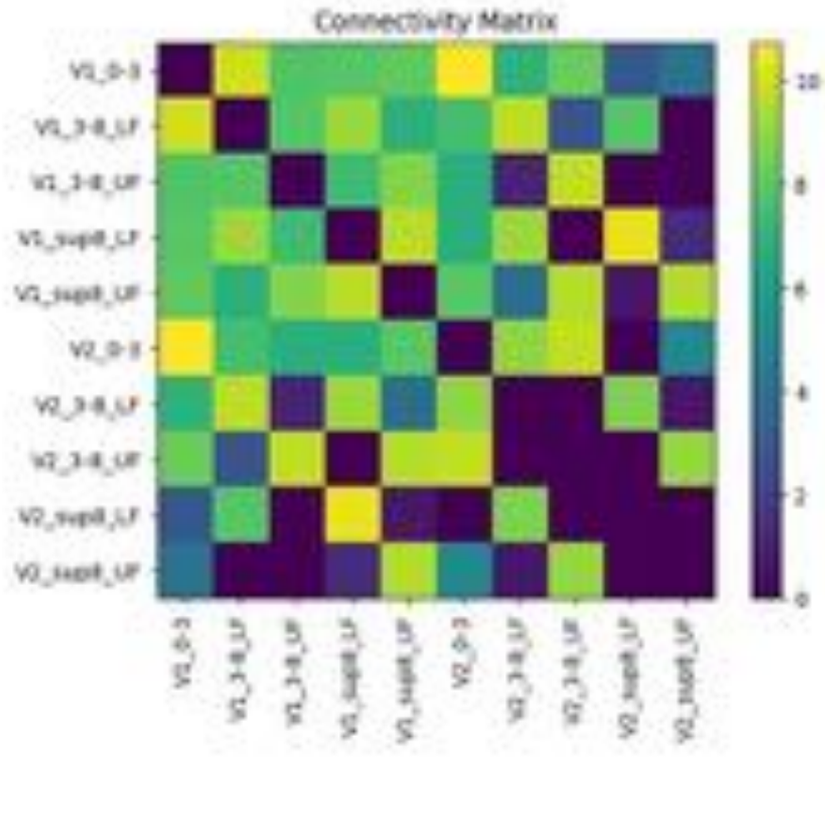
b=2000

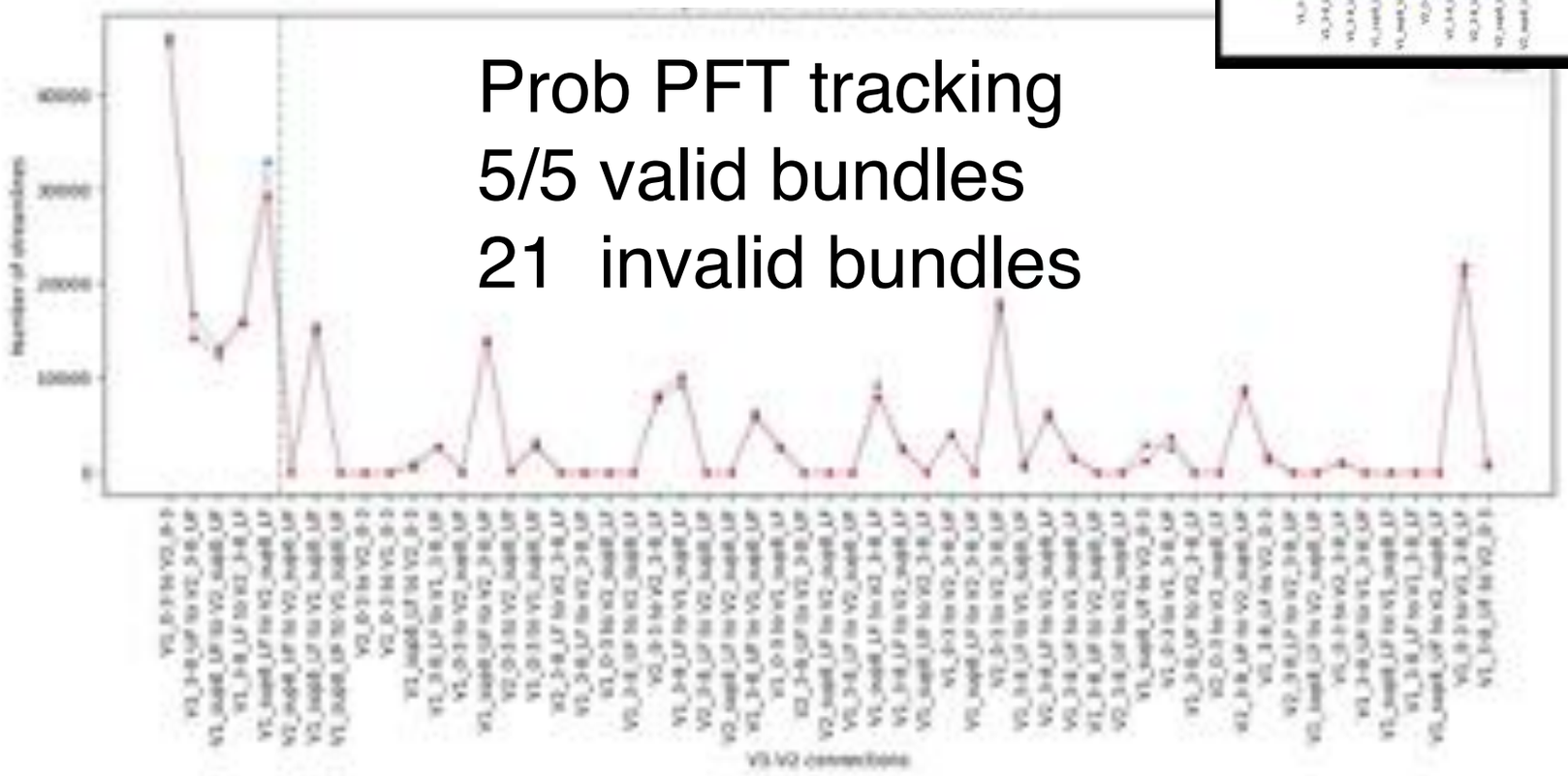
b=4000

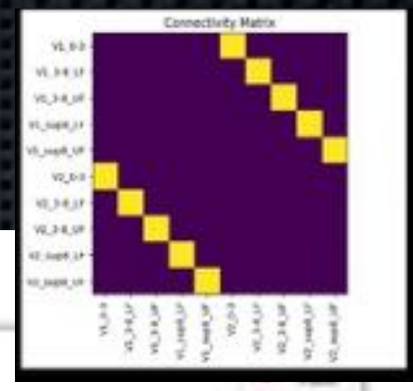
b=6000

[Theaud etal. ISMRM18]

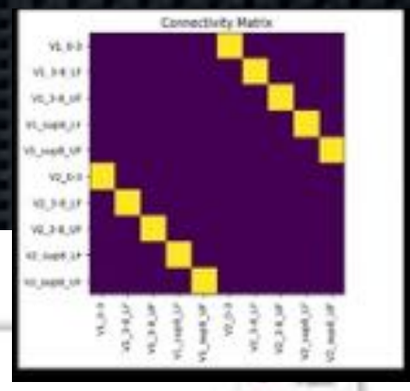
V1-V2 binary connectome

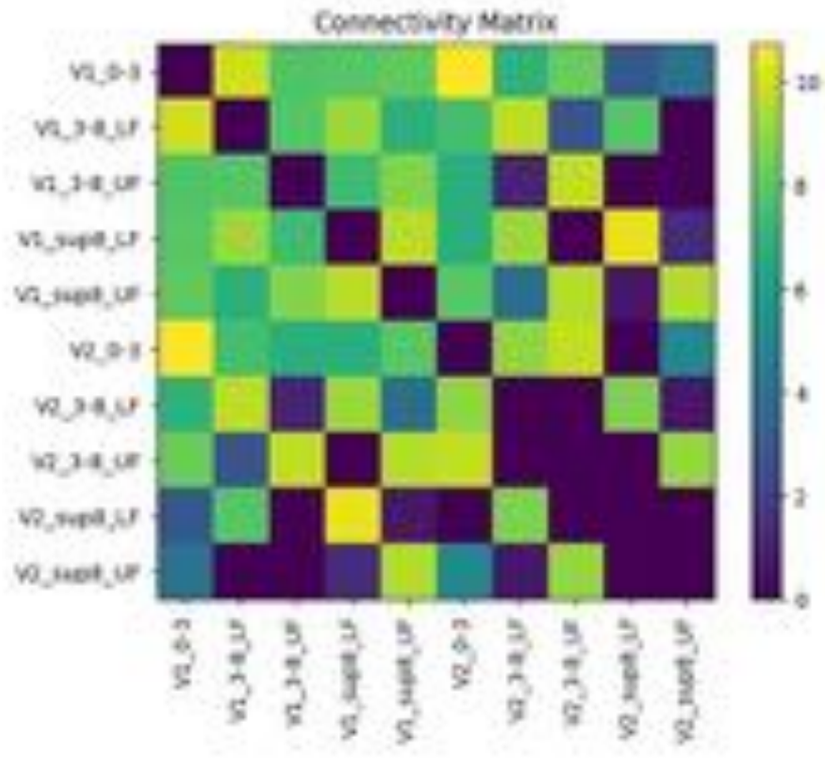


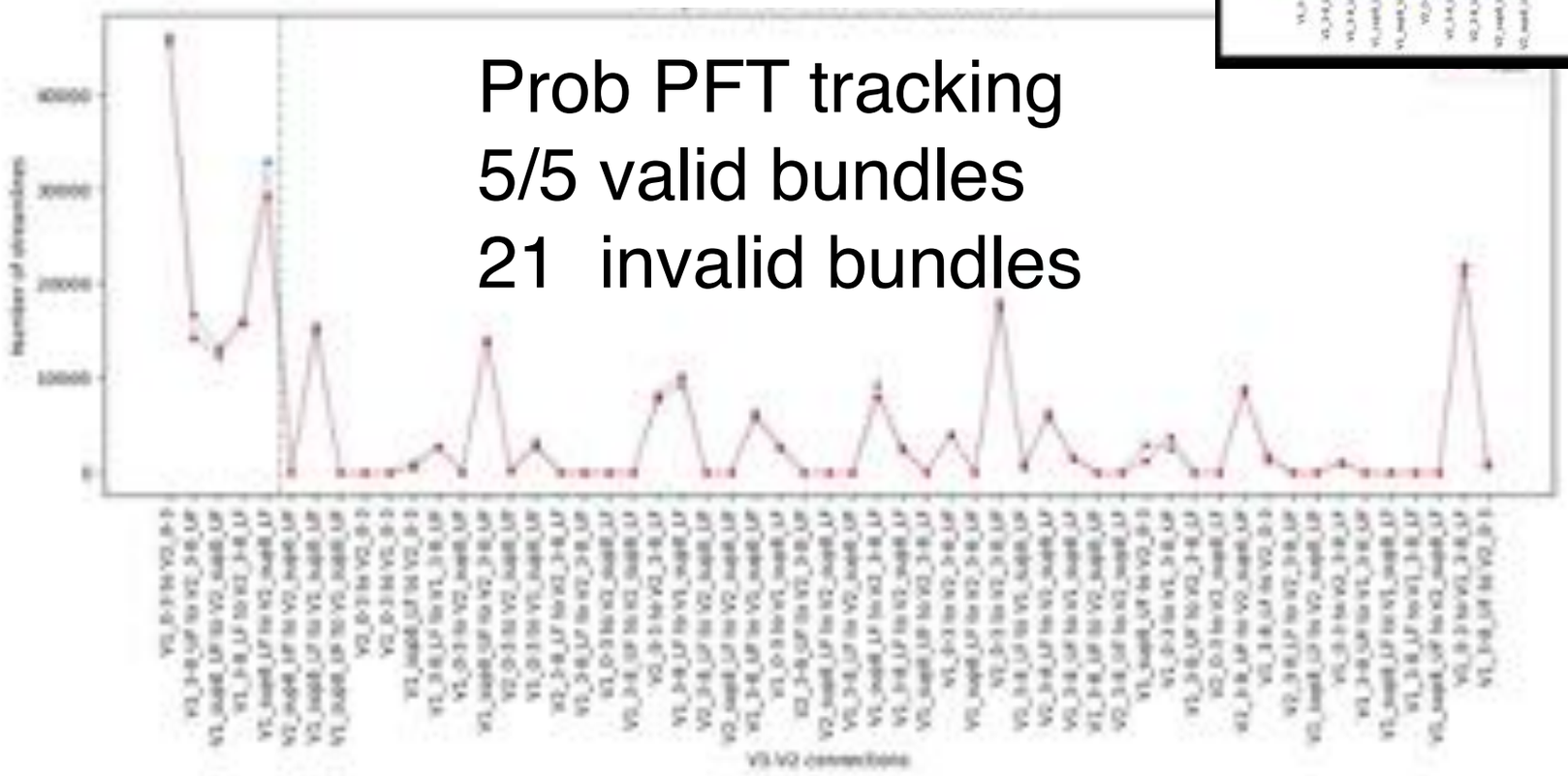


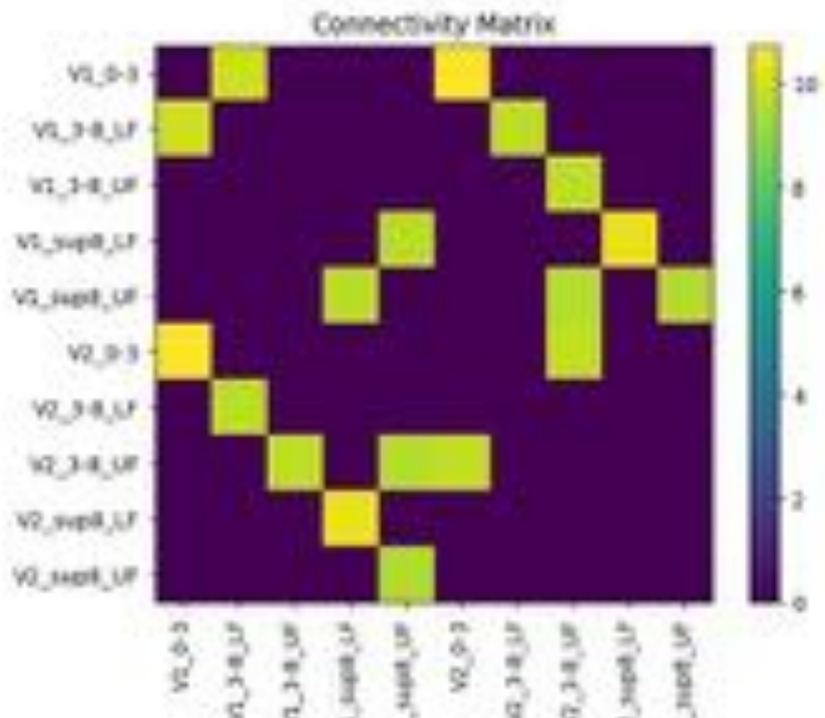


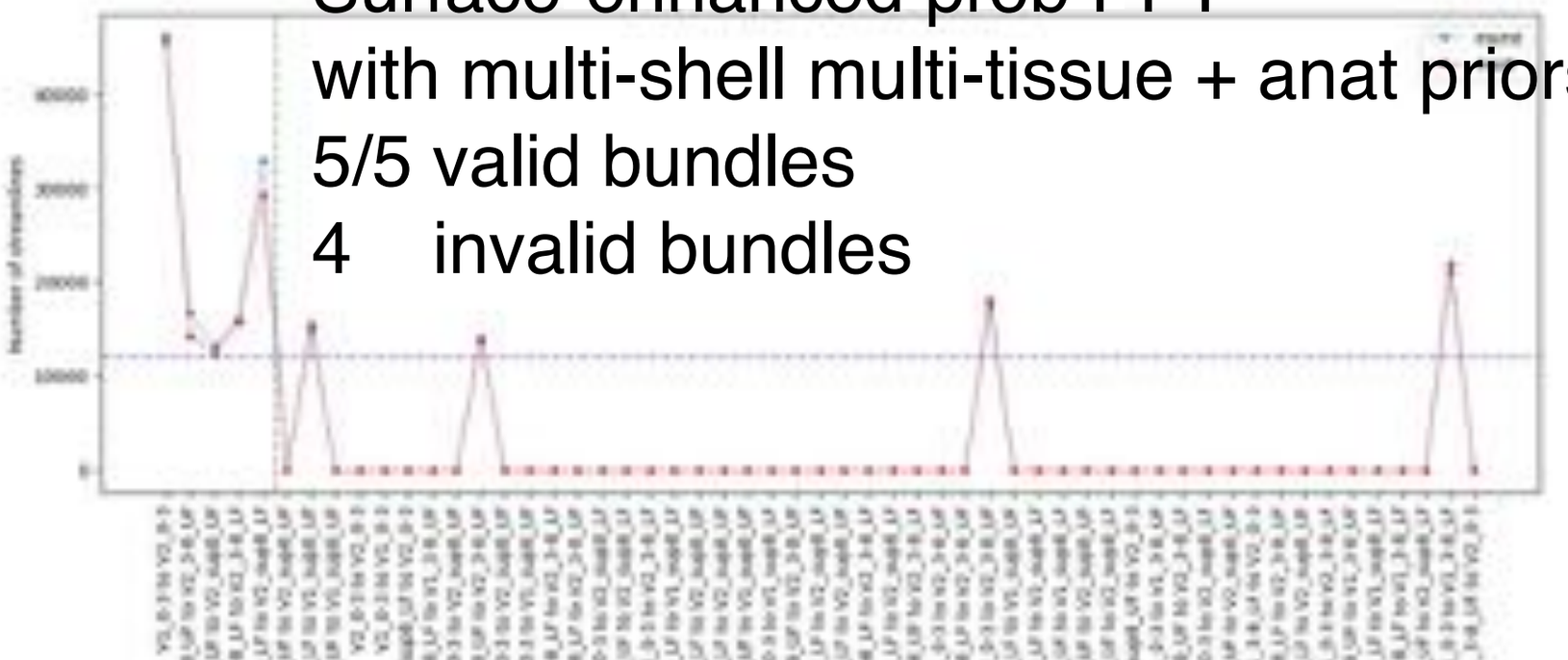
V1-V2 binary connectome









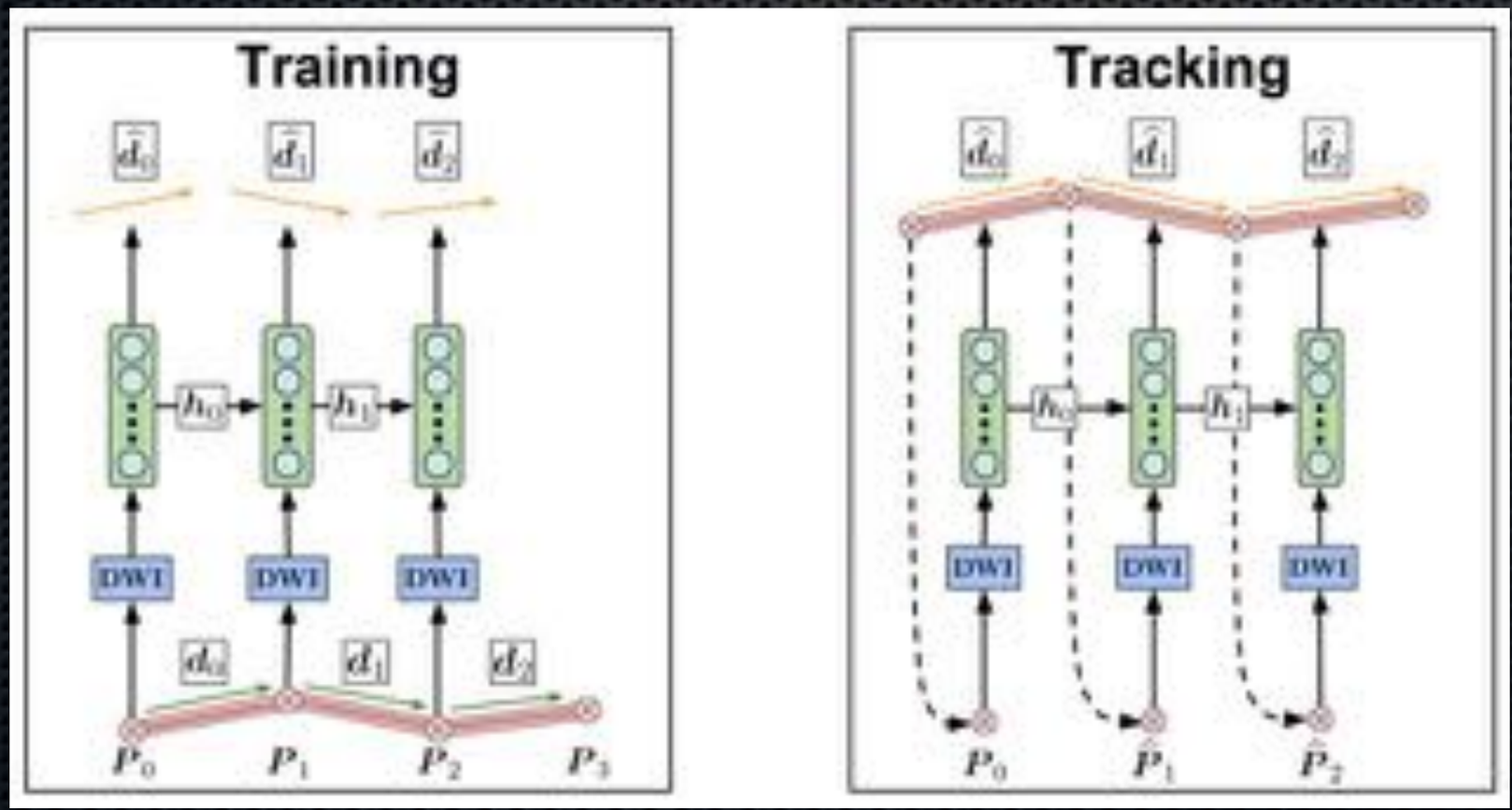


Can machine learning

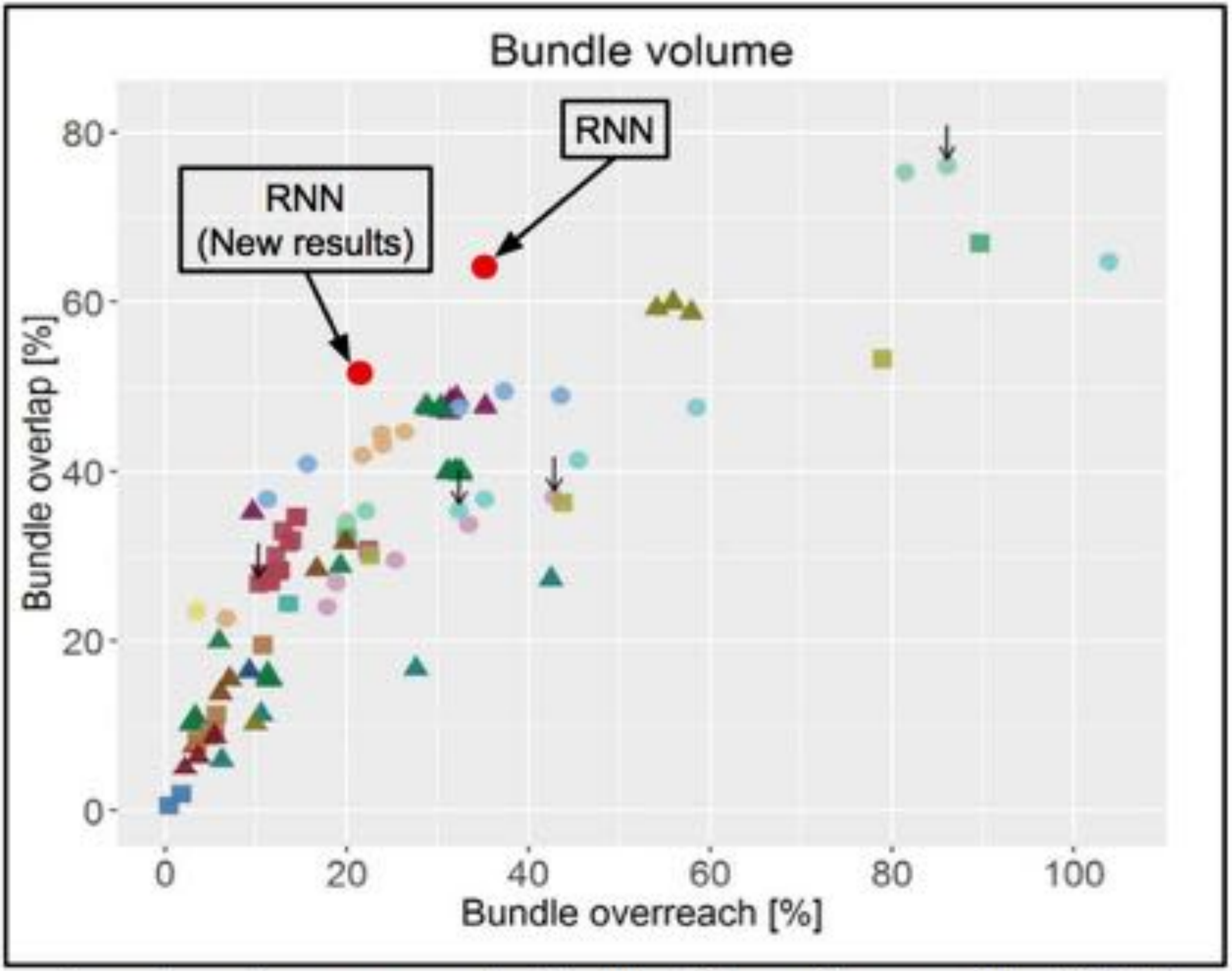
help tractography*?*

Learn to track: Deep learning for tractography

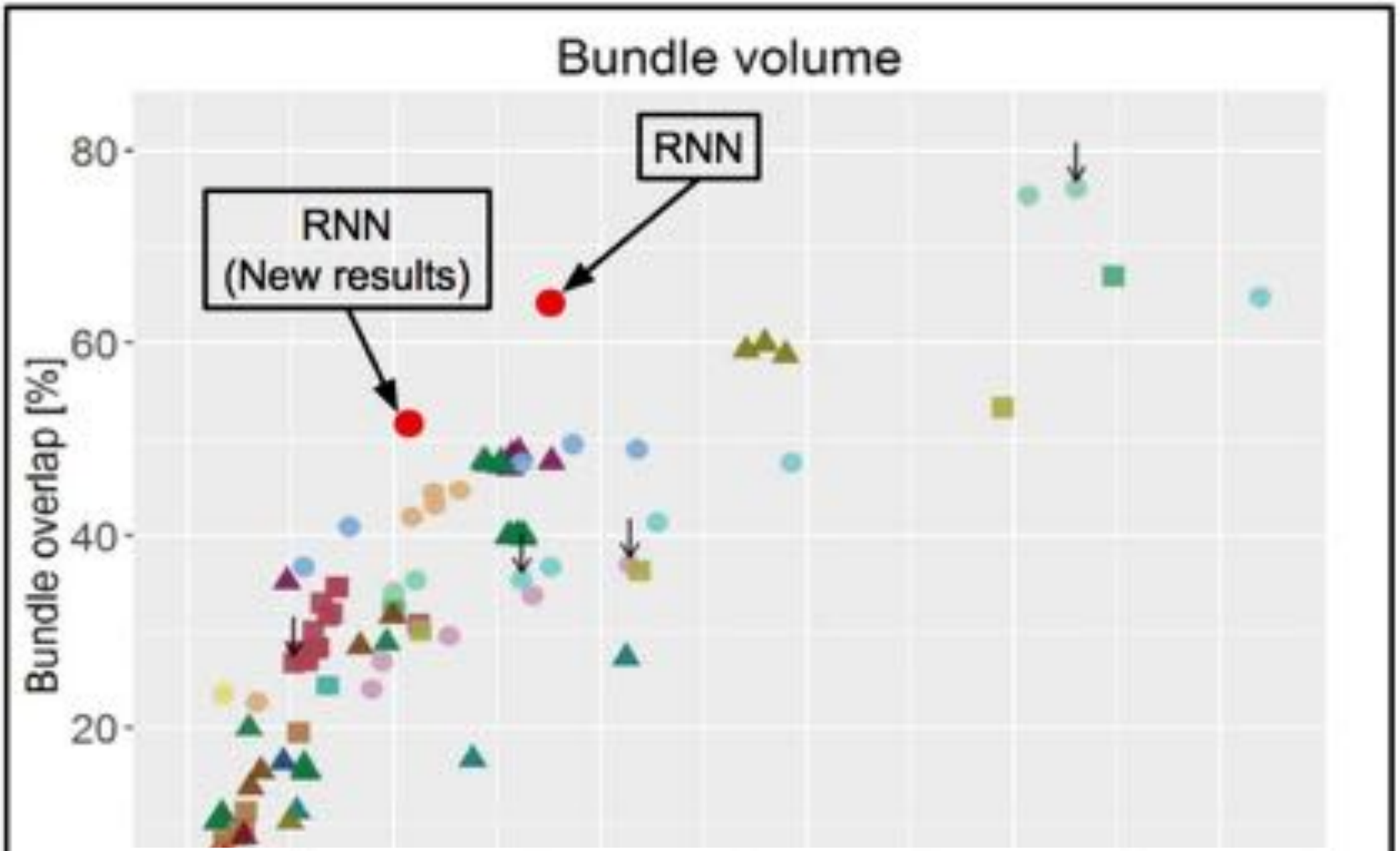
- RNN learns the complicated and complex local/global streamline configurations not to get lost into them
- Learn to avoid invalid connections/bundles
- Notion of history & neighbouring streamlines



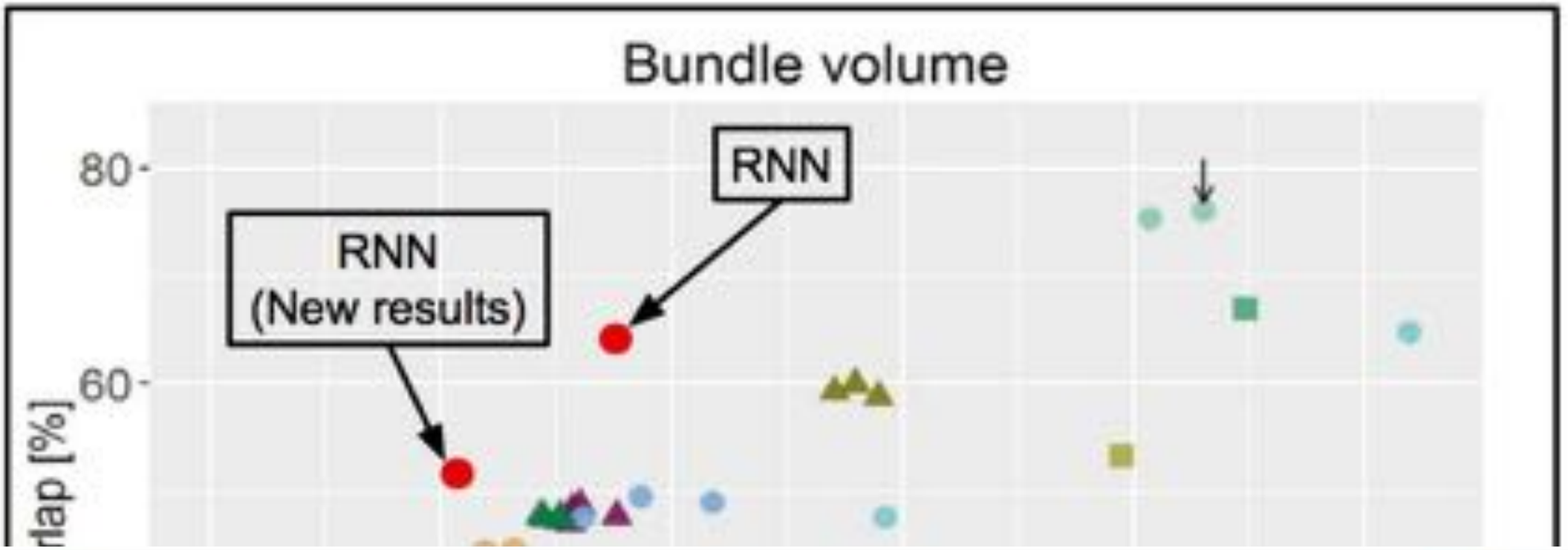
[Poulin et al. MICCAI 2017]

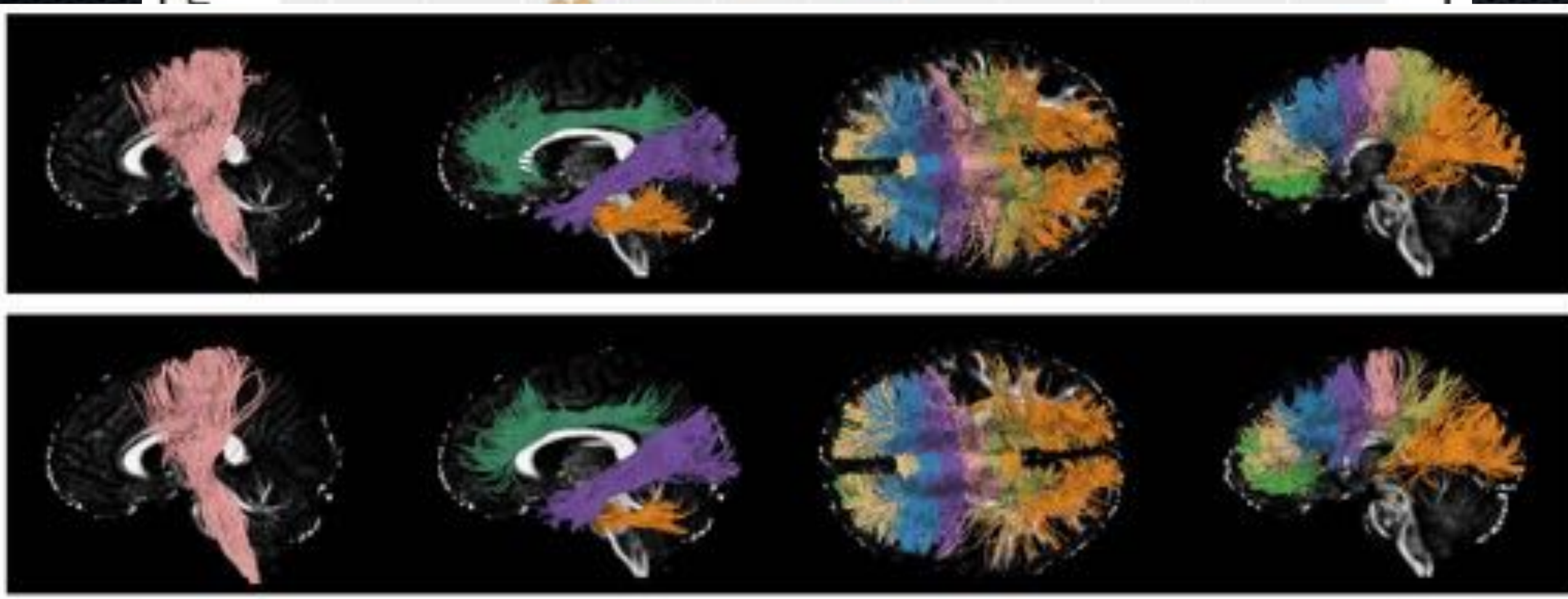


Overview of scores reached by the different teams of the ISMRM 2015 tractography challenge[1]
(Upper-left is best)



	Valid connections	*Valid bundles*	*Invalid bundles*	*Overlap*	*Overreach*
Mean ISMRM 2015 scores	54%	21.4/25	281	31%	23%
RNN (New results)	**85%**	**23/25**	**74**	51%	**21%**





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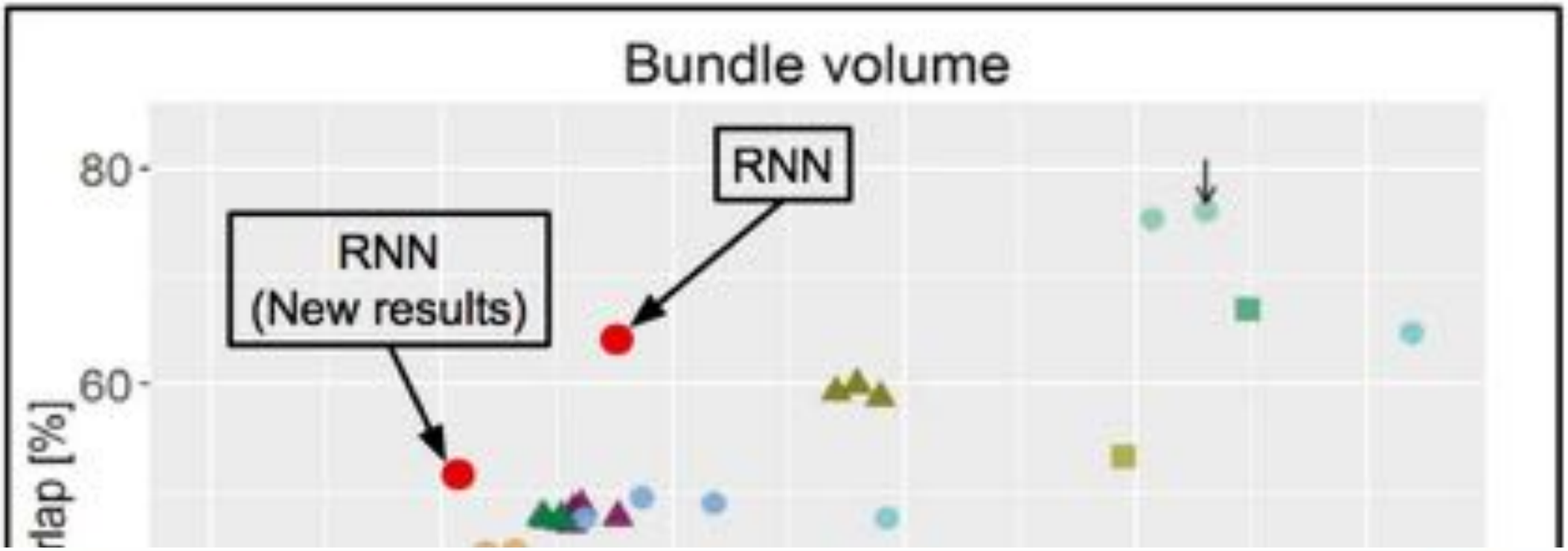
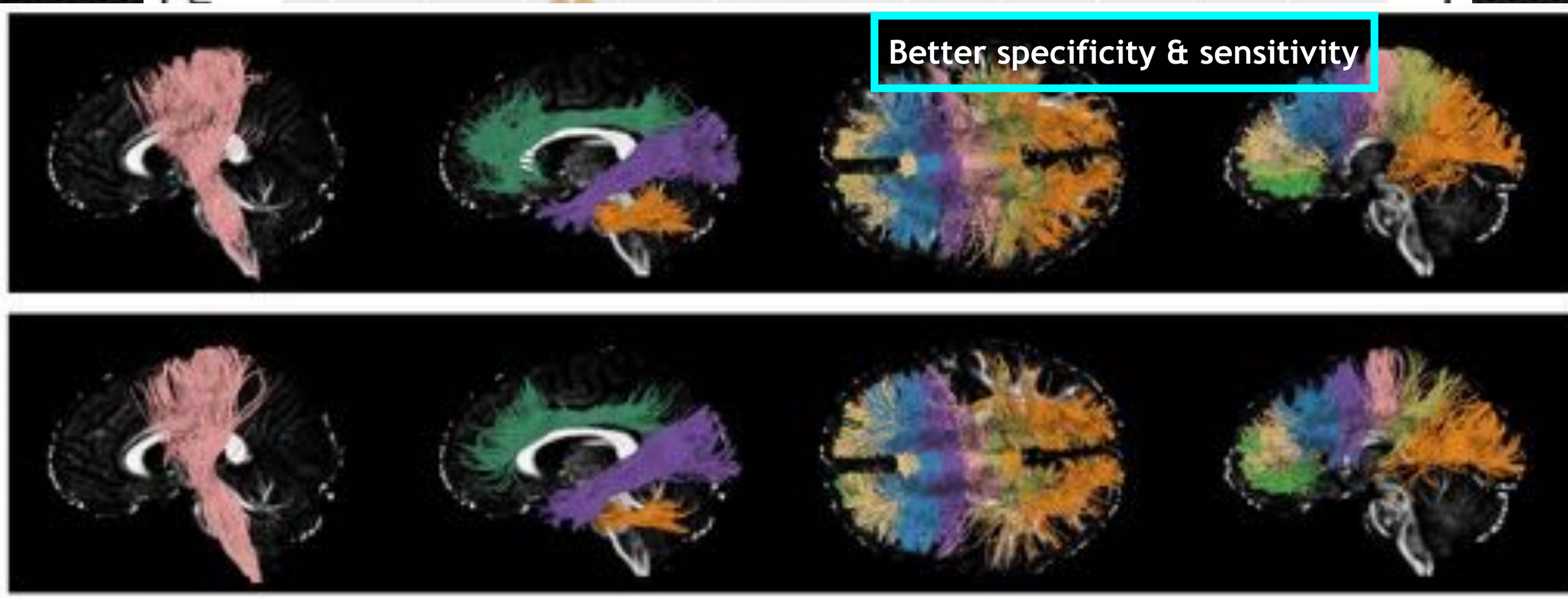
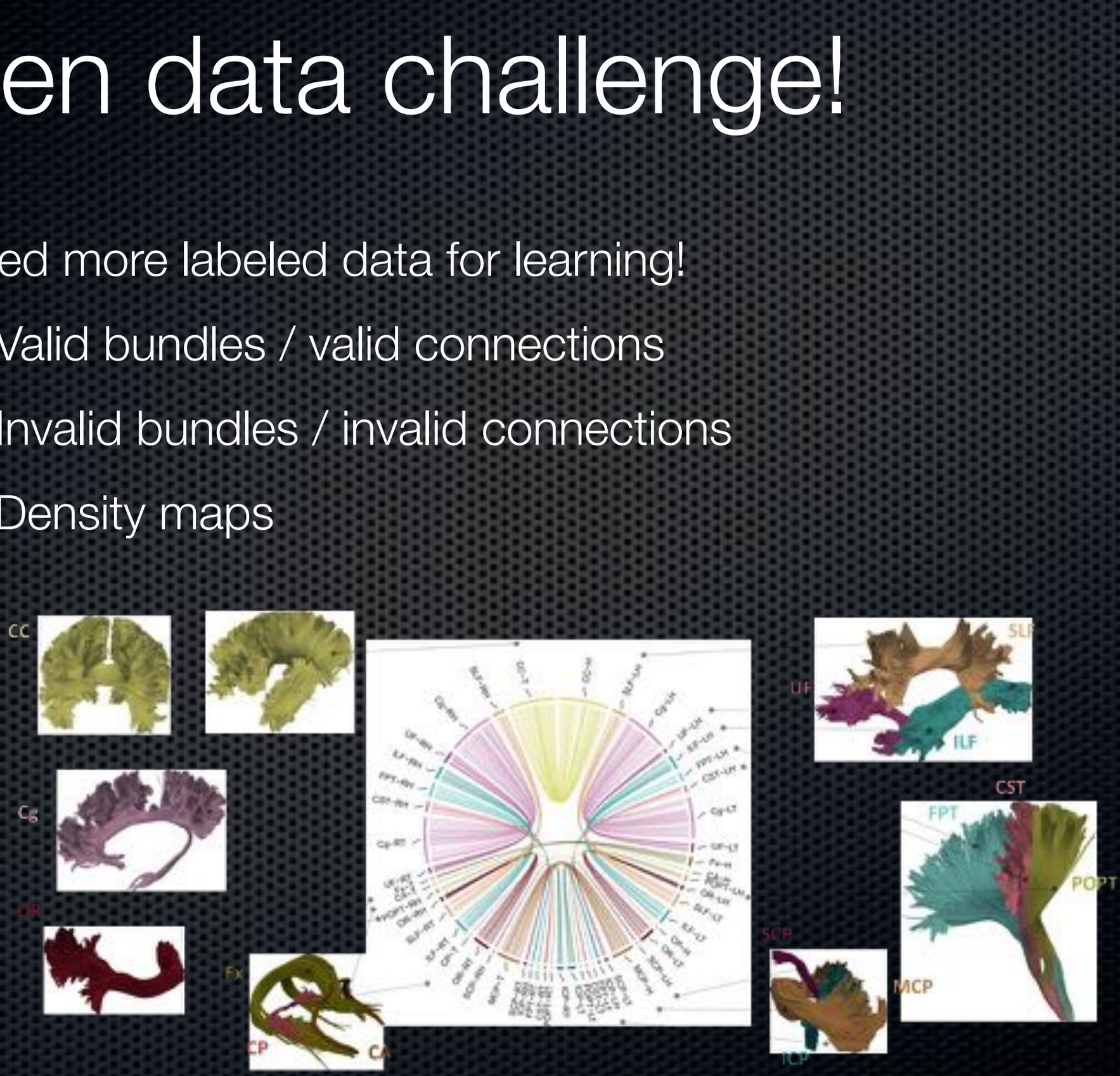




RNN (New results)	**85%**	**23/25**	**74**	51%	**21%**

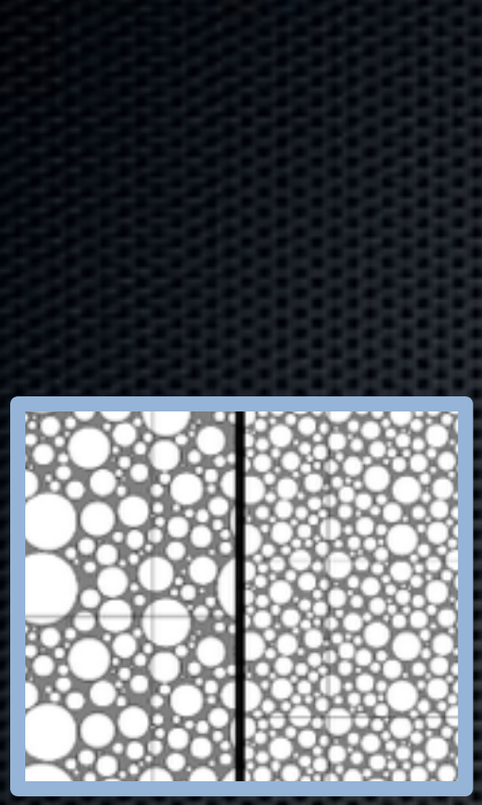
Open data challenge!

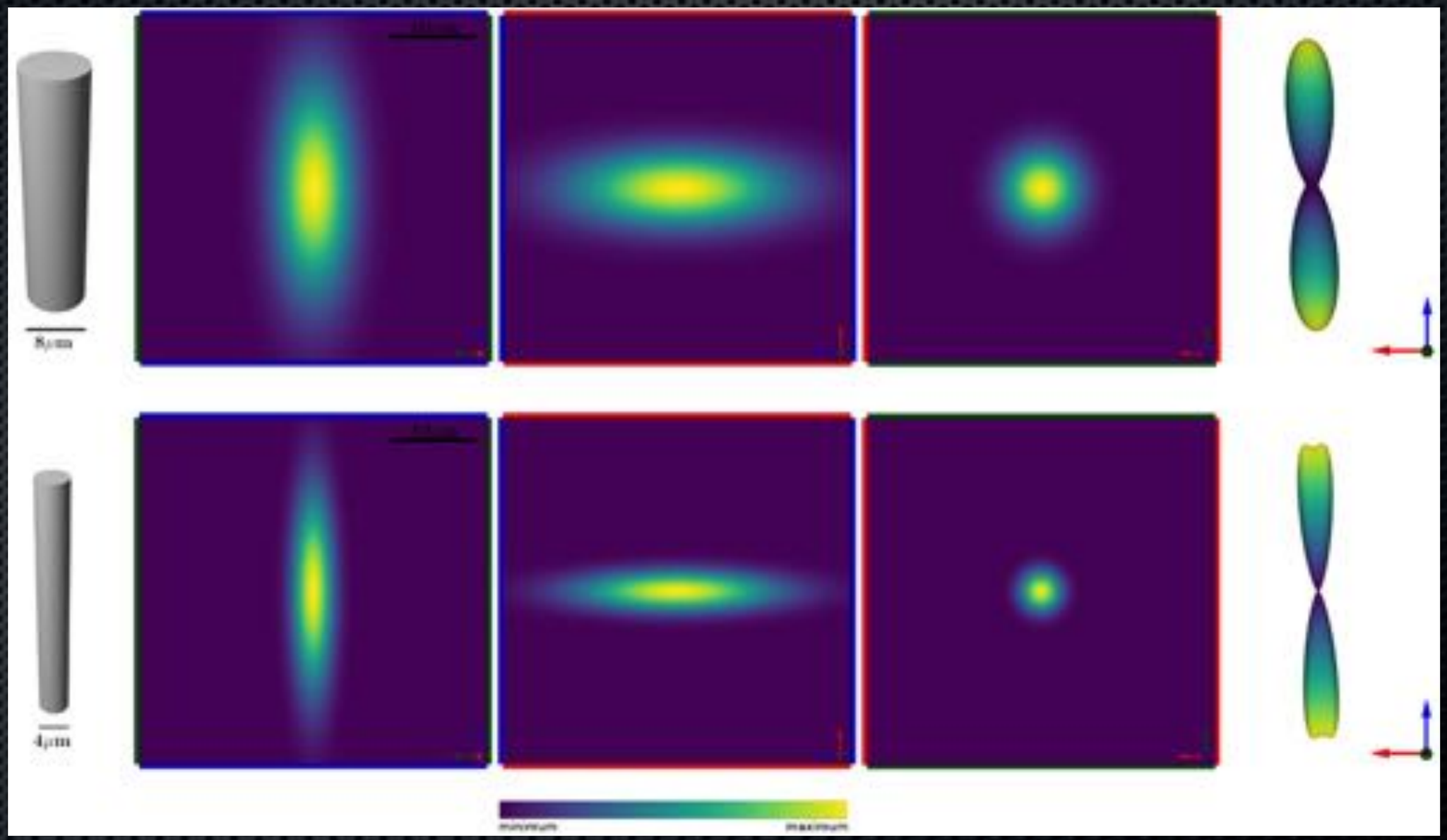
- Need more labeled data for learning!
  - Valid bundles / valid connections
  - Invalid bundles / invalid connections
  - Density maps



- Diffusion microstructure?
- *Can it **reduce***
- ***invalid connections**?*

Diffusion measurements can be sensitive to different axon calibers





Diffusion propagator visualization [Girard et al IPMI 2015]

AxTract: Microstructure-informed tractography

[Gabriel Girard]

- Add microstructure information from the propagator or ActiveAx-like fast solution with AMICO
- Reduce the number of false positives (by reducing the amount of bad turns taken)

HUMAN BRAIN MAPPING

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Research Article

AxTract: Toward microstructure informed tractography

Gabriel Girard, Alessandro Daducci, Laurent Petit, Jean-Philippe Thiran, Kevin Whittingstall, Rachid Deriche, Demian Wassermann, Maxime Descoteaux

First published: 2 August 2017 Full publication history

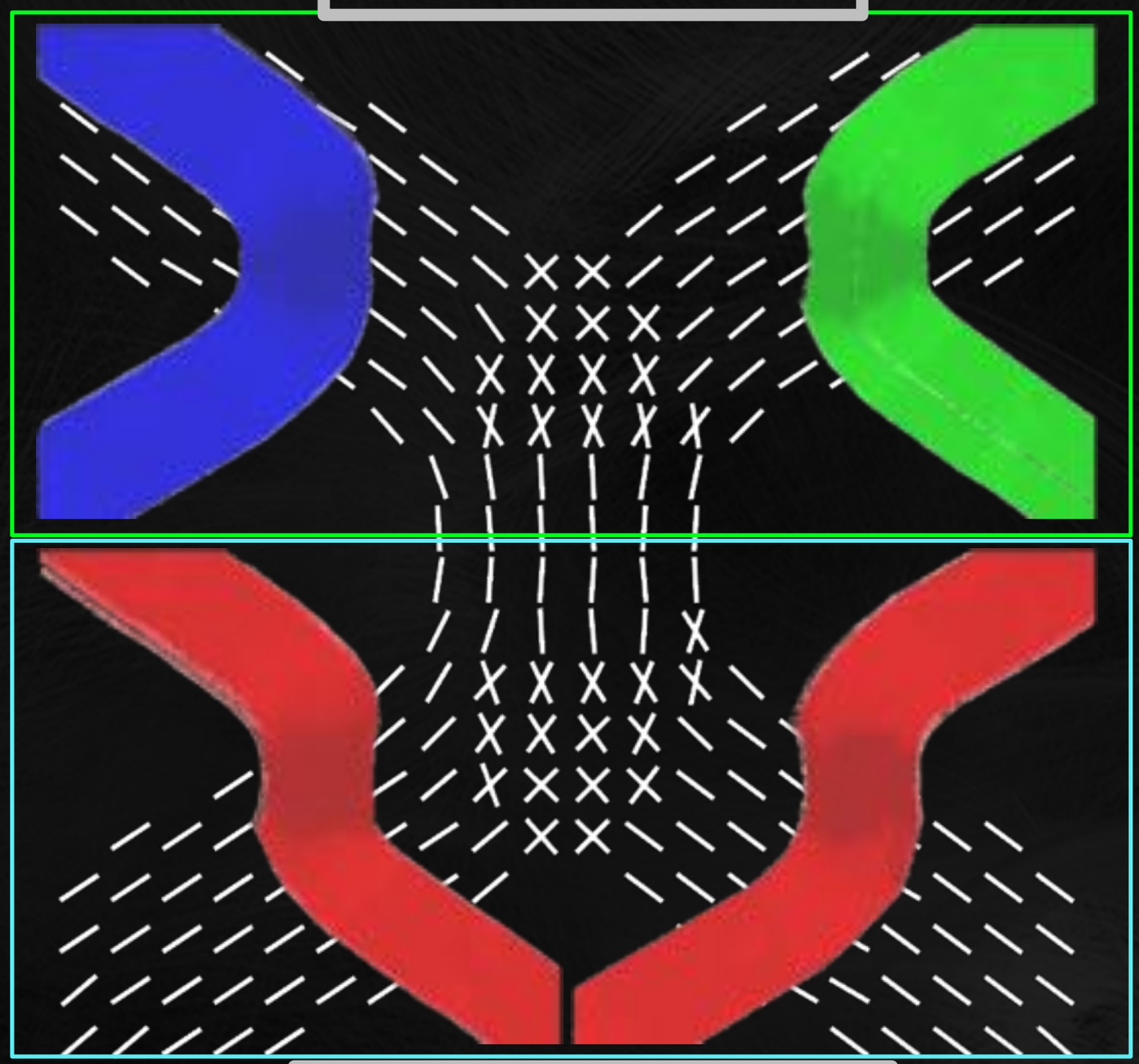
Deterministic HARDI Tractography - Tractometer

Kissing phantom

[Girard et al., HBM 2017]

Deterministic HARDI Tractography - Tractometer

Valid connections



Invalid connections

Kissing phantom

SNR: 20

Valid connections: 53%

Invalid connections: 47%

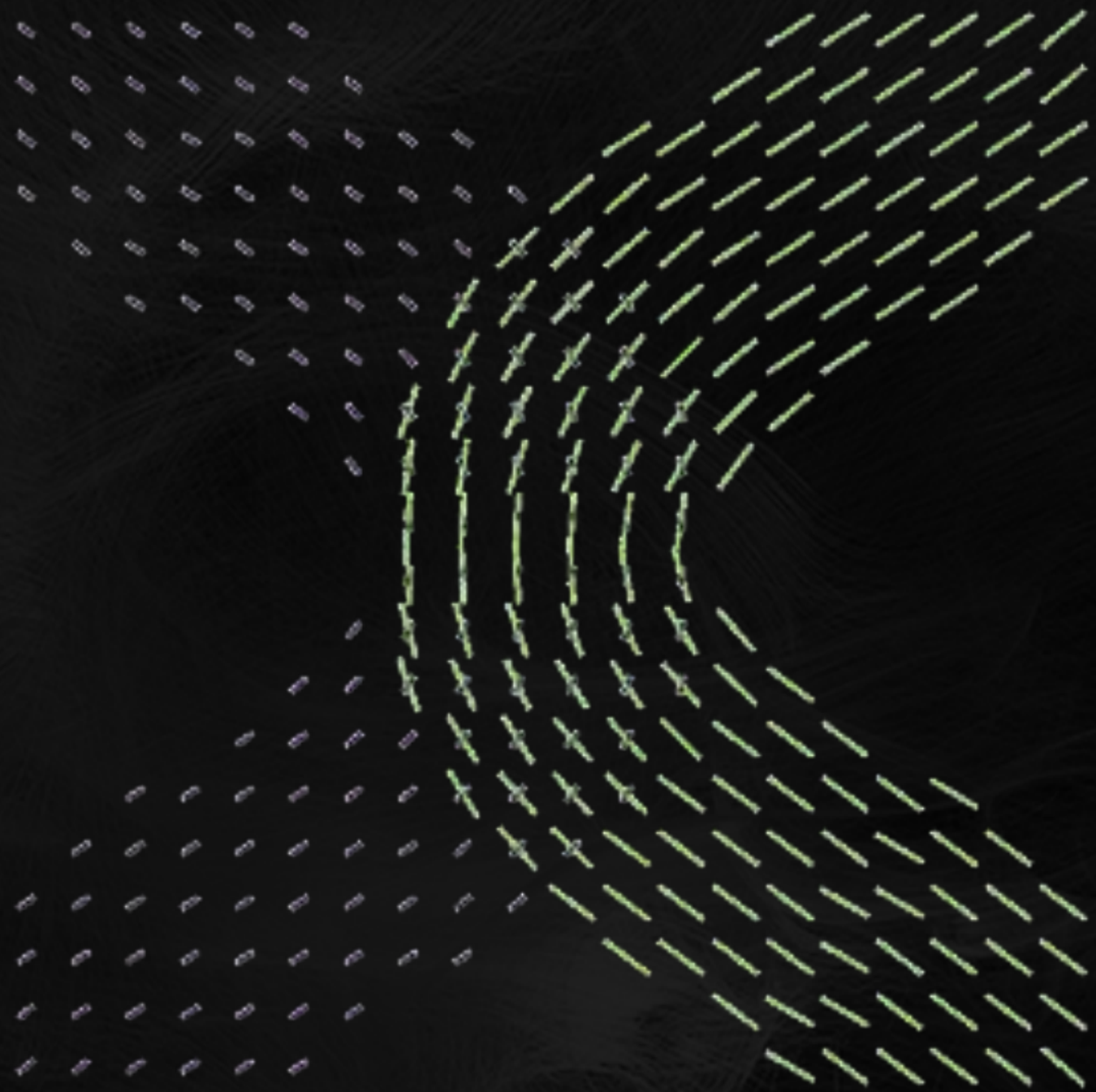
[Girard et al., HBM 2017]

AxTract - Synthetic Data Experiment

[Girard et al., HBM 2017]

AxTract - Synthetic Data Experiment

2.44µm 6.88µm



Geometry : Phantomas
[Caruyer et al., ISMRM, 2014]

DWI Signal : Camino
[Hall and Alexander, TMI, 2009]

[Girard et al., HBM 2017]

AxTract - Synthetic Data Experiment

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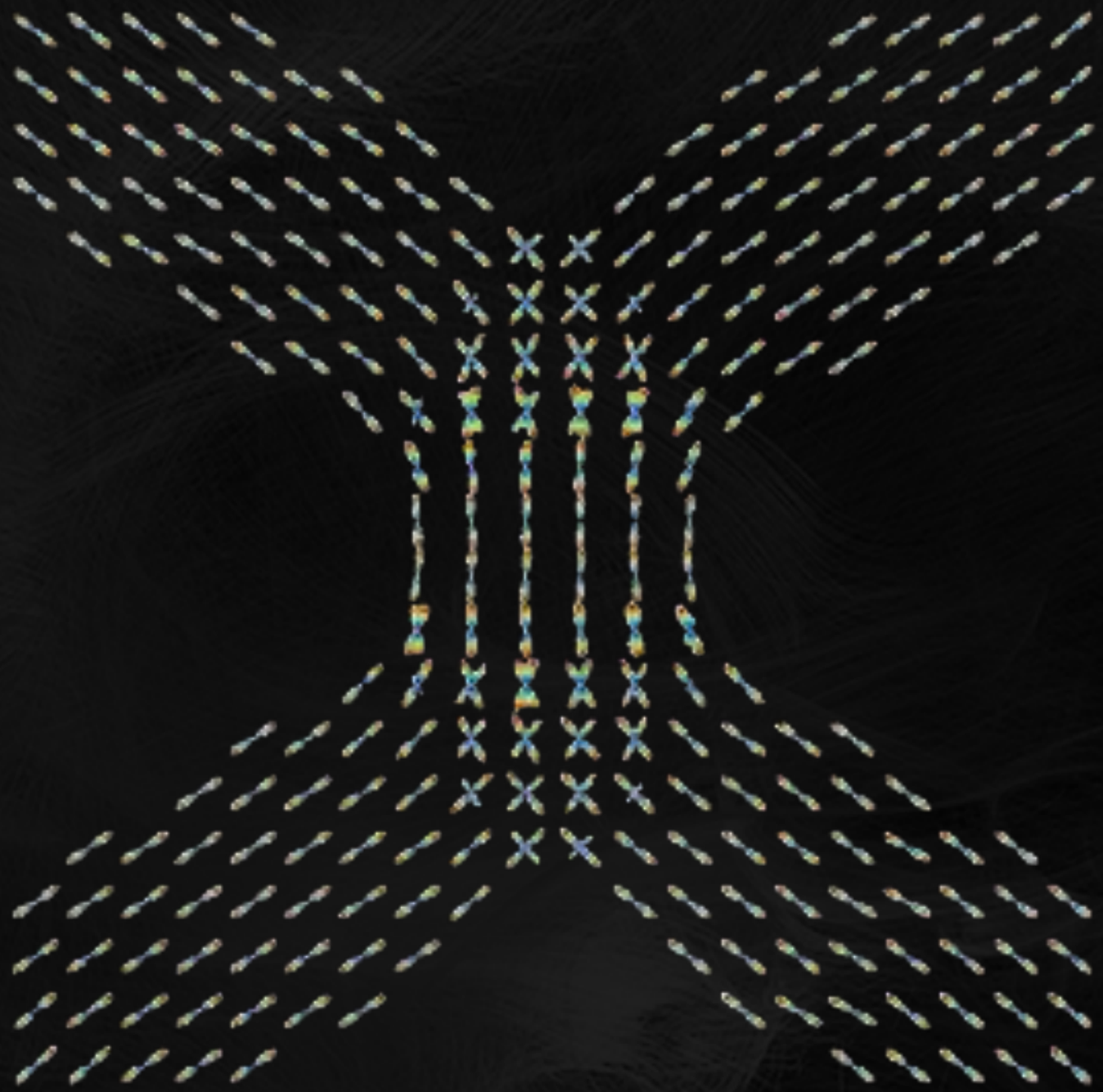
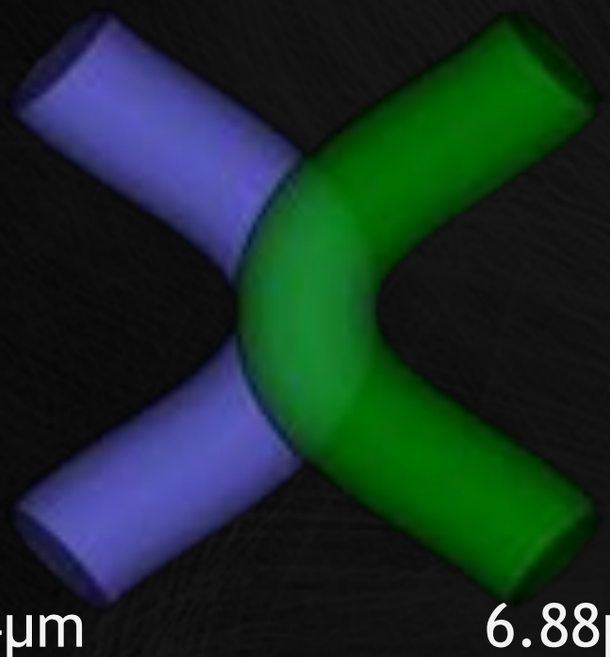


[Girard et al., HBM 2017]

AxTract - Synthetic Data Experiment



2.44µm 6.88µm

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[Caruyer et al., ISMRM, 2014]

DWI Signal : Camino
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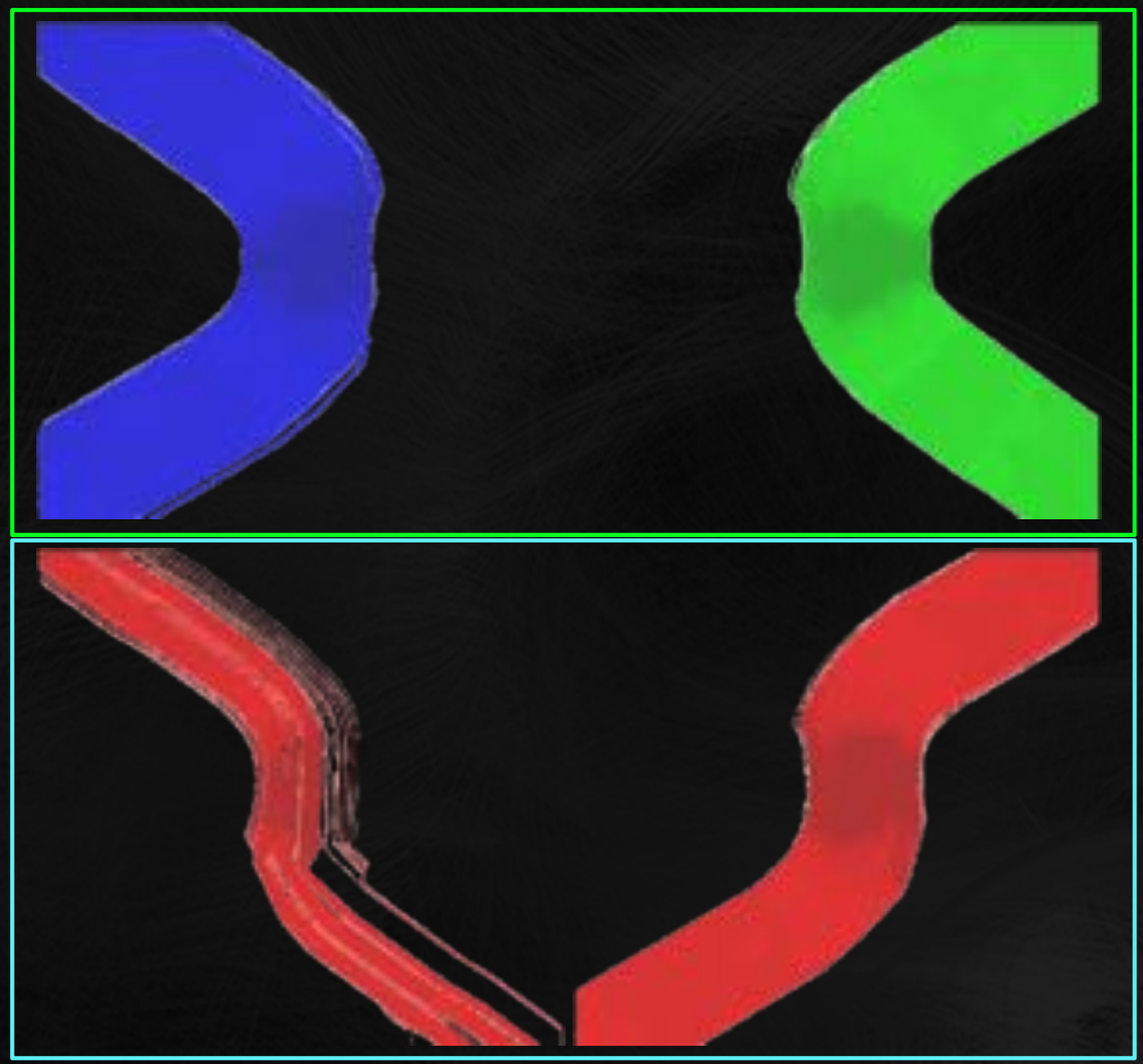
[Girard et al., HBM 2017]

AxTract - Tractometer Analysis

[Girard et al., HBM 2017]

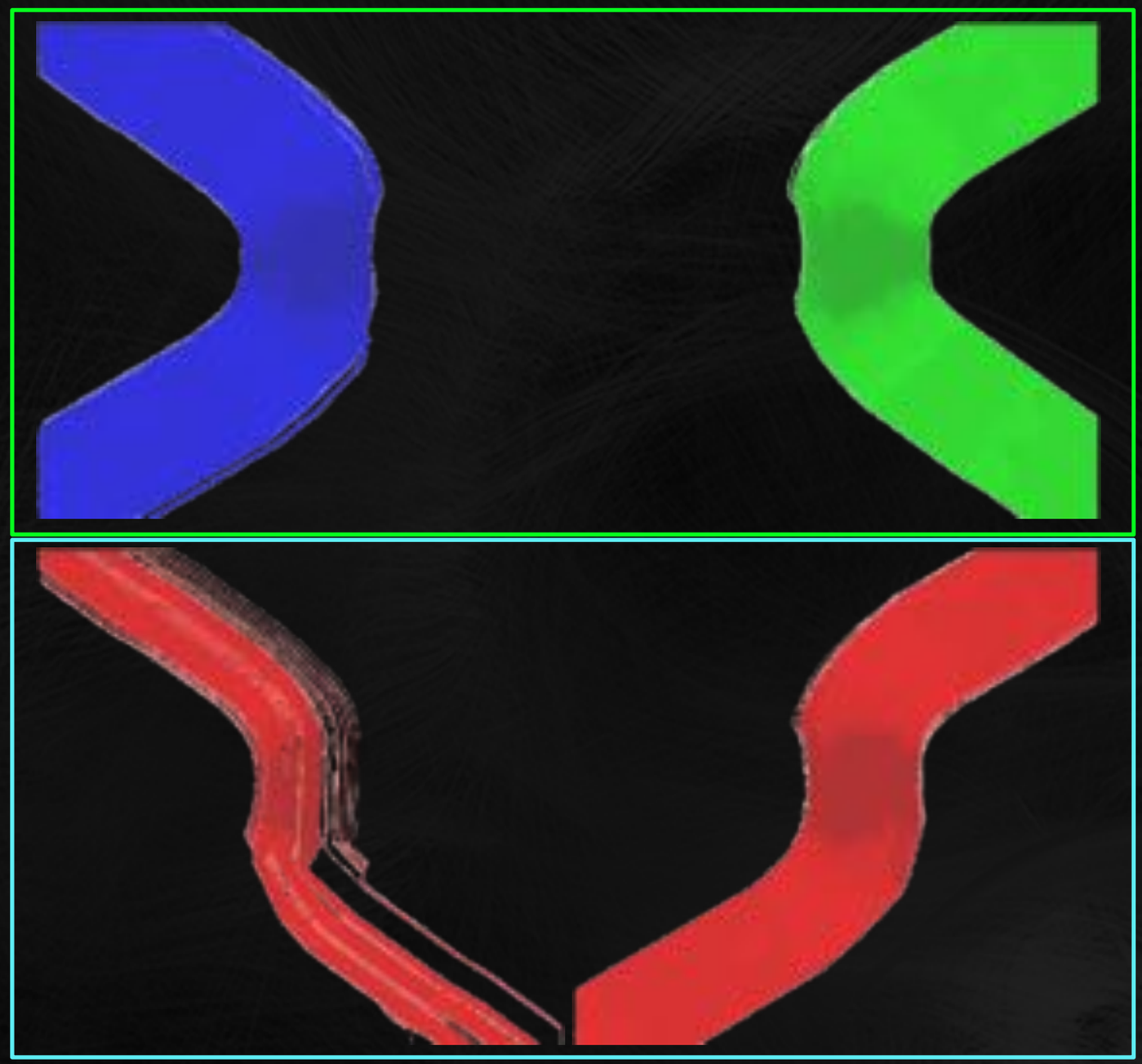
AxTract - Tractometer Analysis



2.44µm 6.88µm

[Girard et al., HBM 2017]

AxTract - Tractometer Analysis



2.44µm 6.88µm

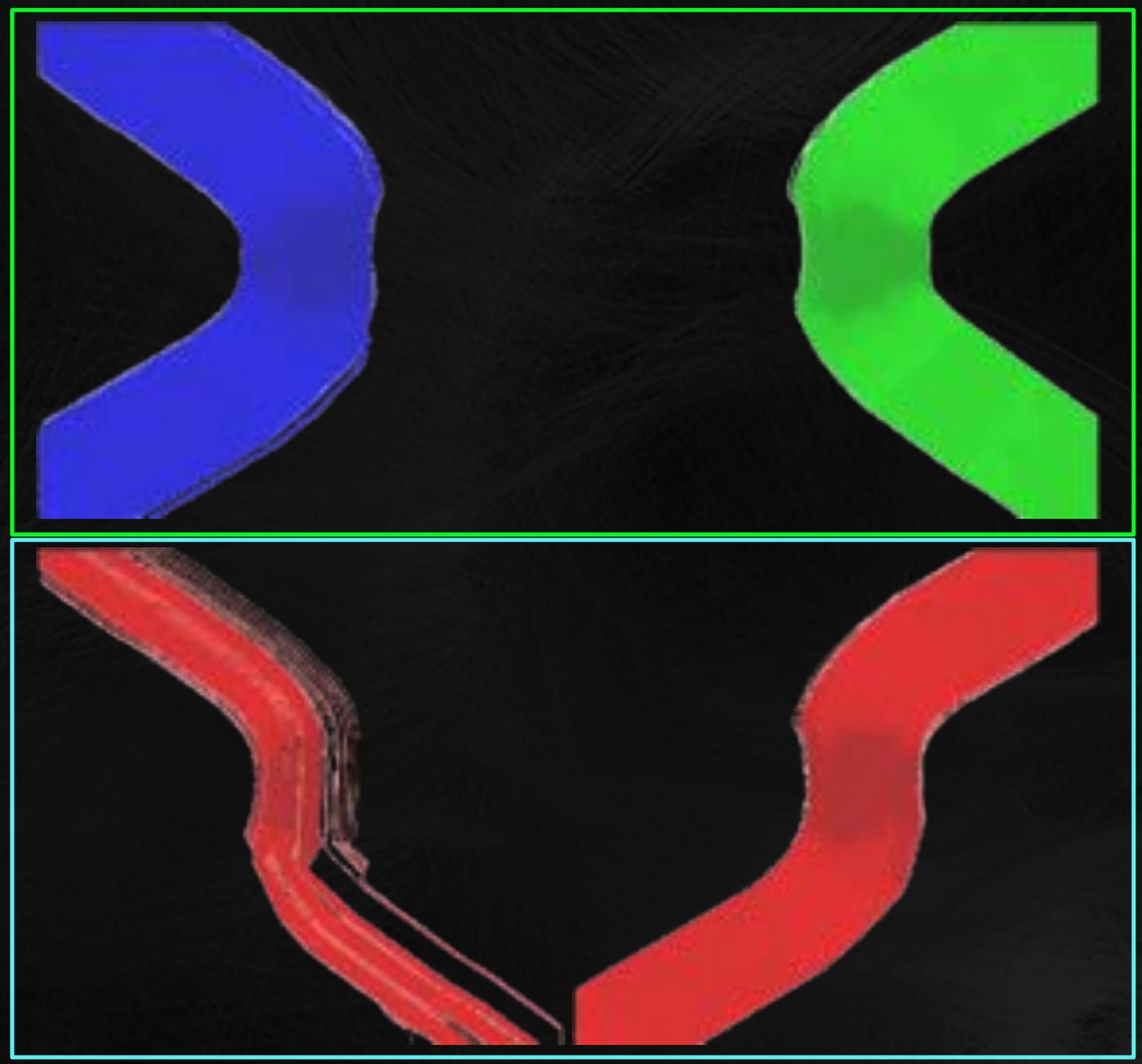
SNR:20

Valid connections:
87%

Invalid connections:
13%

[Girard et al., HBM 2017]

AxTract - Tractometer Analysis



2.44µm 6.88µm

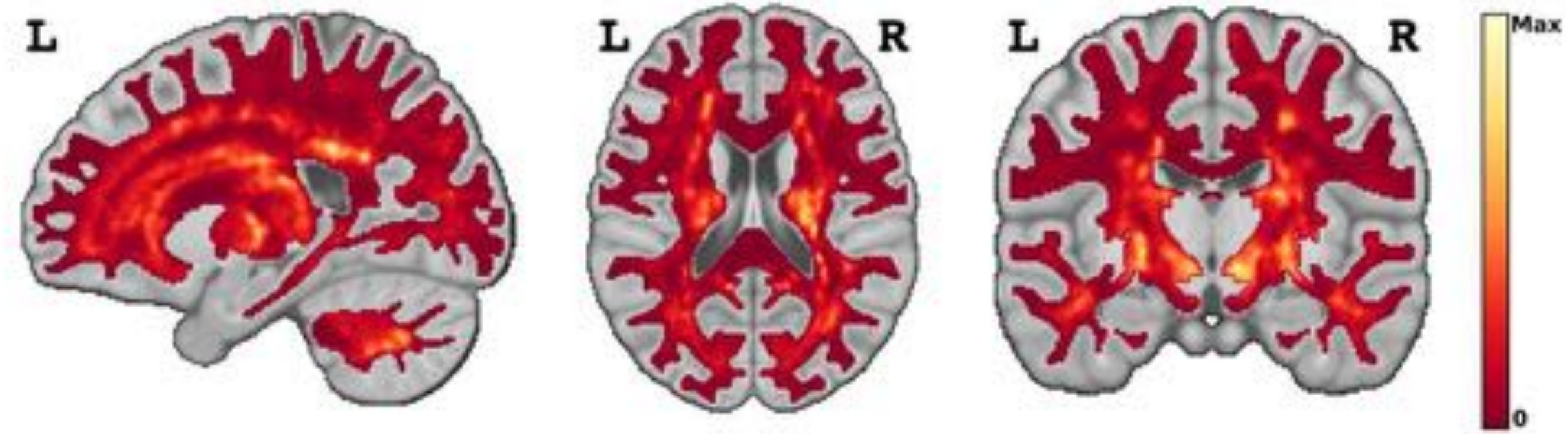
SNR:20

Valid connections:
87%

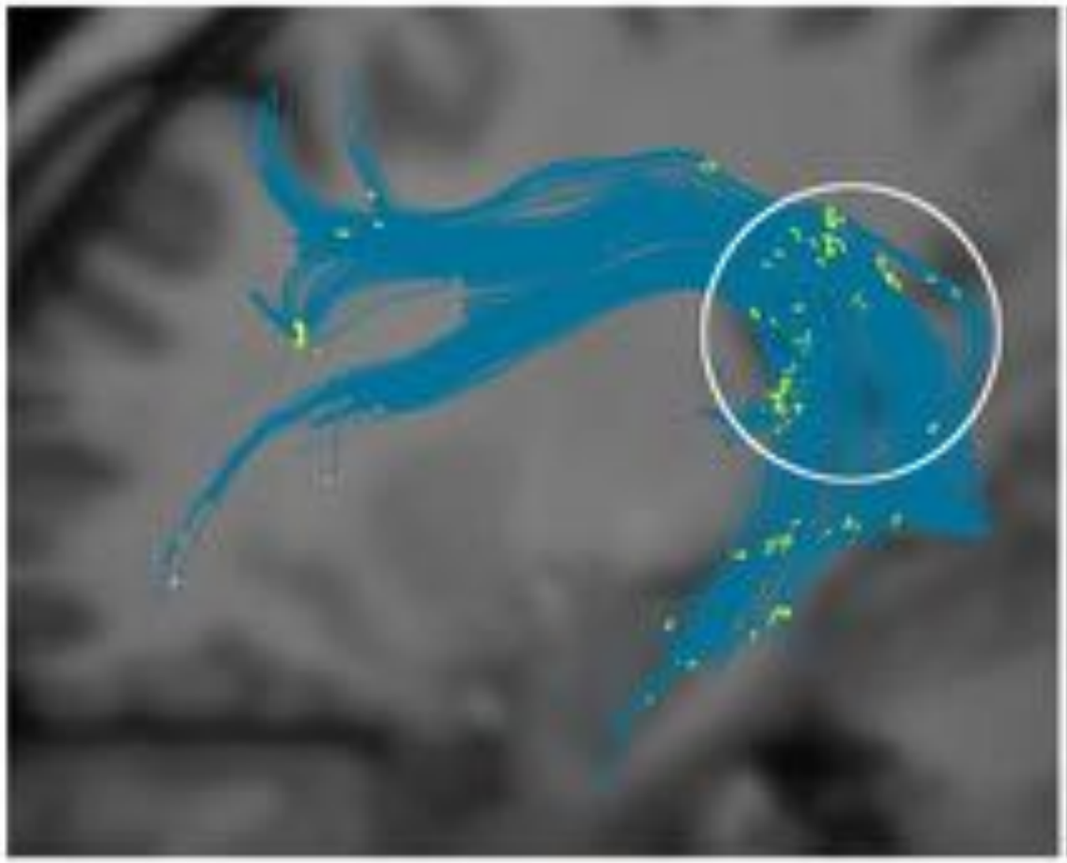
Invalid connections:
13%

[Girard et al., HBM 2017]

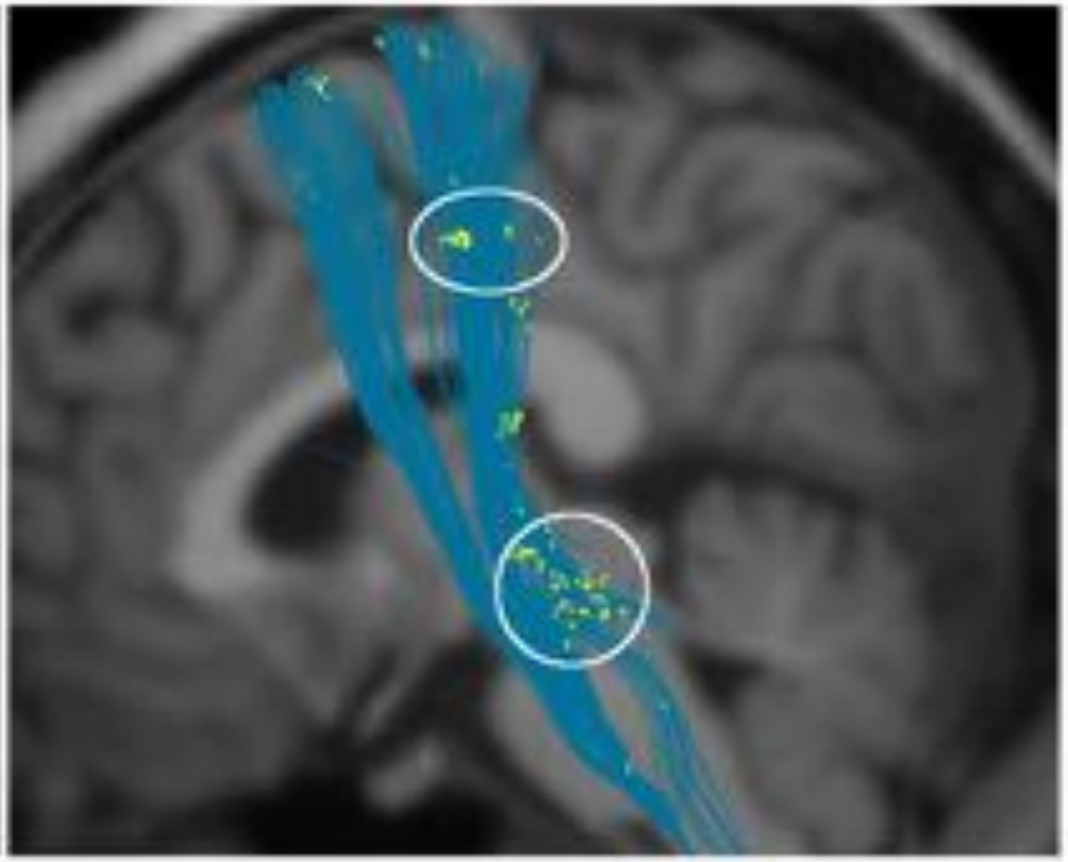
HCP MGH data:
34 subjects - 5 shells b1000-10000



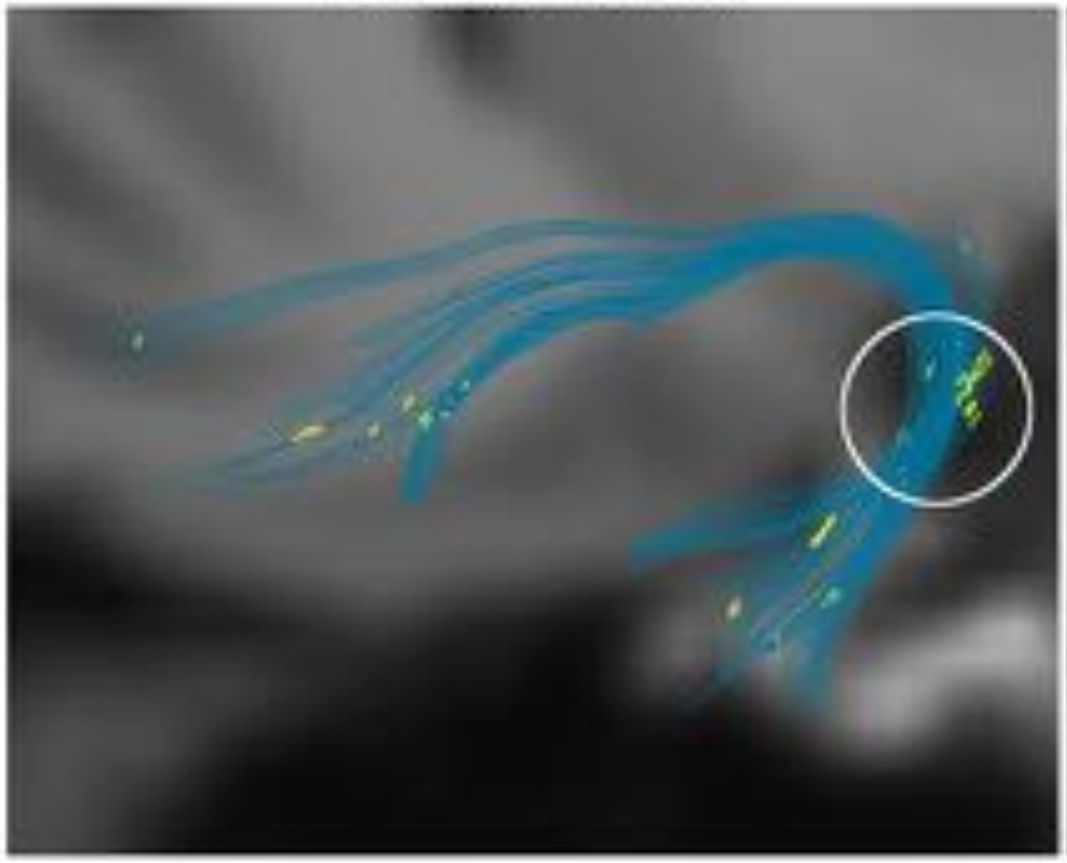
Average occurence map where local directions was picked differently than standard tractography



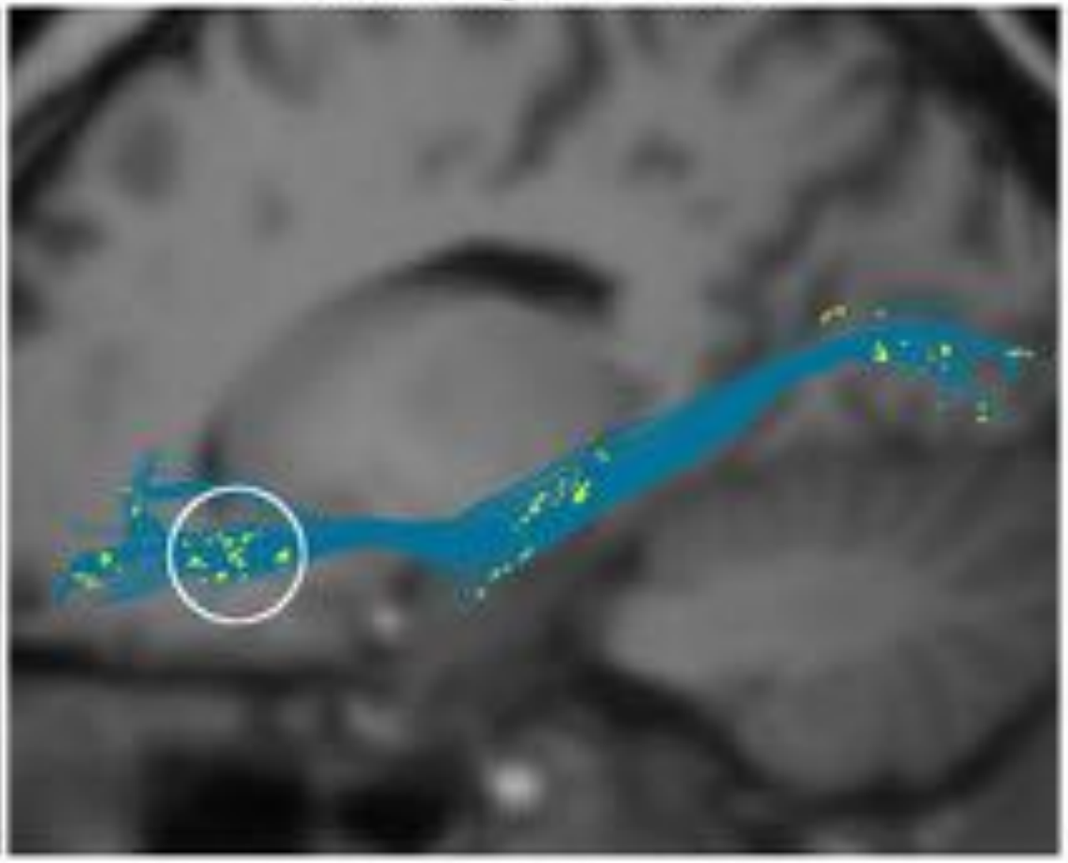
Arcuate Fasciculus



Corticospinal Tract



Uncinate Fasciculus

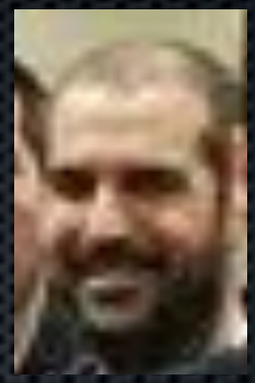


Inferior Fronto-Occipital Fasciculus

Can functional imaging
help tractography*?*

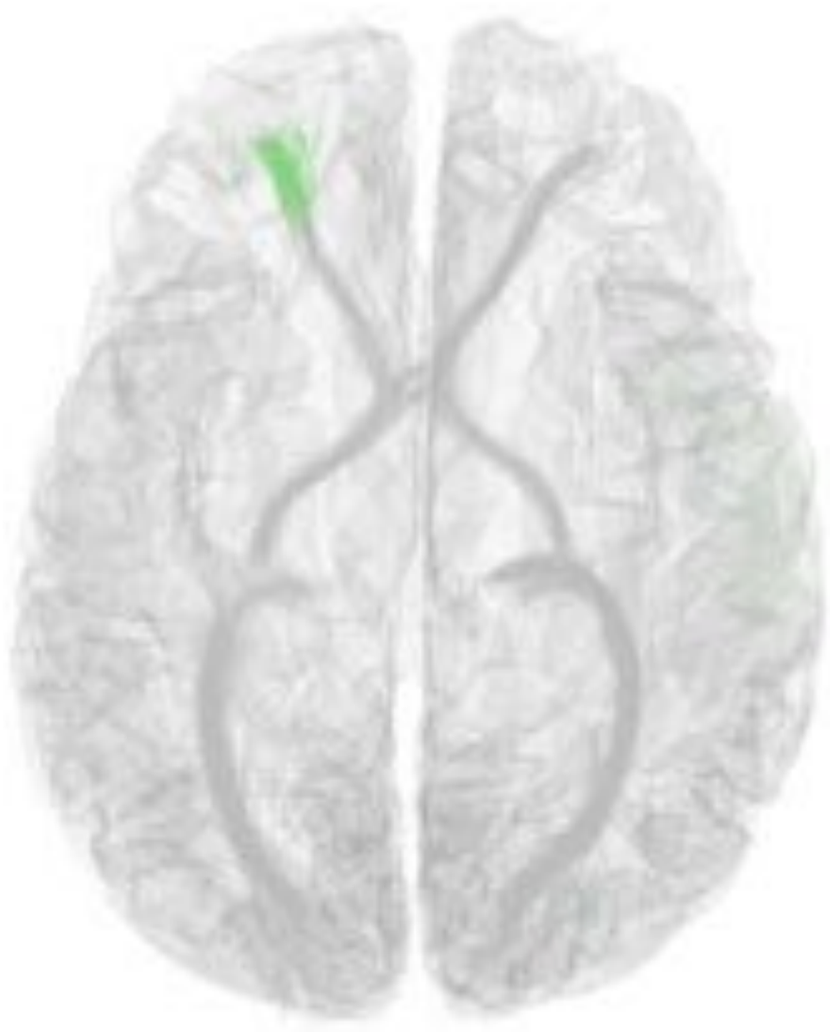
Fibre directionality and information flow through the white matter: Preliminary results on the fusion of diffusion MRI and EEG

Samuel Deslauriers-Gauthier, Jean-Marc Lina, Russell Butler,
Kevin Whittingstall, Pierre-Michel Bernier, Maxime Descoteaux



- Exploiting **time delay** from EEG data

[Deslauriers *et al. ISMRM* 2016]
[Deslauriers *et al. MICCAI* 2017]



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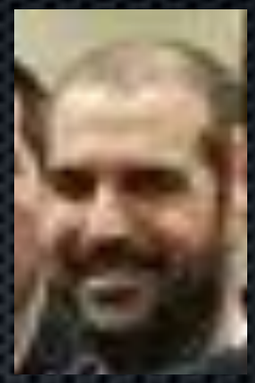

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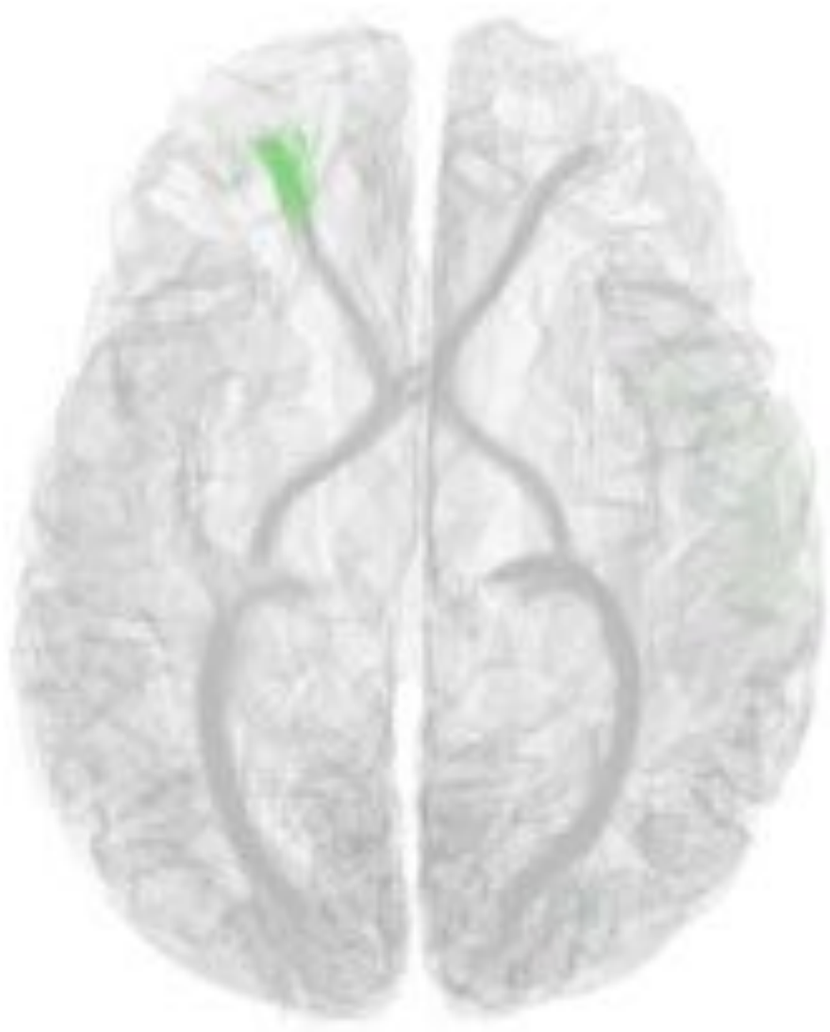
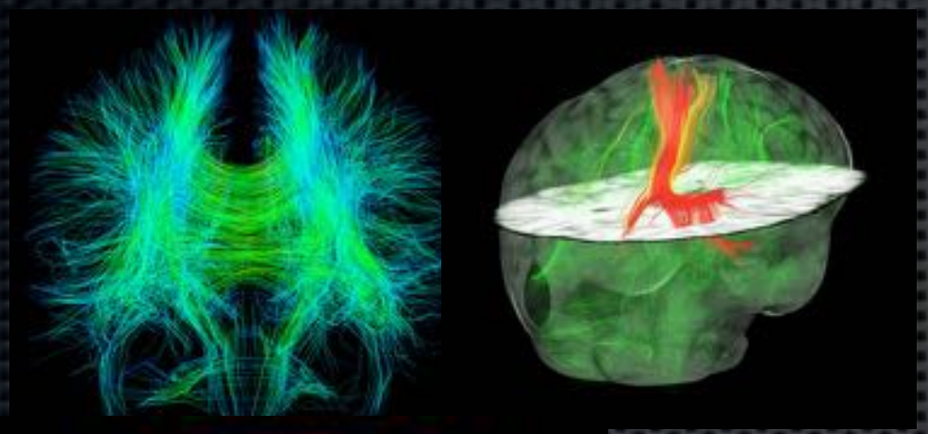


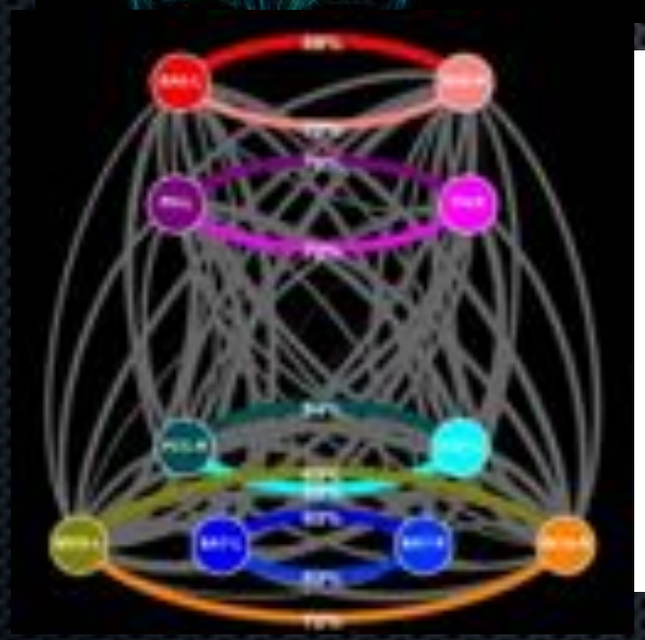
- Conclusion

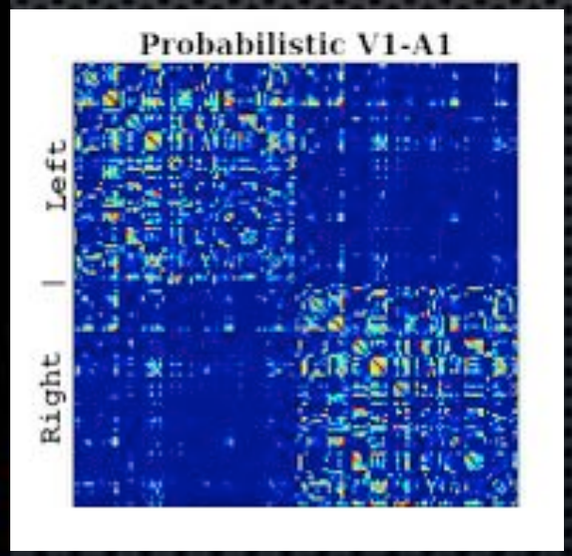
Towards quantitative connectomics

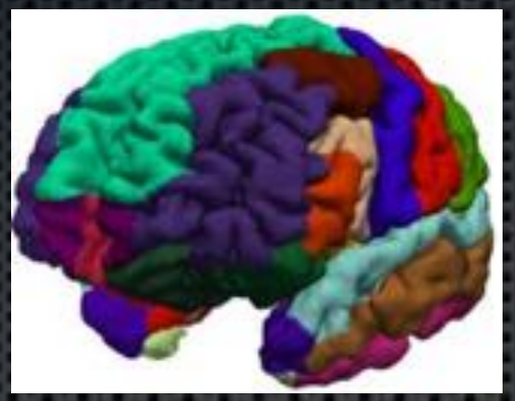
Connectomics

Tractography
Tractometry
Connectomics

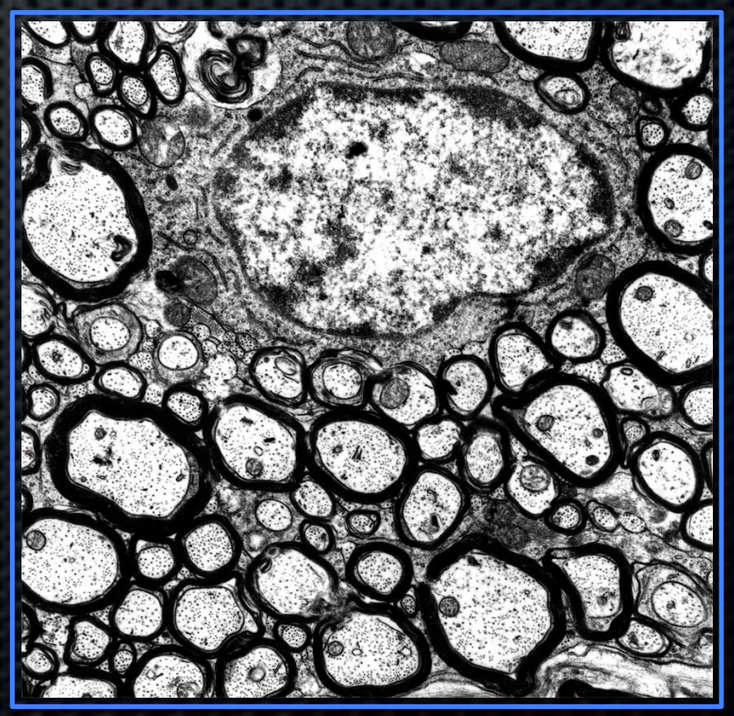








Tissue properties
local modelling
microstructure
(axon diameter,
g-ratio,
intra-extra axonal)



[Daducci, Descoteaux et al. Frontiers 2016]

Improving connectivity

- **Adaptive** tractography (position bias)
- Notion of **neighbours** (hybrid/global tracking)
- Need for **advanced filtering** (no space for everyone)
- Notion of **anatomy** (priors) & **microstructure** (AxTract)
- **Validation** and reproducibility (simulations and work on real data with tract-tracing/PLI/others)
- Bring **multi-modal imaging** in the picture (myelin & functional)

Diffusion in DIPY (Diffusion in Python)

DIPY

www.dipy.org

- Pre-processing, registration, denoising & data quality
- Reconstruction of the local diffusion phenomena
- Tractography with anatomical priors
- Bundle analysis & streamlines post-processing
- Connectomics
- Visualization

Thank you!

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NSERC CRSNG

Fonds de recherche sur la nature et les technologies Québec

UNIVERSITÉ DE SHERBROOKE

Dipy
Diffusion Imaging in Python