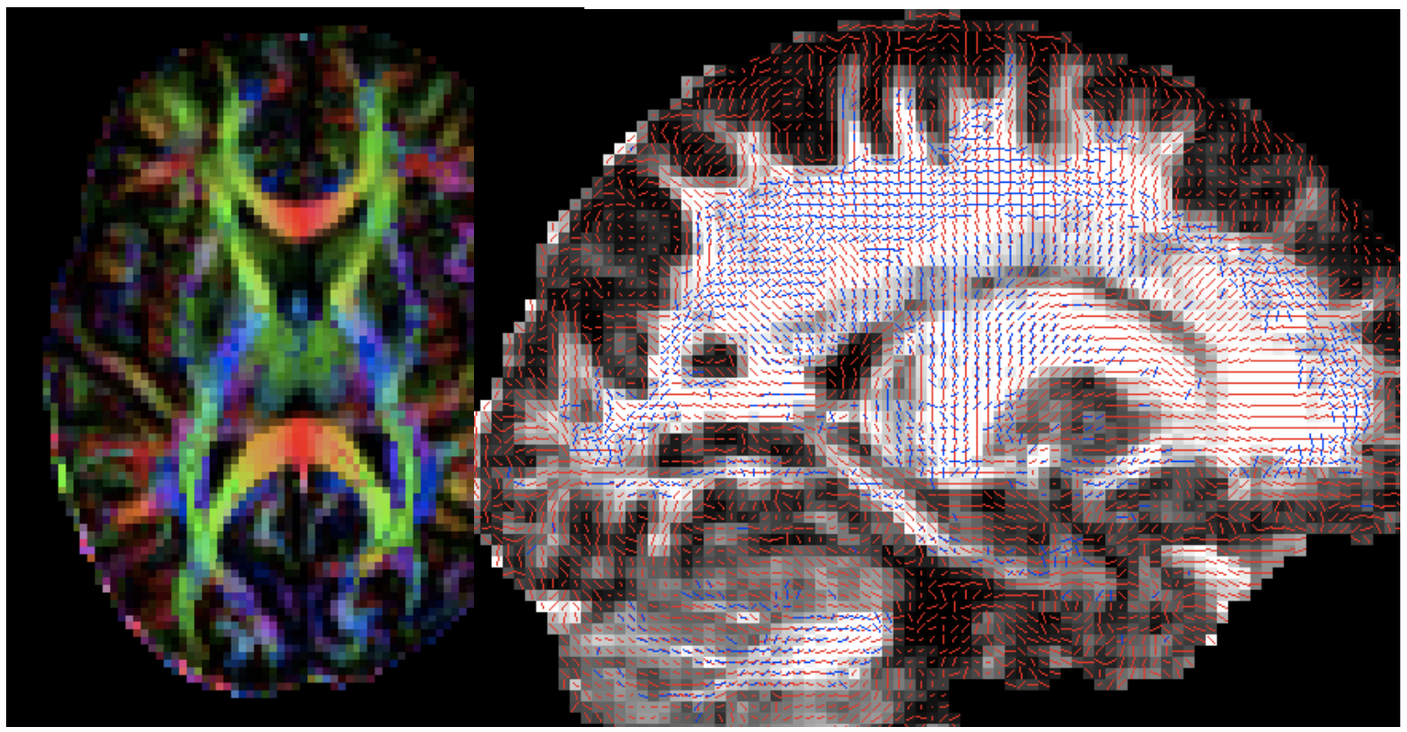
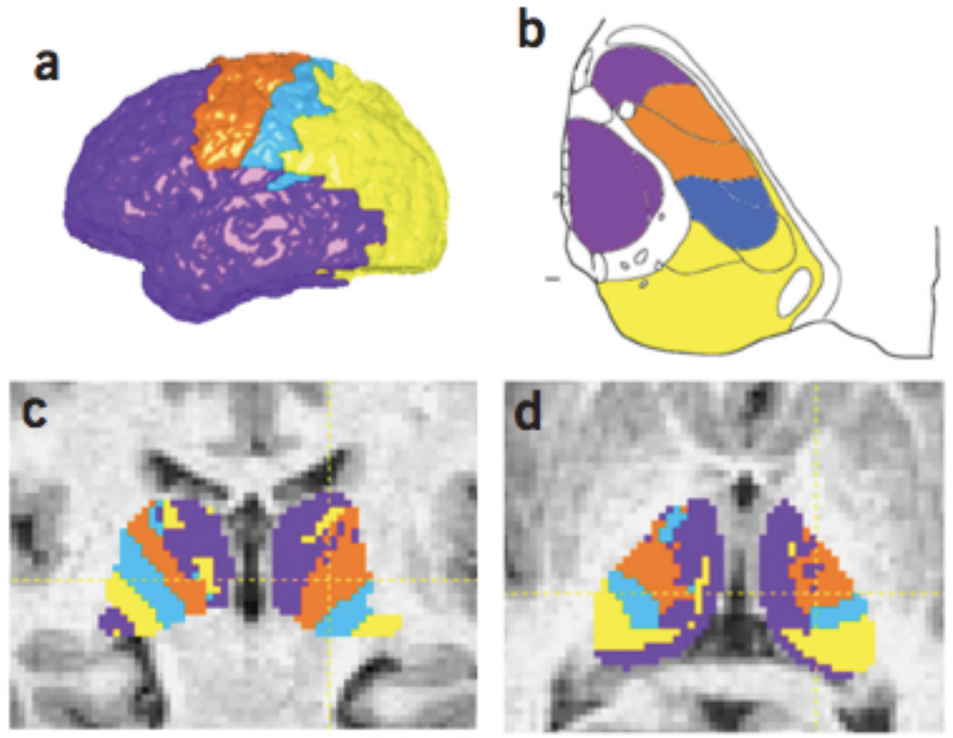
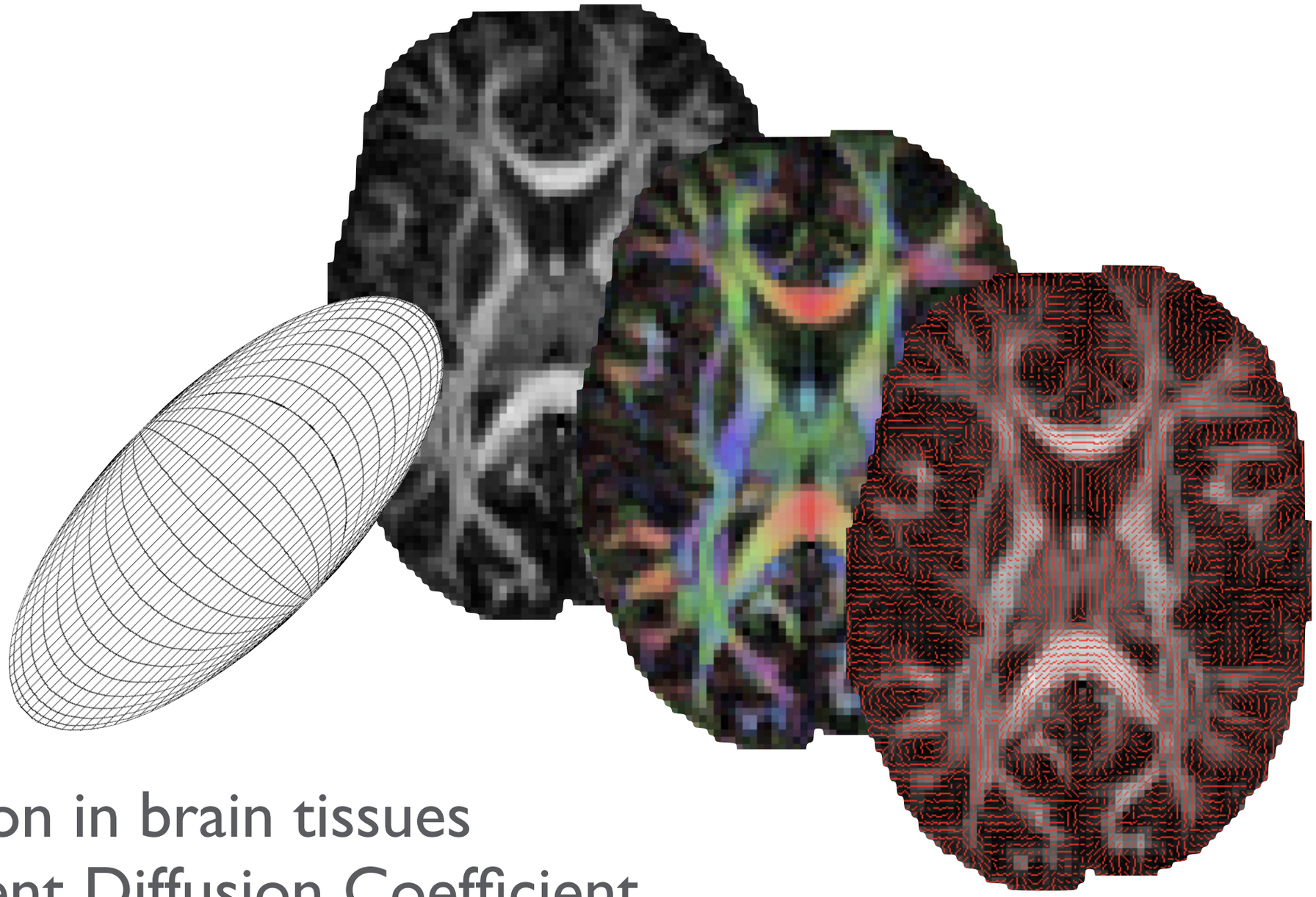
FMRIB Diffusion Toolbox

- DTI model fit
- Eddy current correction
- Voxel-Based diffusion analysis (TBSS)
- BEDPOSTX modelling crossing fibres
- PROBTRACKX propagating uncertainty in tractography





Diffusion Tensor Imaging - basic principles

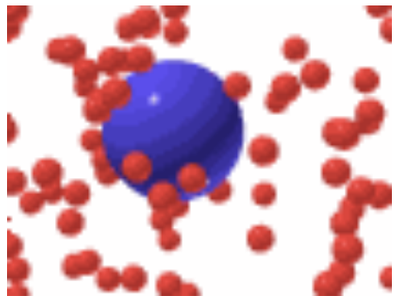


- Diffusion in brain tissues
- Apparent Diffusion Coefficient
- Diffusion Tensor model
- Tensor-derived measures

Brownian motion

Robert Brown (1773-1858)

Molecules are in constant motion



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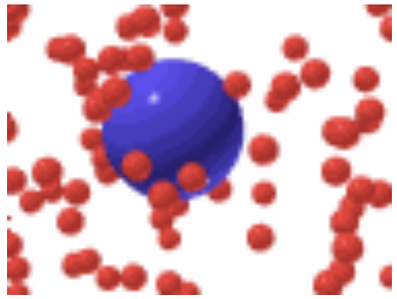

Adolf Fick (1829-1901)

diffusion coefficient

flux

concentration

$$J = -D\nabla\phi.$$

$$\frac{\partial\phi}{\partial t} = D\,\frac{\partial^2\phi}{\partial x^2}$$

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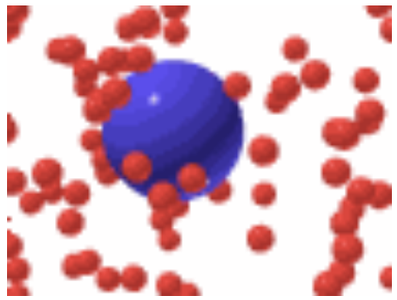

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$$J = -D\nabla\phi.$$

$$\frac{\partial\phi}{\partial t} = D\frac{\partial^2\phi}{\partial x^2}$$

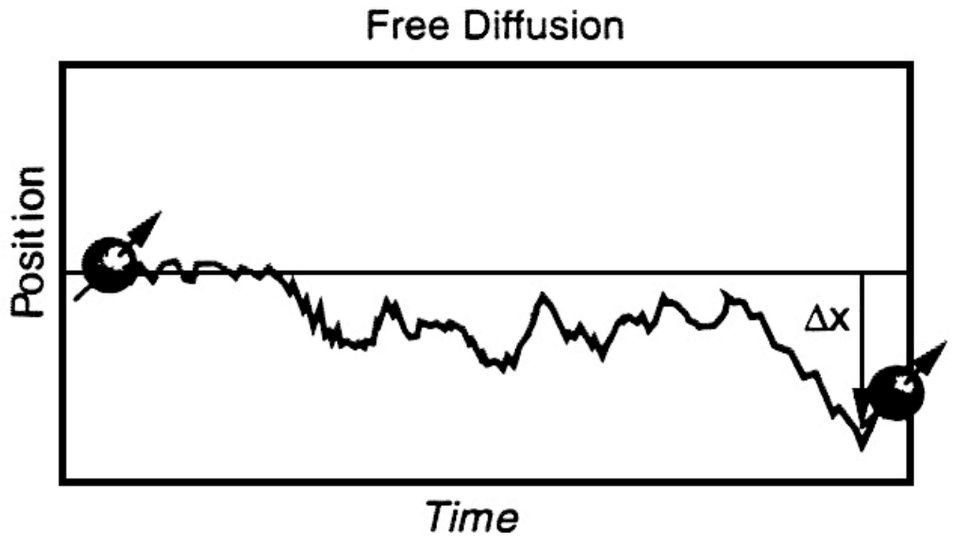
Albert Einstein (1879-1955)

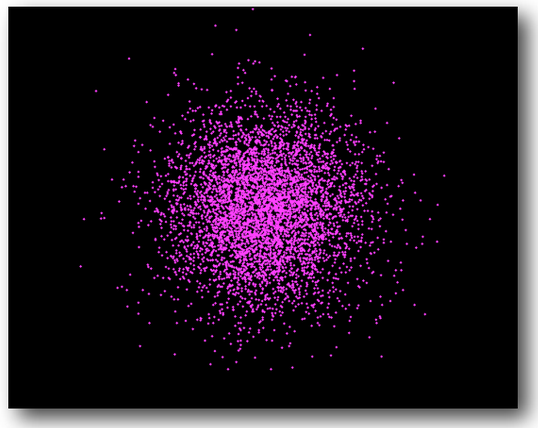
$$< x^2 >= 2nDt$$

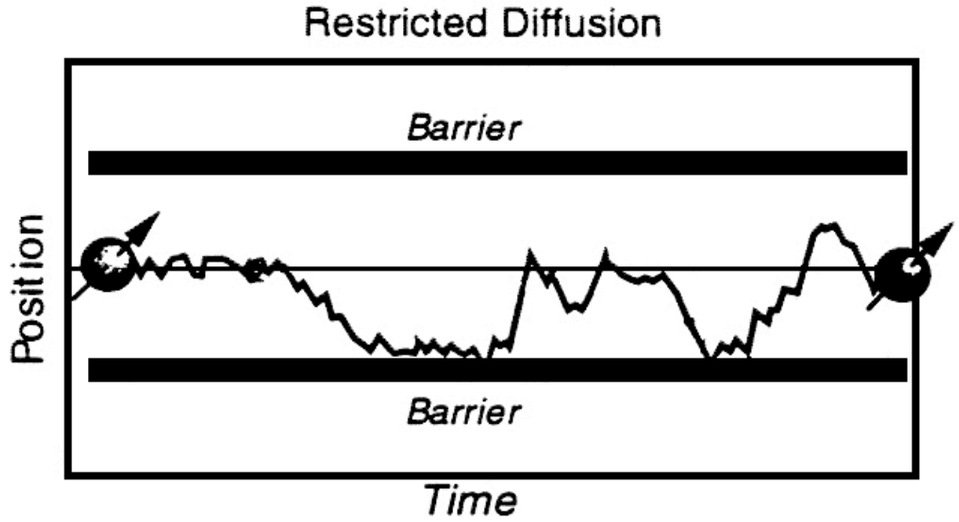
displacement

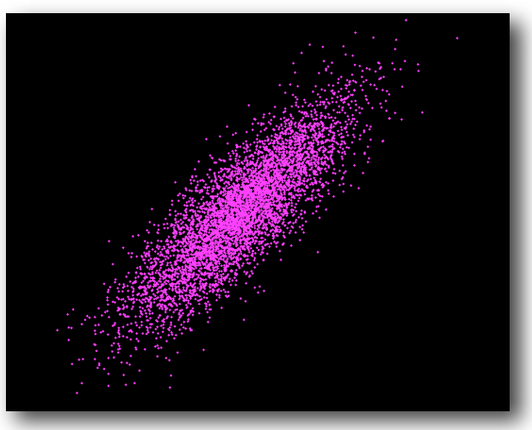
time

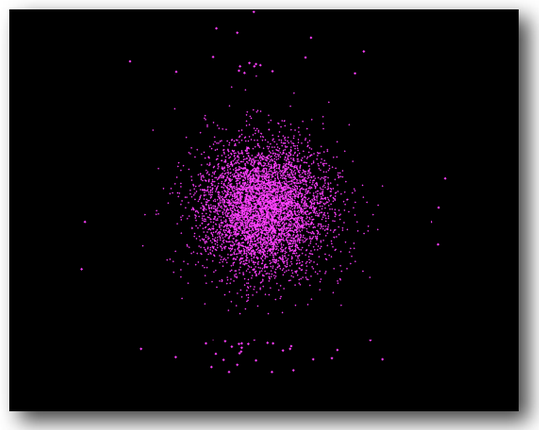
Diffusion in tissues



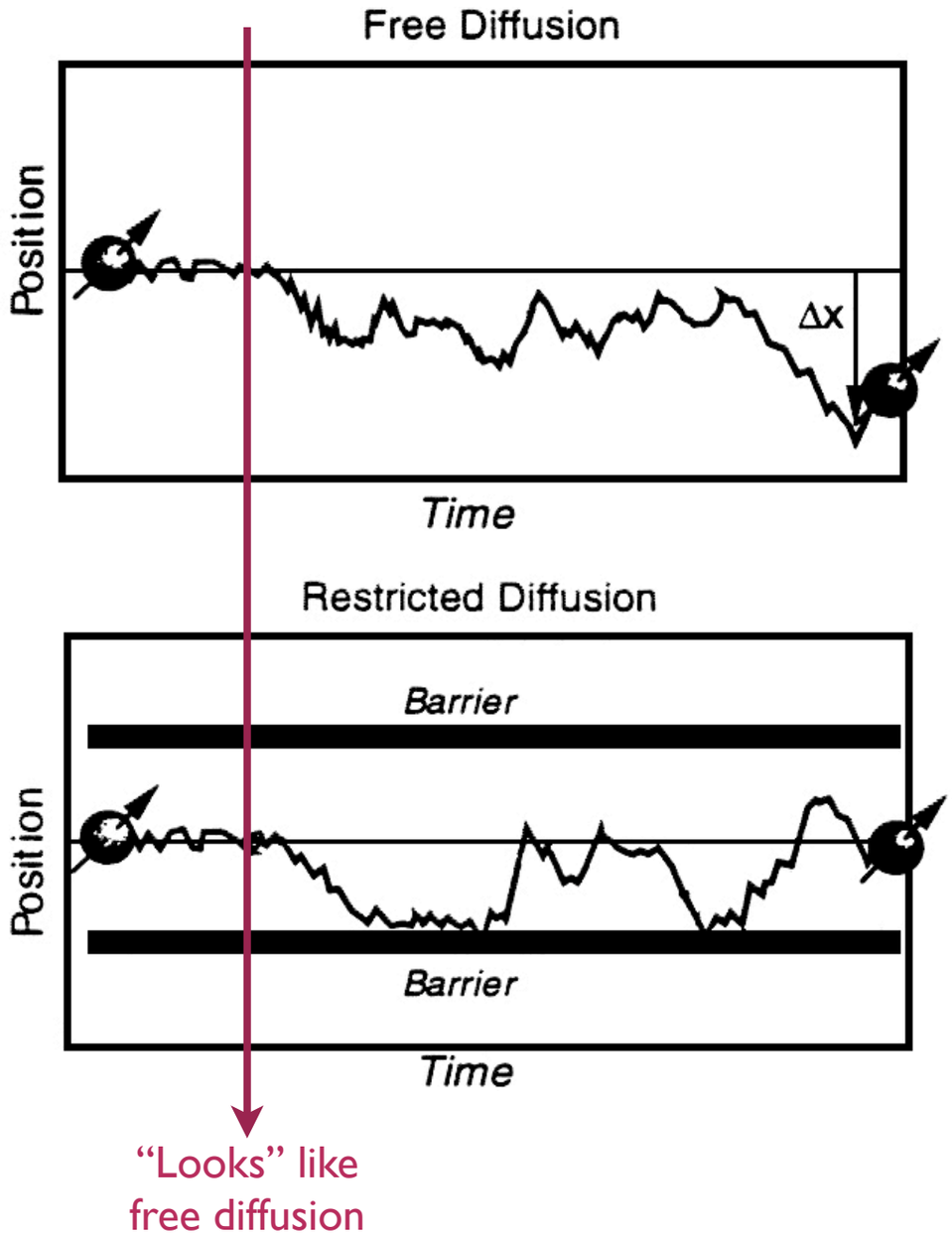


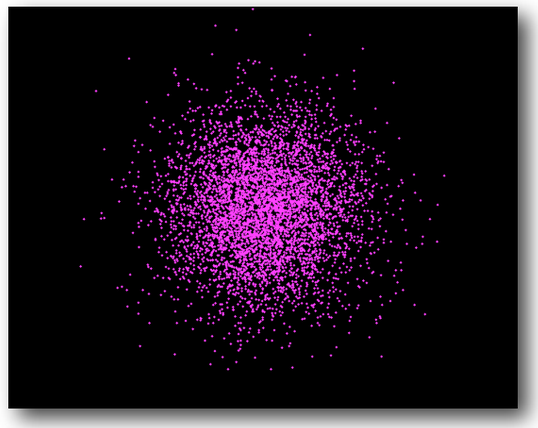


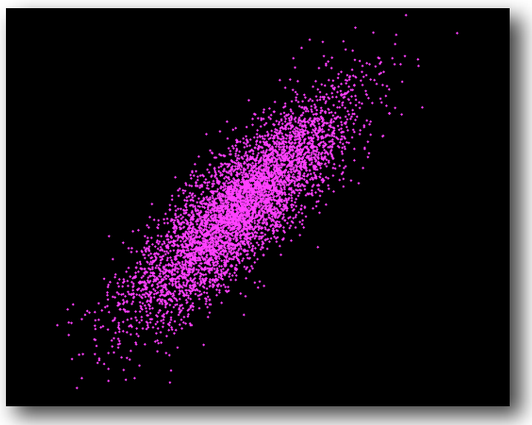


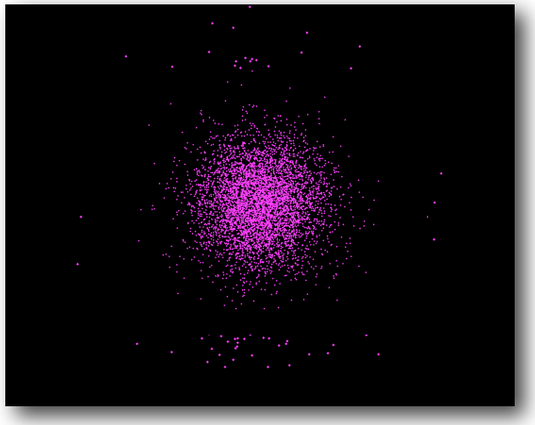


Diffusion in tissues

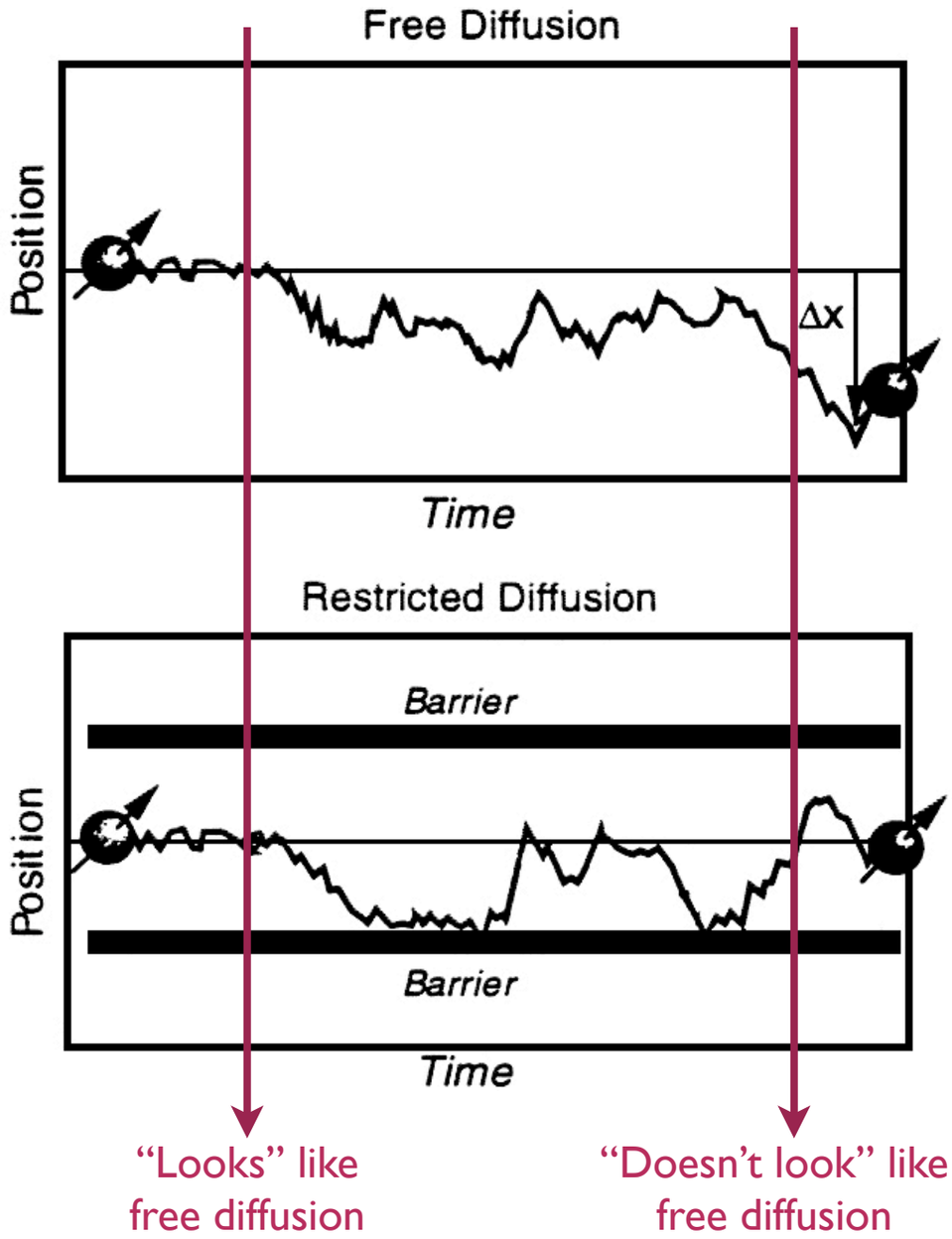


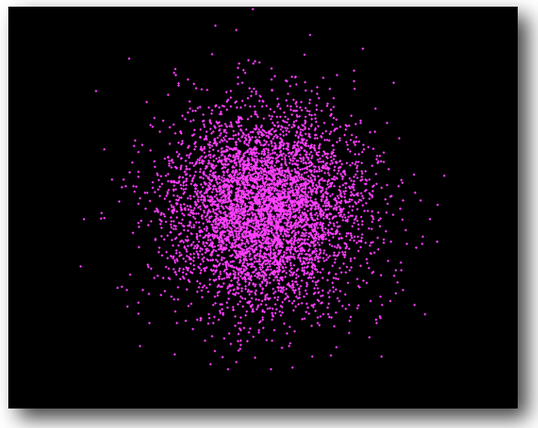


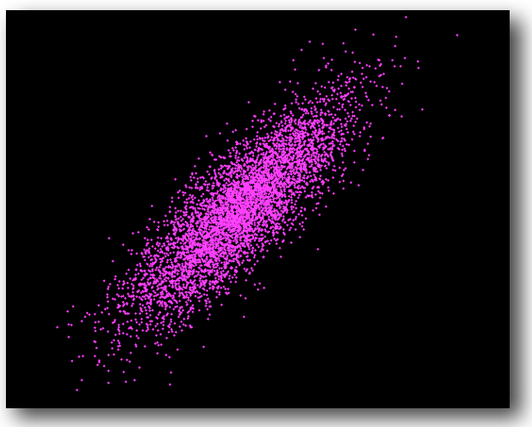


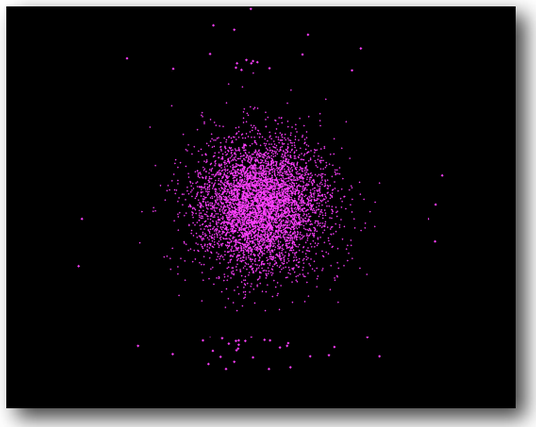


Diffusion in tissues

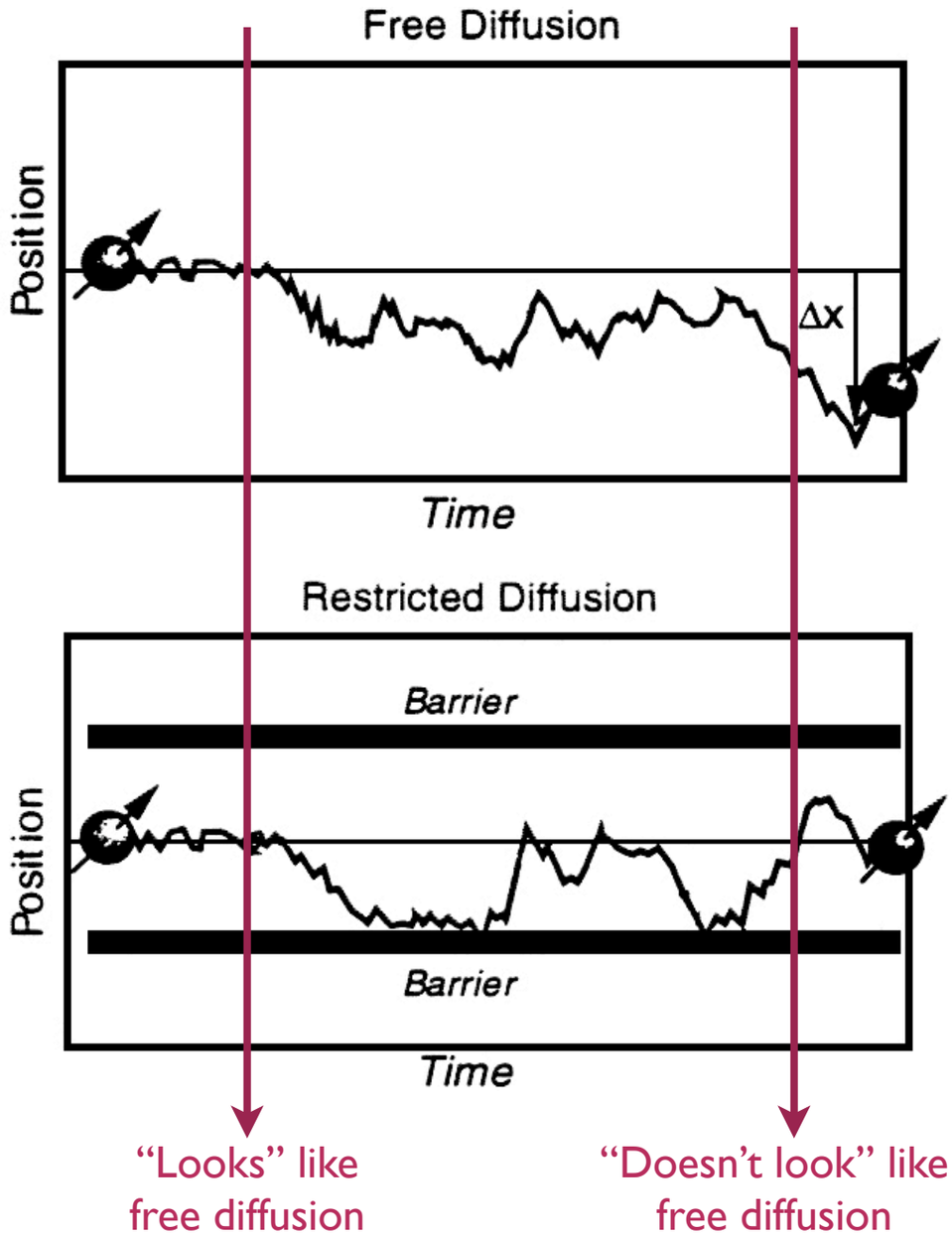


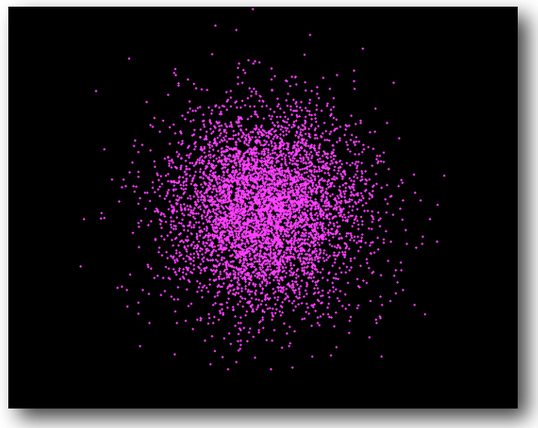


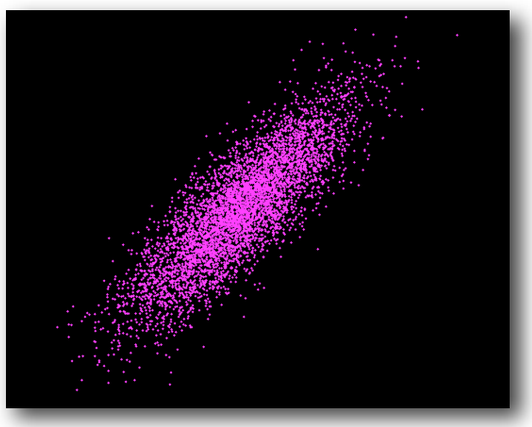


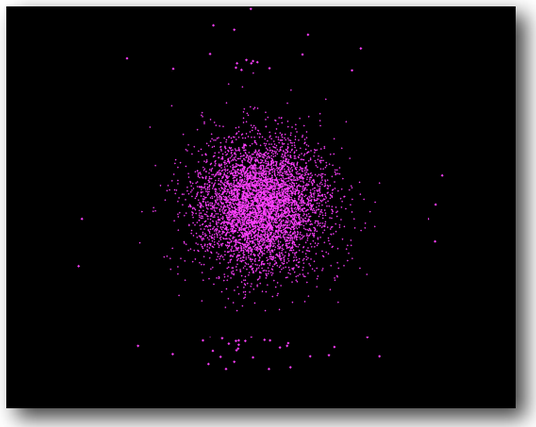


Diffusion in tissues



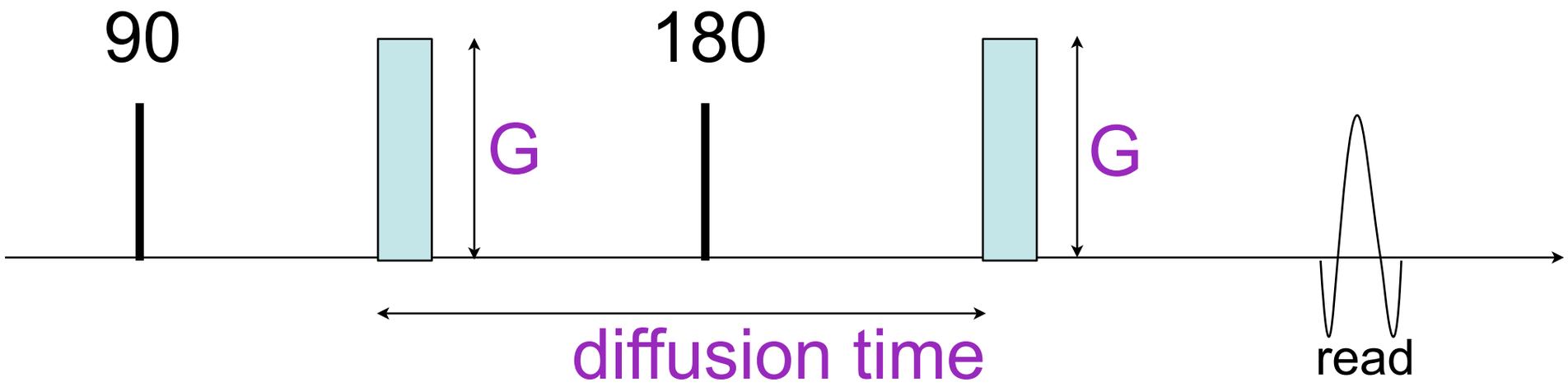


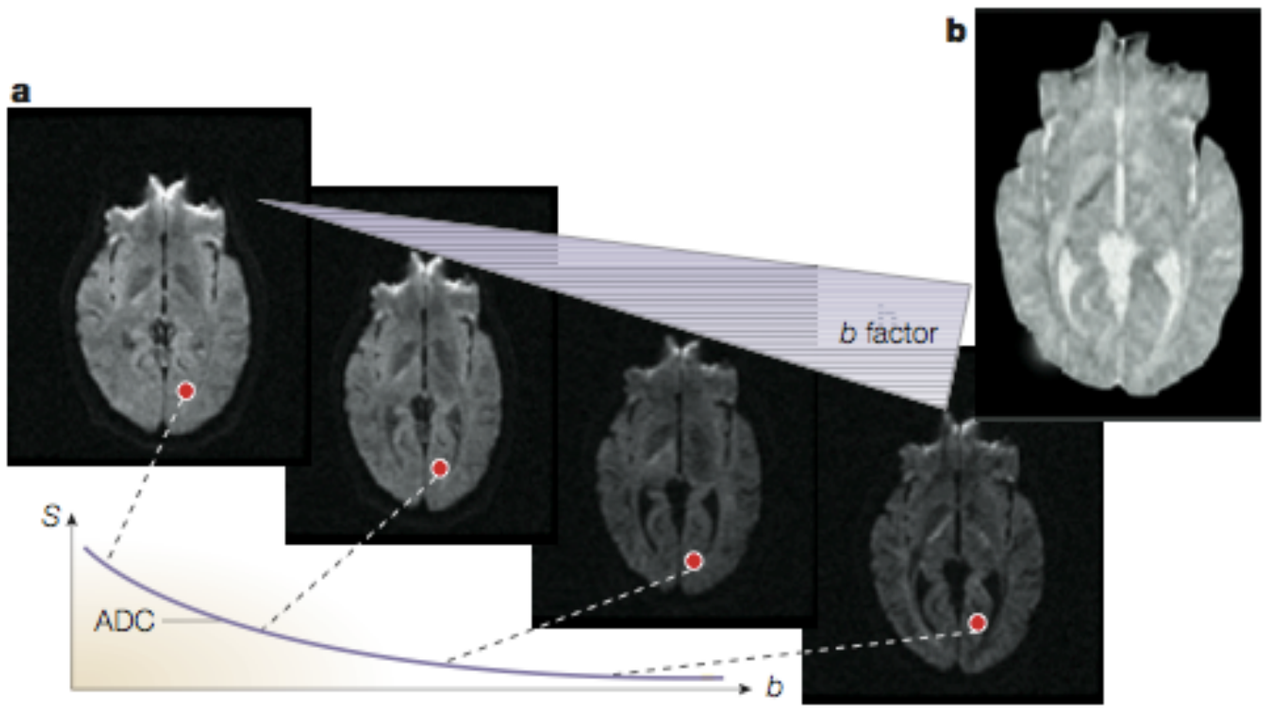




"Apparent" diffusion coefficient (ADC) depends on the diffusion experiment!

Measuring diffusion with MRI



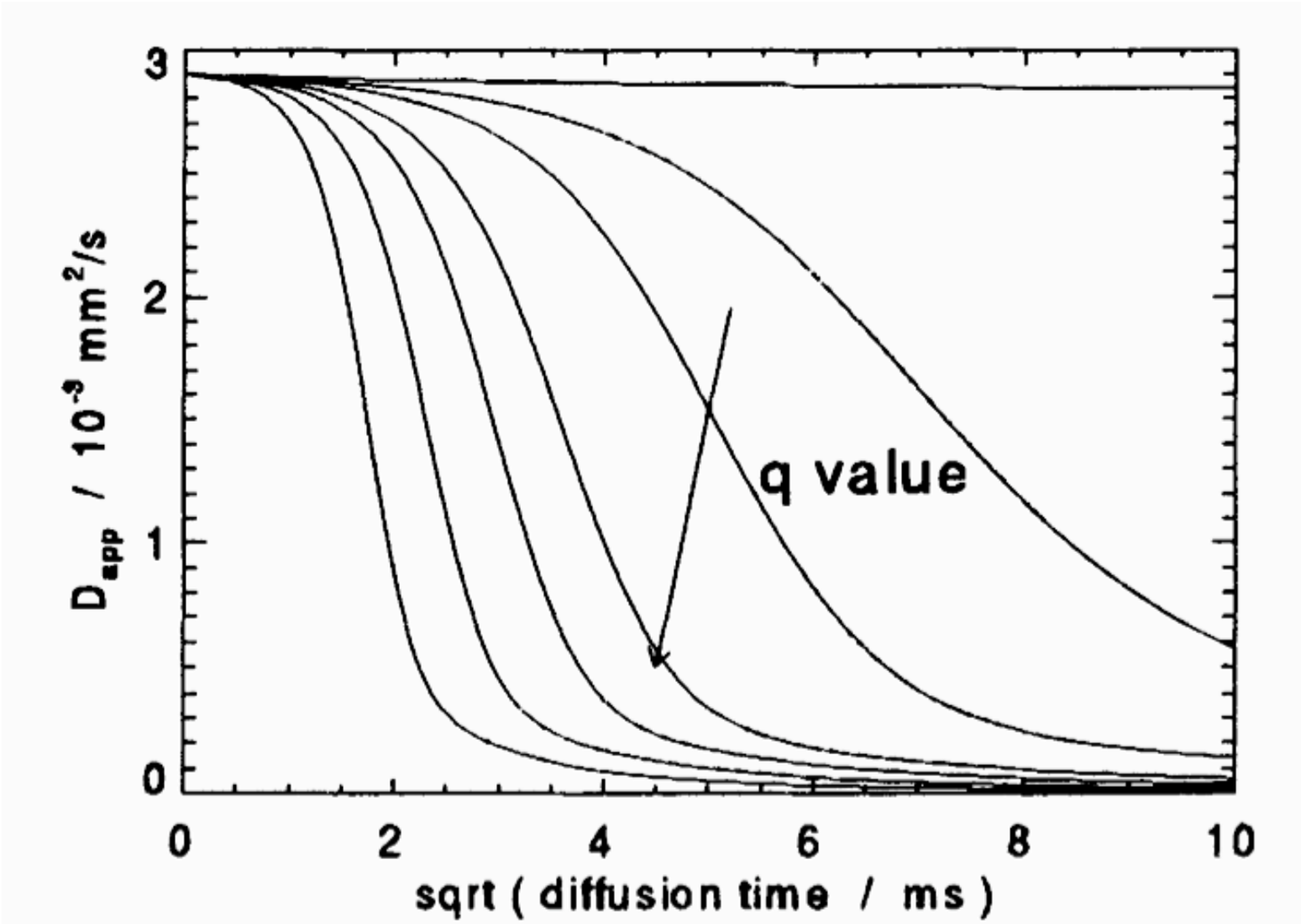


Diffusion contrast is modulated by:

. Gradient **strength**
. Gradient **orientation**
. Diffusion **time**

Apparent diffusion coefficient

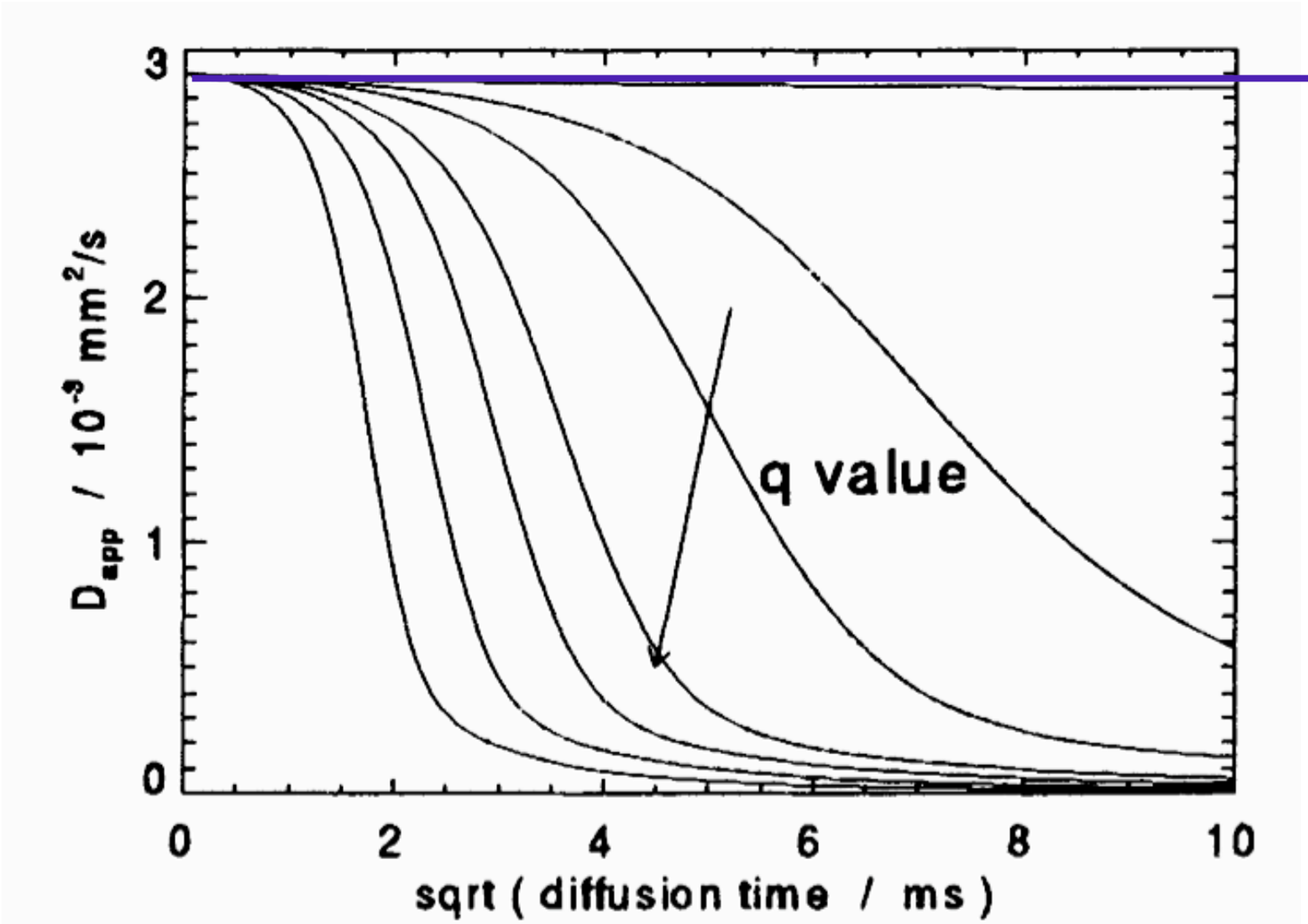
Remember:
q ~ gradient strength



Pfeuffer et al, NMR Biomed 1998

Apparent diffusion coefficient

Remember:
q ~ gradient strength

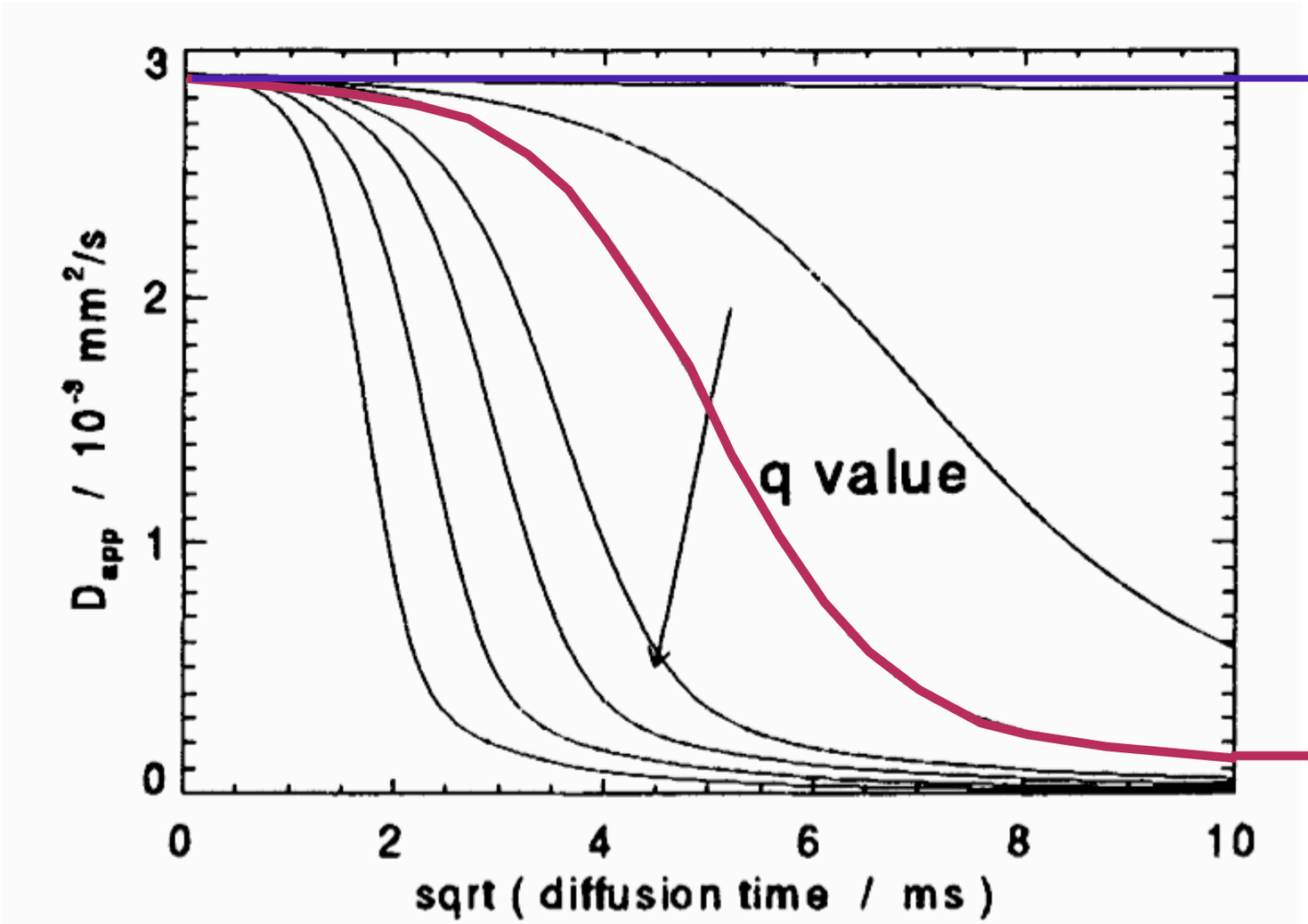


"intrinsic" diffusion coefficient

Pfeuffer et al, NMR Biomed 1998

Apparent diffusion coefficient

Remember:
q ~ gradient strength



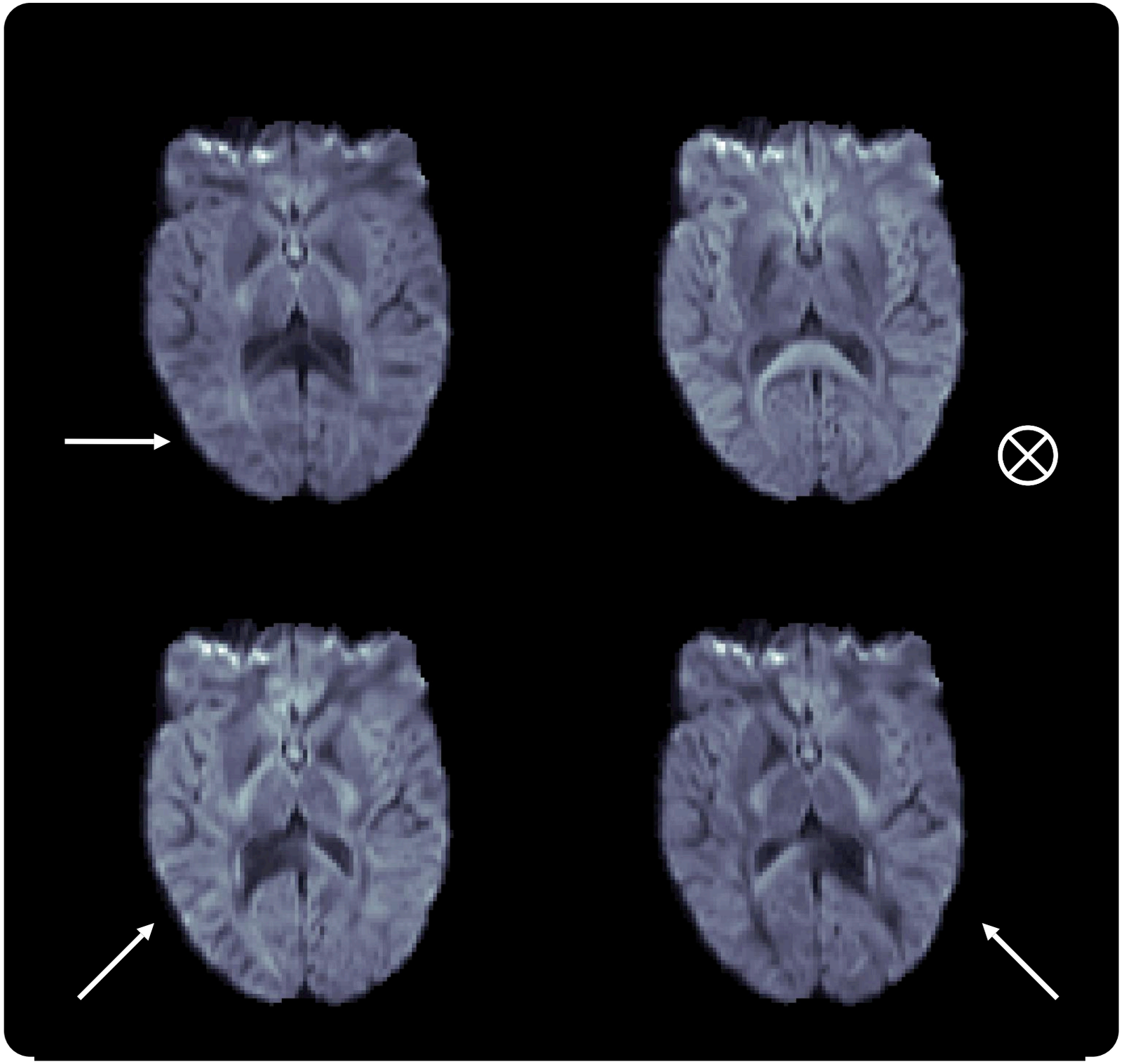
Pfeuffer et al, NMR Biomed 1998

"intrinsic" diffusion coefficient

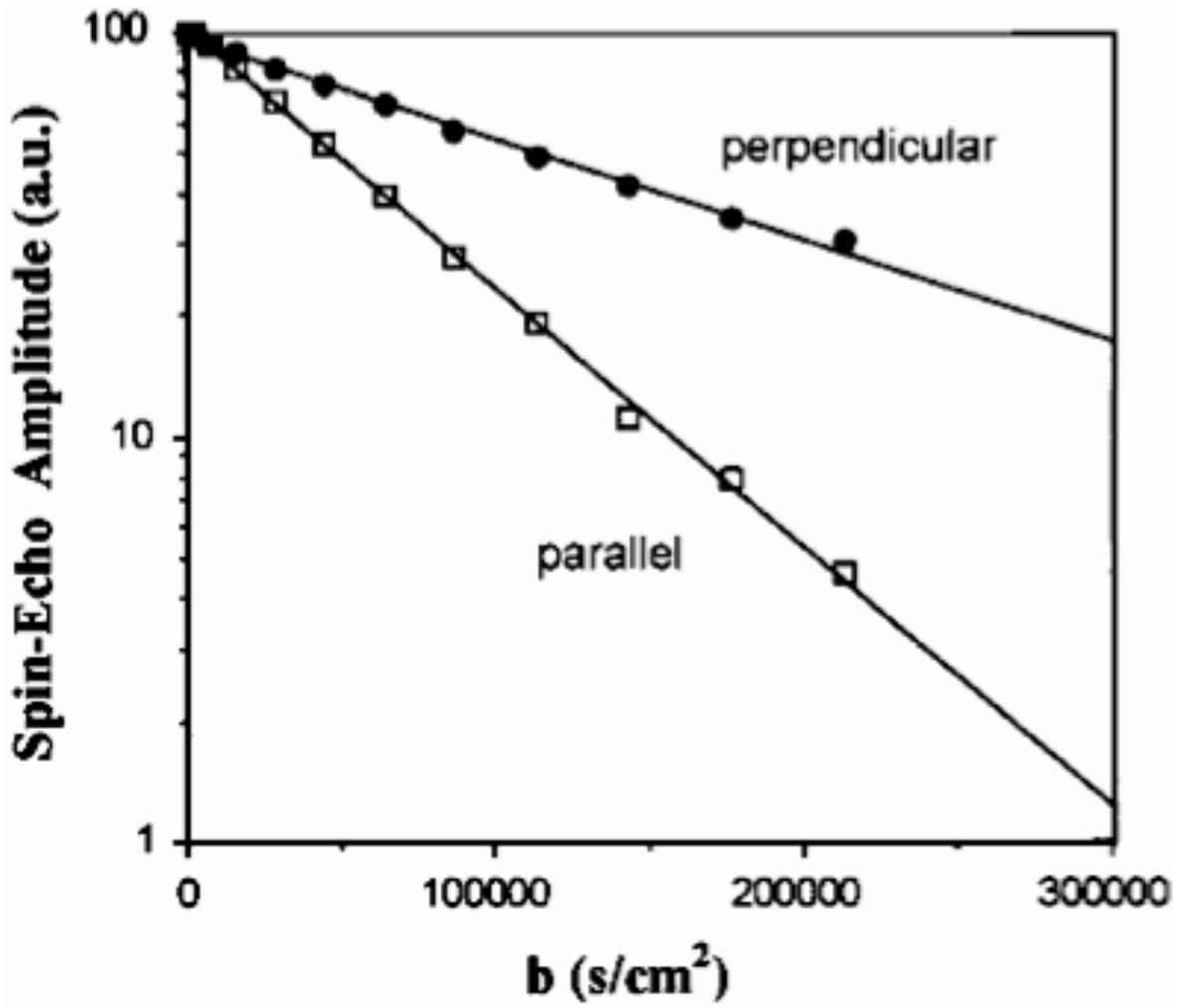
"apparent" diffusion coefficient

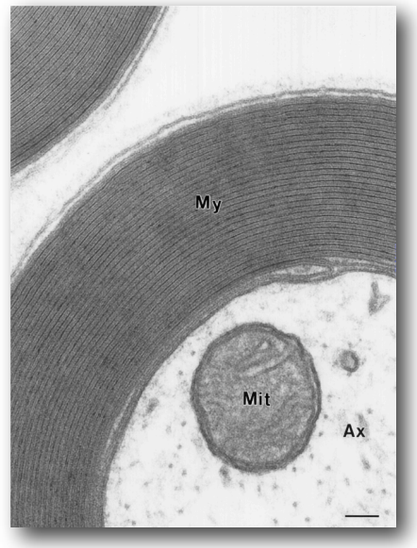
Typical experiment (50-100 ms)

Orientation contrast in Diffusion MR



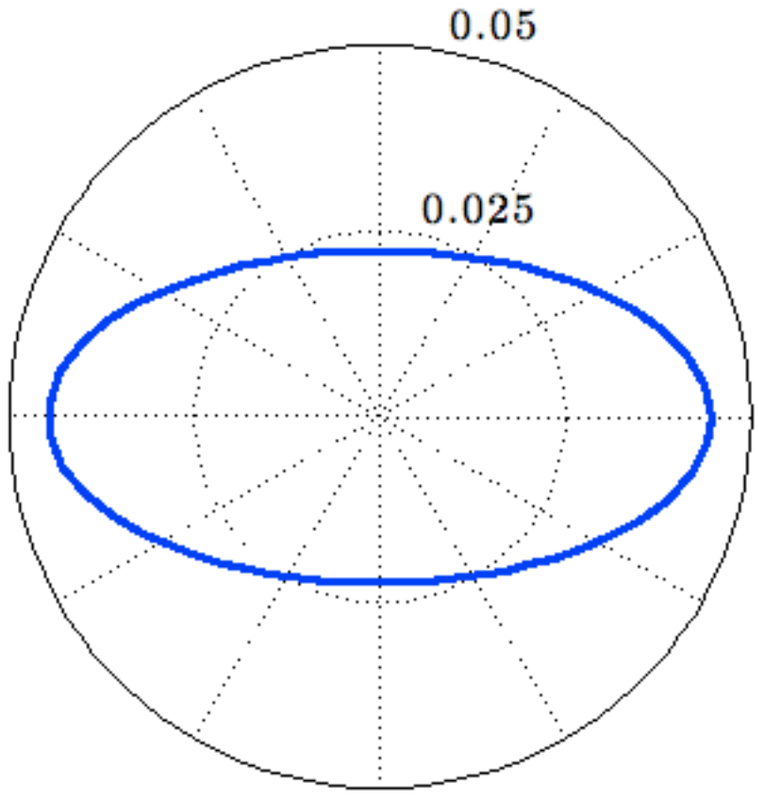
Anisotropy of the Apparent diffusion coefficient





Beaulieu, NMR Biomed 2002

Diffusion tensor model

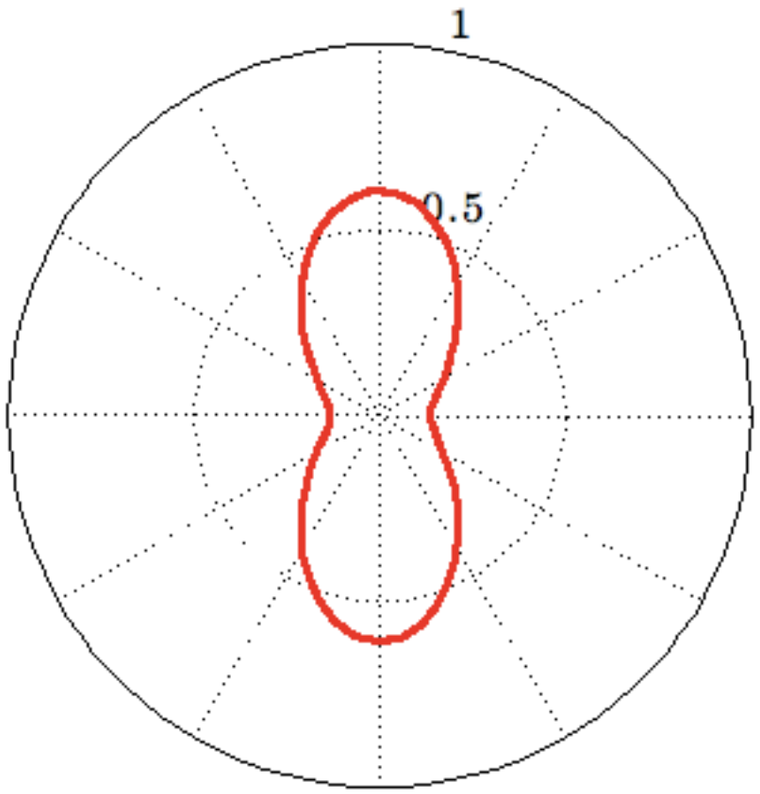


Iso-probability contour

$$\mathcal{N}(0, 2\tau\mathbf{D})$$

mean squared displacement

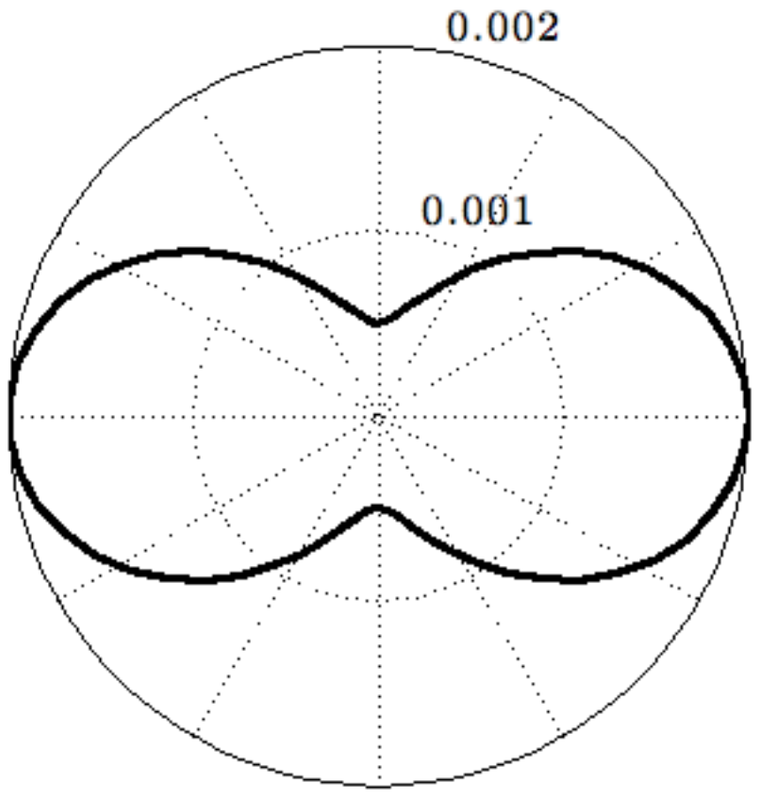
Diffusion tensor model



diffusion MRI signal

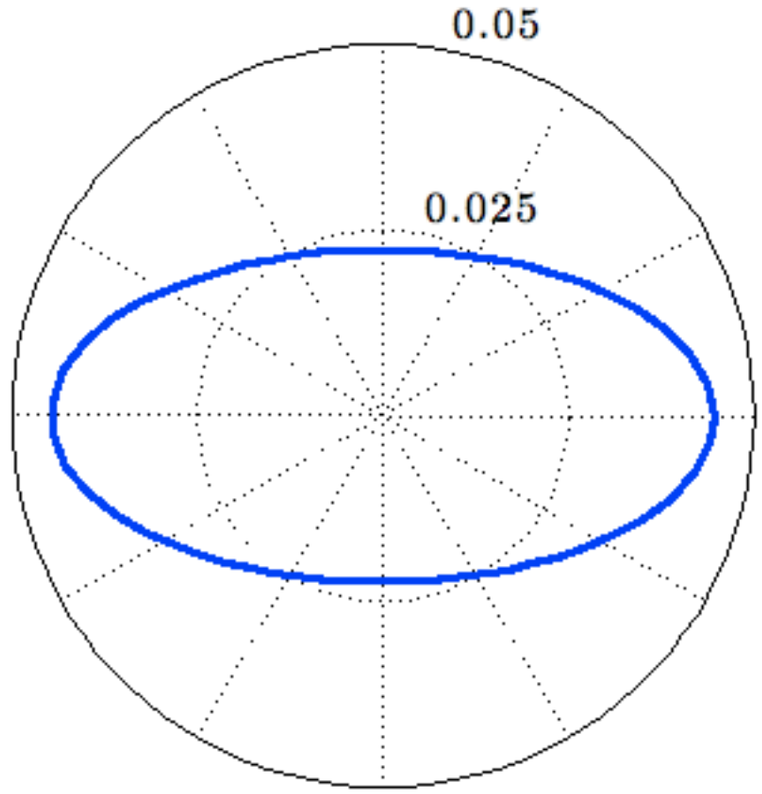
$$\exp(-b\mathbf{x}^T\mathbf{D}\mathbf{x})$$

signal attenuation



ADC profile
(mm^2/s)

$$\mathbf{x}^T\mathbf{D}\mathbf{x}$$



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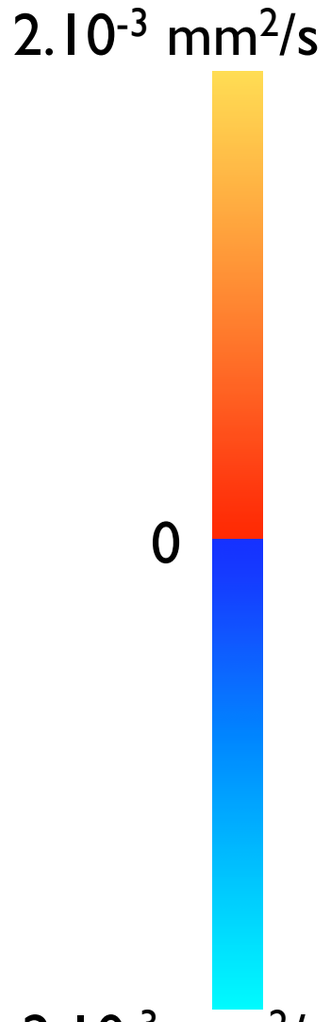
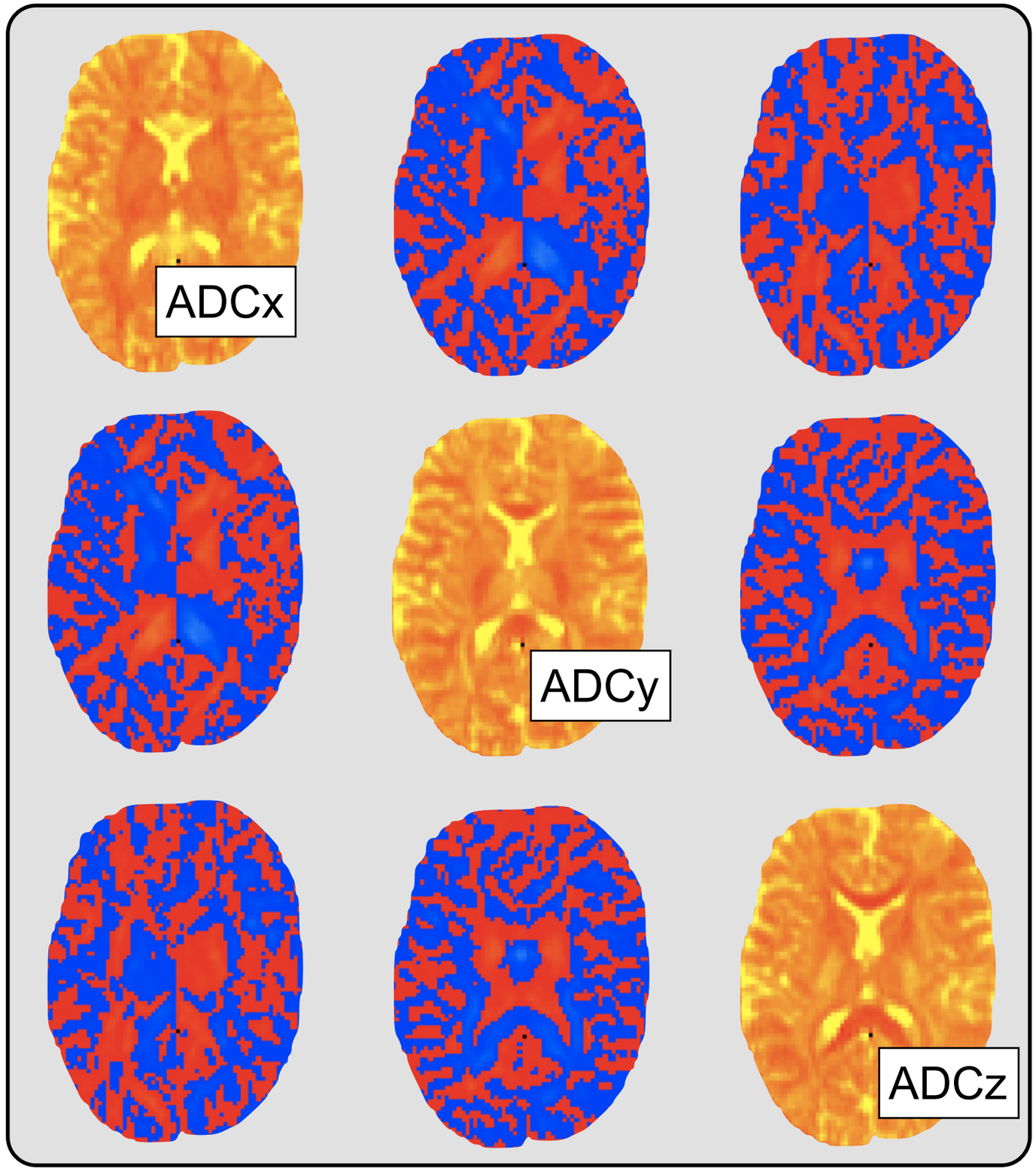
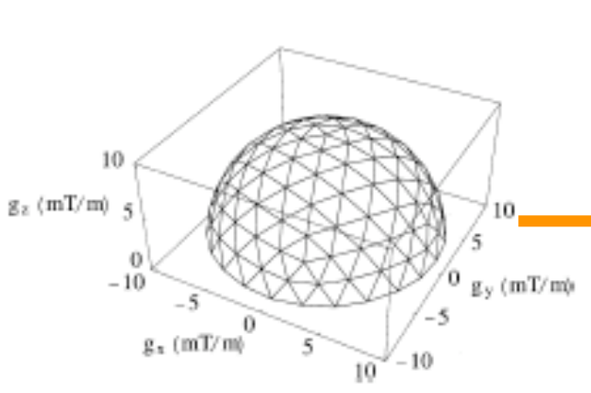
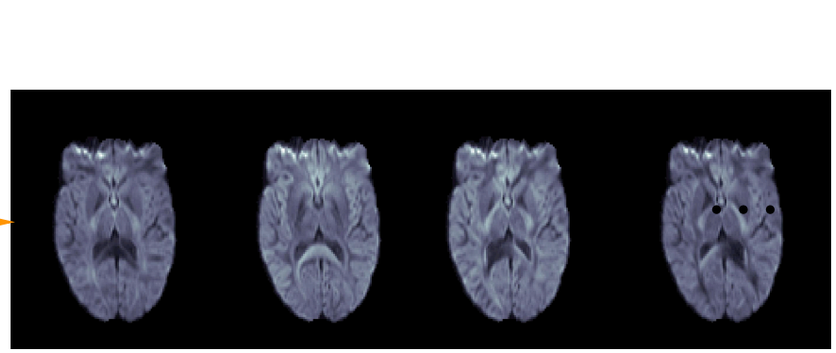
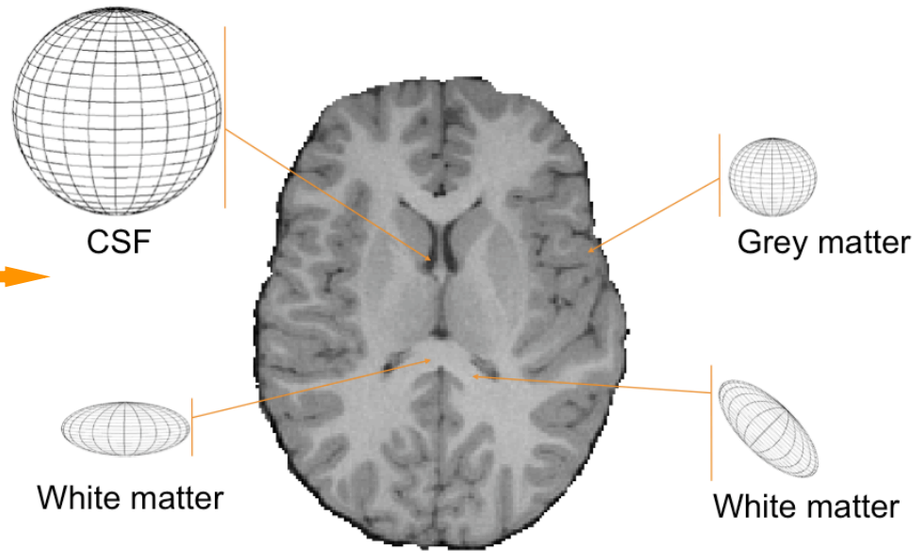




Diffusion tensor model Estimation

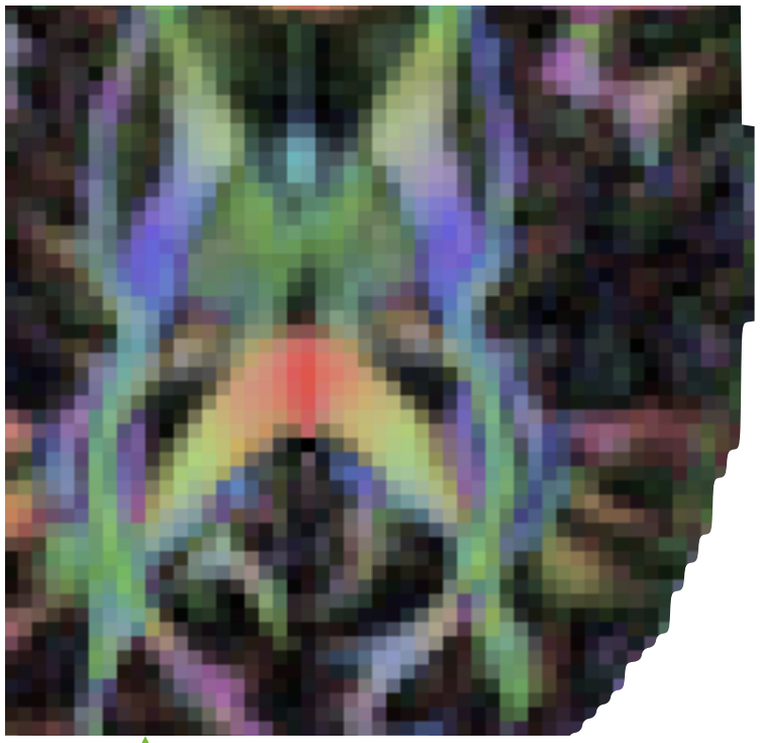


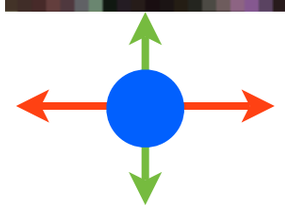


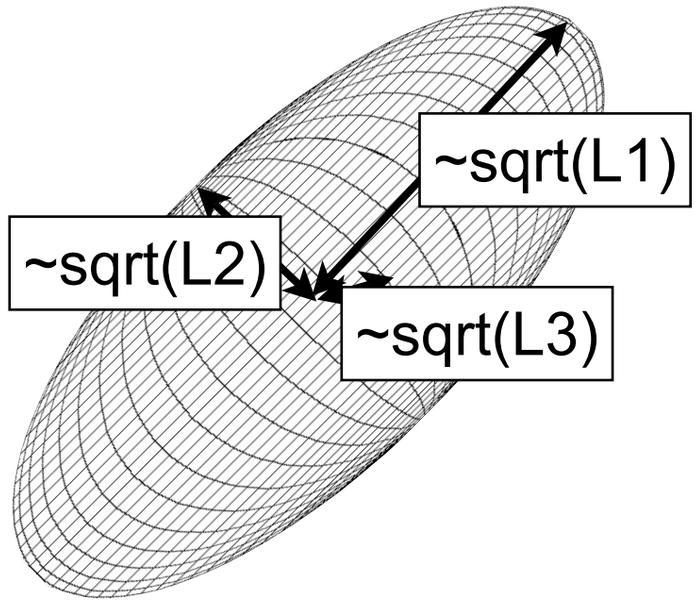


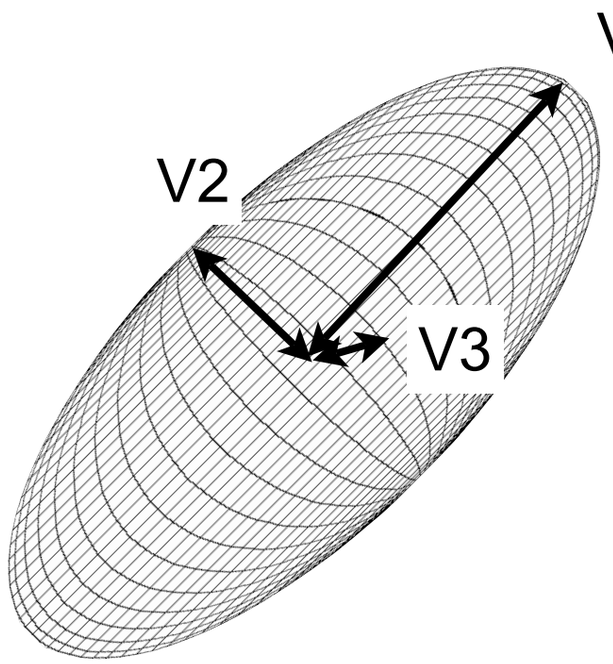
Diffusion tensor model eigenspectrum

V1 map





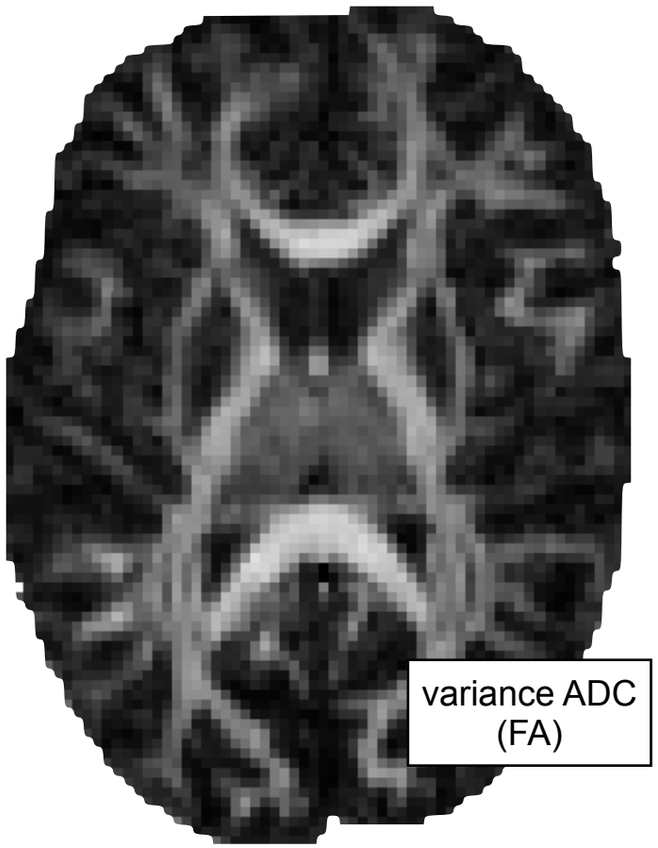




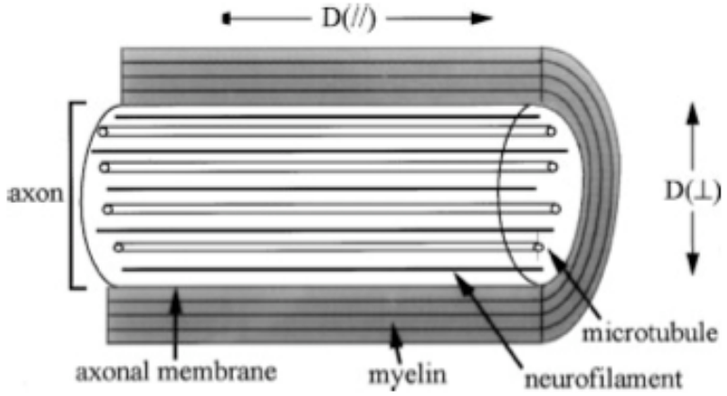
L1=ADCmax
L3=ADCmin

L1+L2+L3 = 3x(average ADC)

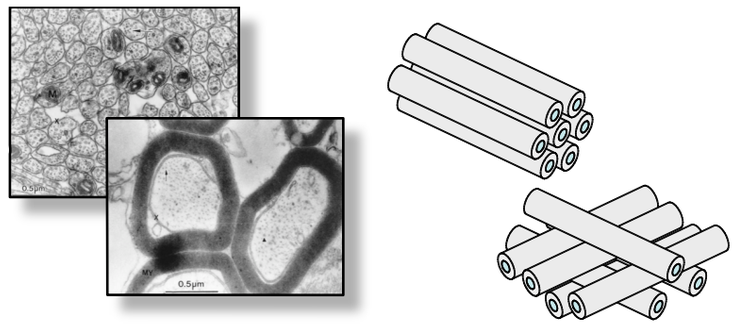
Tensor-derived measures



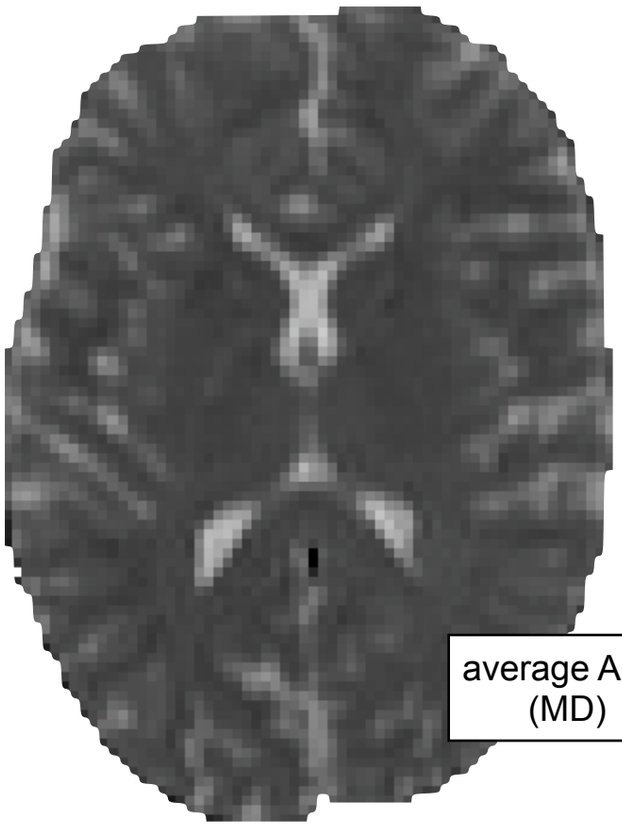
variance ADC
(FA)



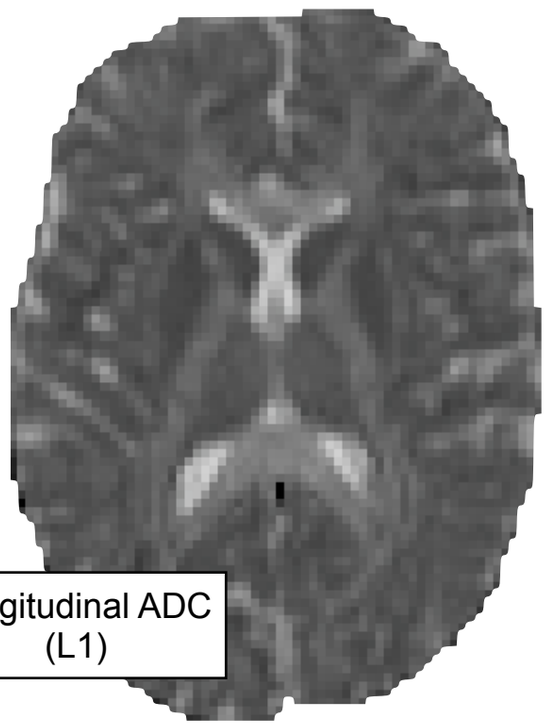
biophysical properties



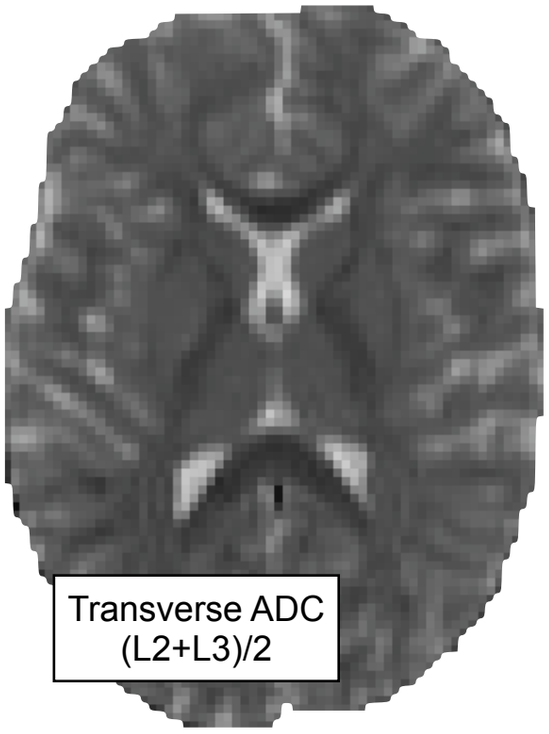
geometric properties



average ADC
(MD)

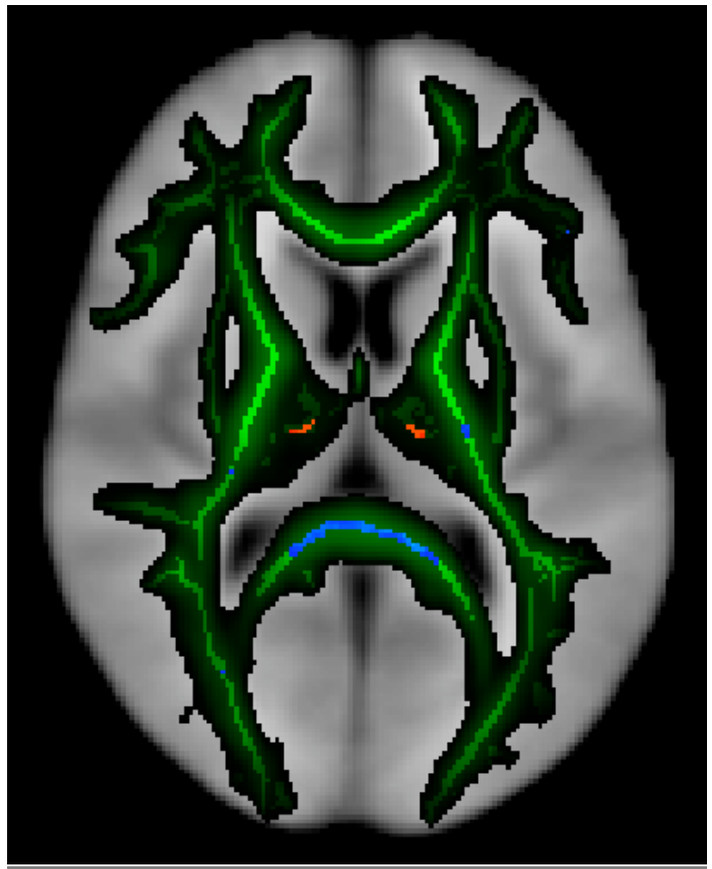


Longitudinal ADC
(L1)



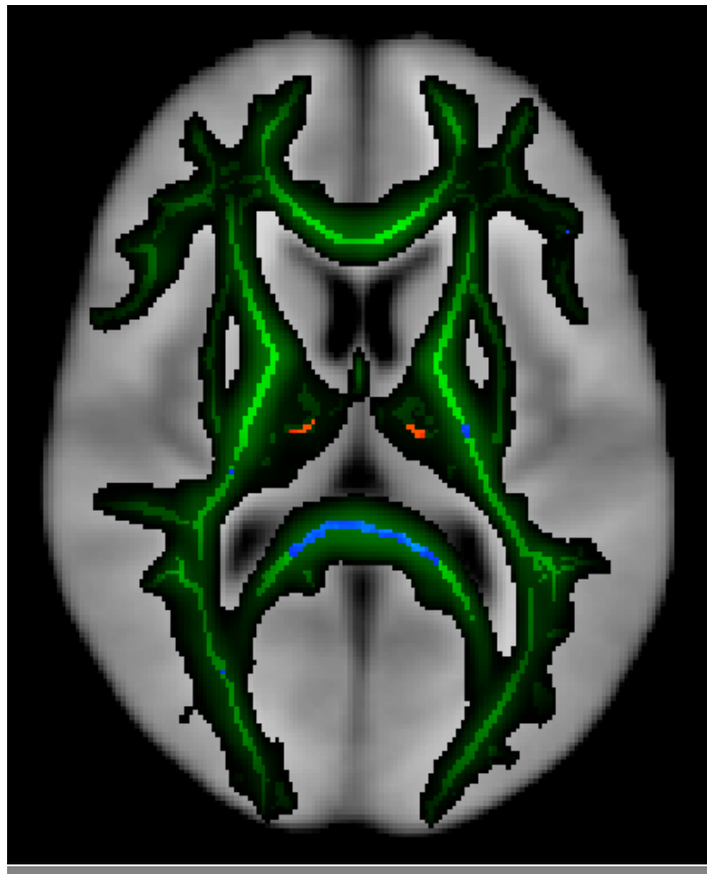
Transverse ADC
(L2+L3)/2

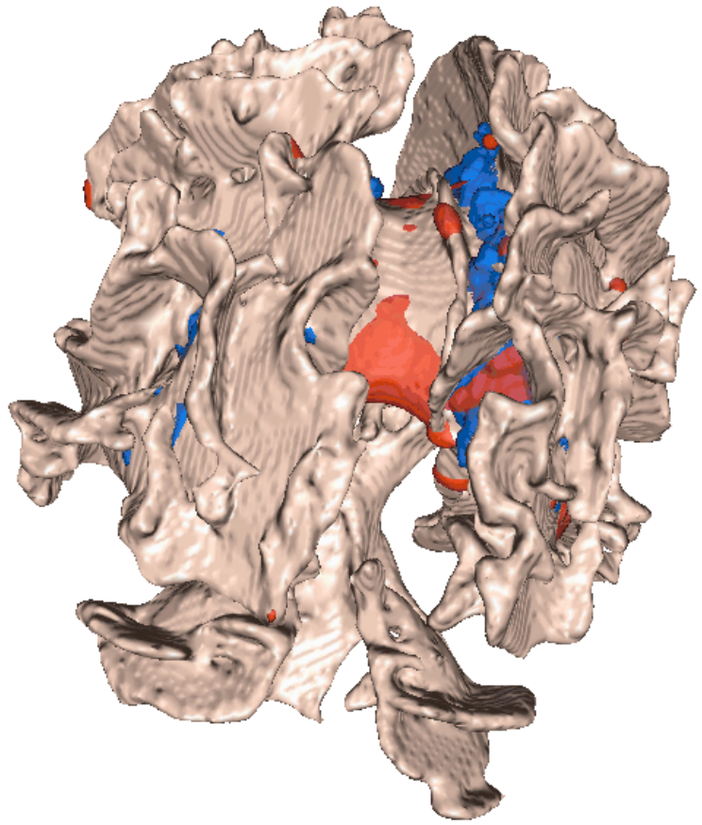
TBSS : Tract-Based Spatial Statisics



- Need: robust “voxelwise” cross-subject stats on DTI
- Problem: alignment issues confound valid local stats
- TBSS: solve alignment using alignment-invariant features:
- Compare FA taken from tract centres (via skeletonisation)

TBSS : Tract-Based Spatial Statisics





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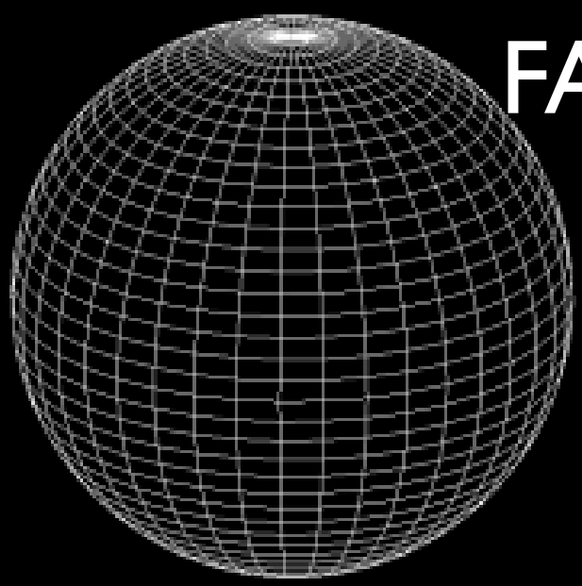
- TBSS: solve alignment using alignment-invariant features:
- Compare FA taken from tract centres (via skeletonisation)

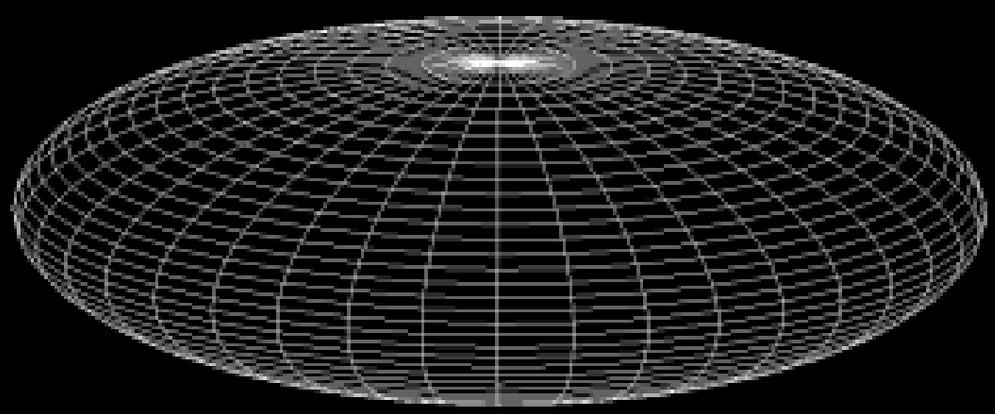
Tensor-derived parameters: Fractional Anisotropy

- FA encodes how strongly directional diffusion is
  - (derived from diffusion tensor eigenvalues)
- Hence good marker for WM integrity
  - i.e., good marker for disease, development, etc.

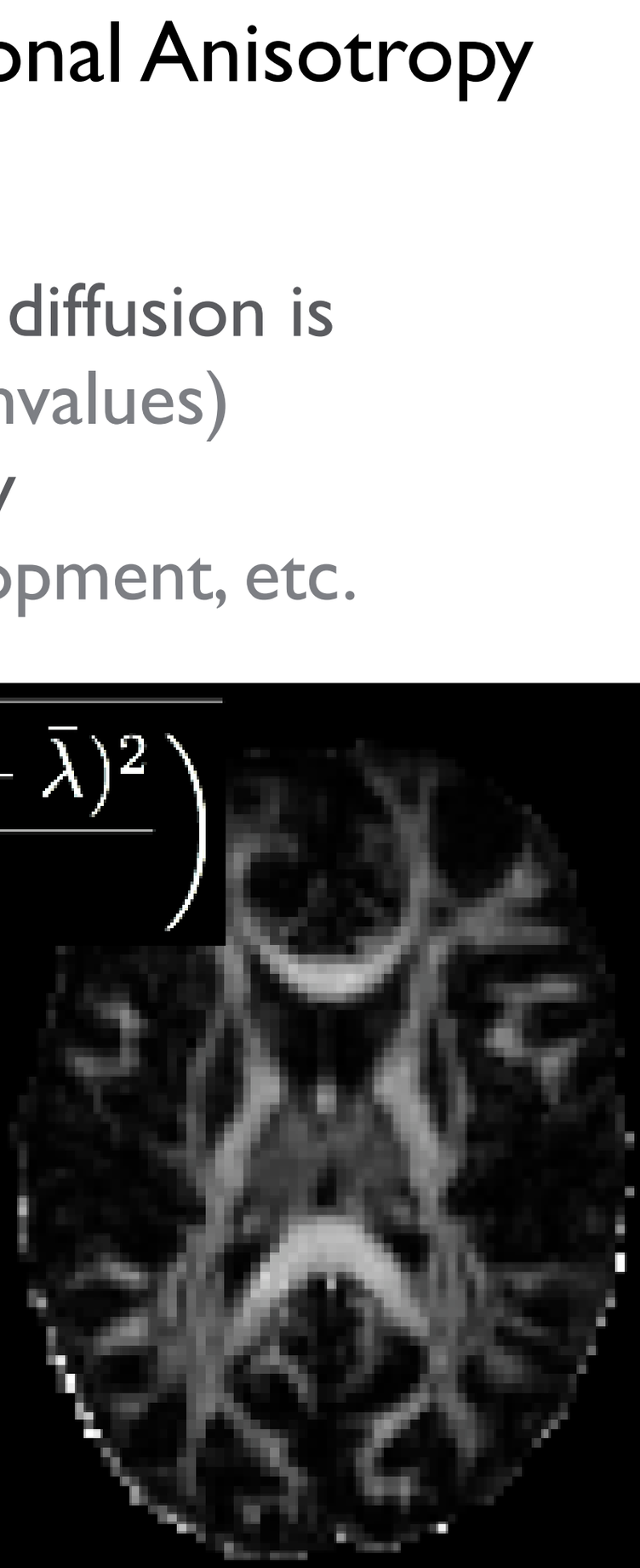
$$\mathrm{FA} = \sqrt{\frac{3}{2}\left(\frac{(\lambda_1-\bar{\lambda})^2+(\lambda_2-\bar{\lambda})^2+(\lambda_3-\bar{\lambda})^2}{\lambda_1^2+\lambda_2^2+\lambda_3^2}\right)}$$



FA=0

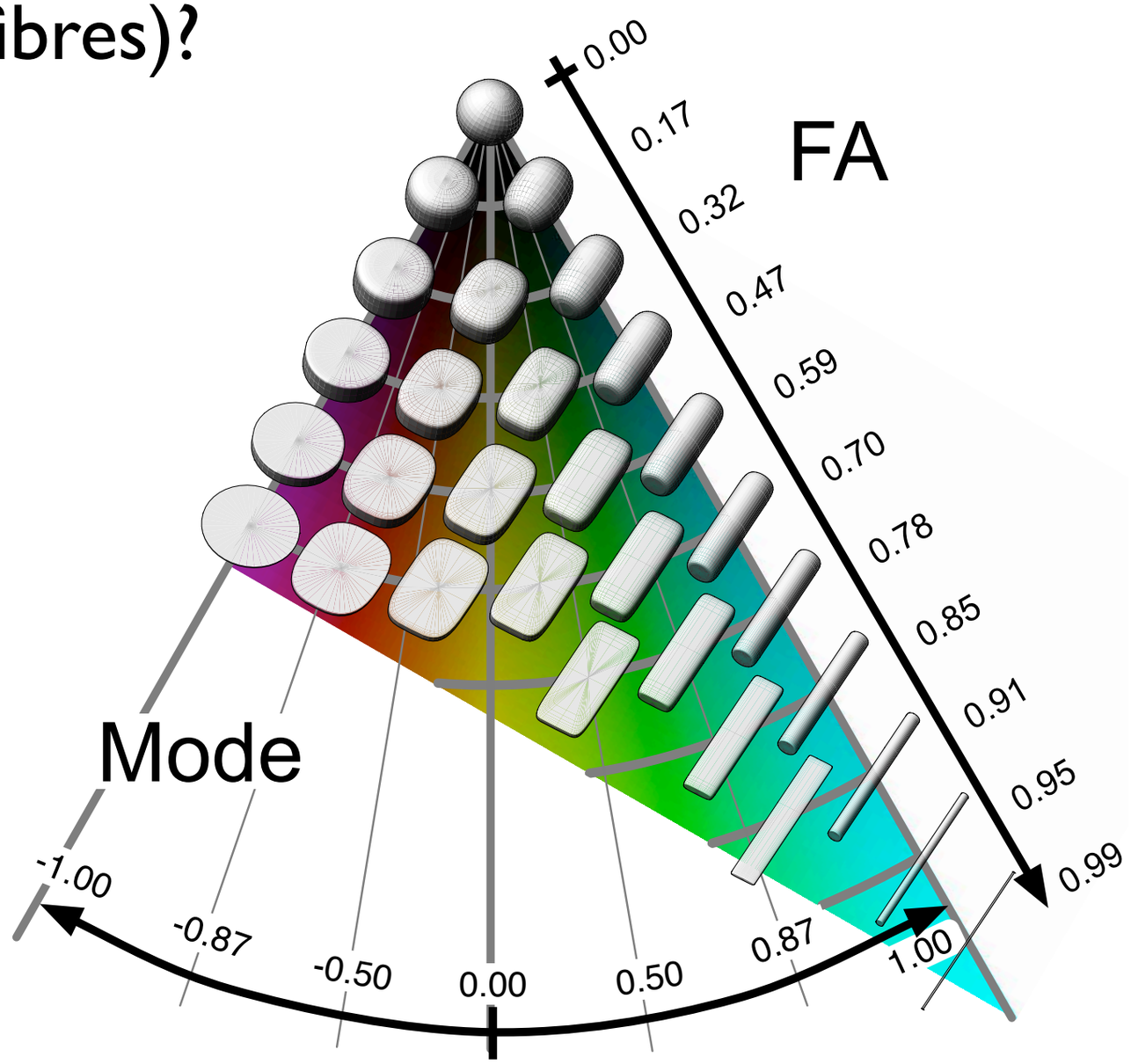


FA=0.8



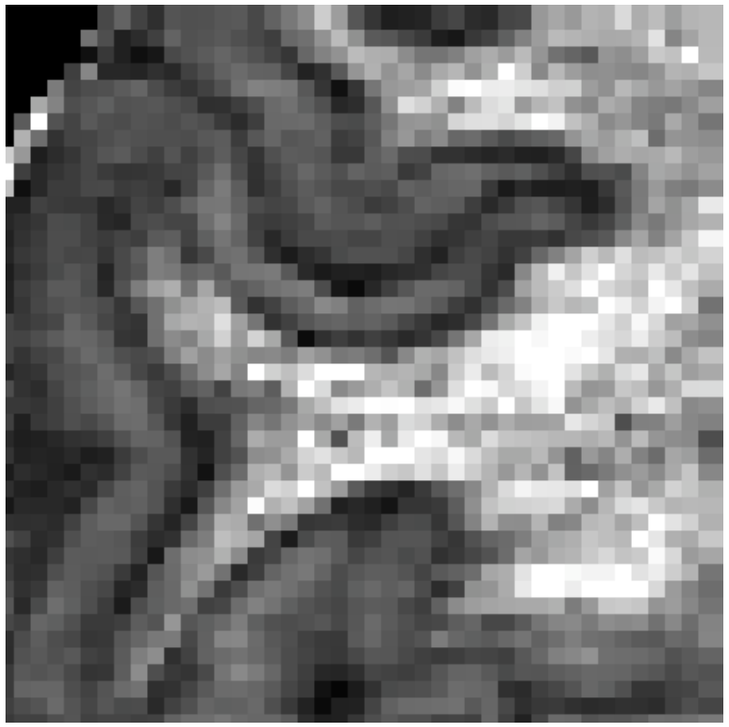
Orthogonal Tensor Invariants (Kindlmann, TMI 2007)

- Nice to have 3 orthogonal (independent) tensor-derived measures: MD, FA & "Mode"
- Mode: is the tensor tubular (one strong fibre) or flat-cylindrical (two strong fibres)?



At “normal” resolutions, tracts appear thinner than they really are

primarily because of the interference between orthogonal anisotropy in GM and WM



original 0.7mm data -> FA

data smoothed to match
2mm data -> FA

data smoothed to match
3.5mm data -> FA

high-resolution ex-vivo diffusion data:
McNab & Miller (FMRIB)

computation resources:
Jones, Stathakis & Wise (CUBRIC cluster)

VBM-style Analysis of FA

- VBM [Ashburner 2000, Good 2001]
- Align all subjects' data to standard space
- Segment -> grey matter segmentation
- Smooth GM
- Do voxelwise stats (e.g. controls-patients)

- VBM on FA [Rugg-Gunn 2001, Büchel 2004, Simon 2005]
- Like VBM but no segmentation needed

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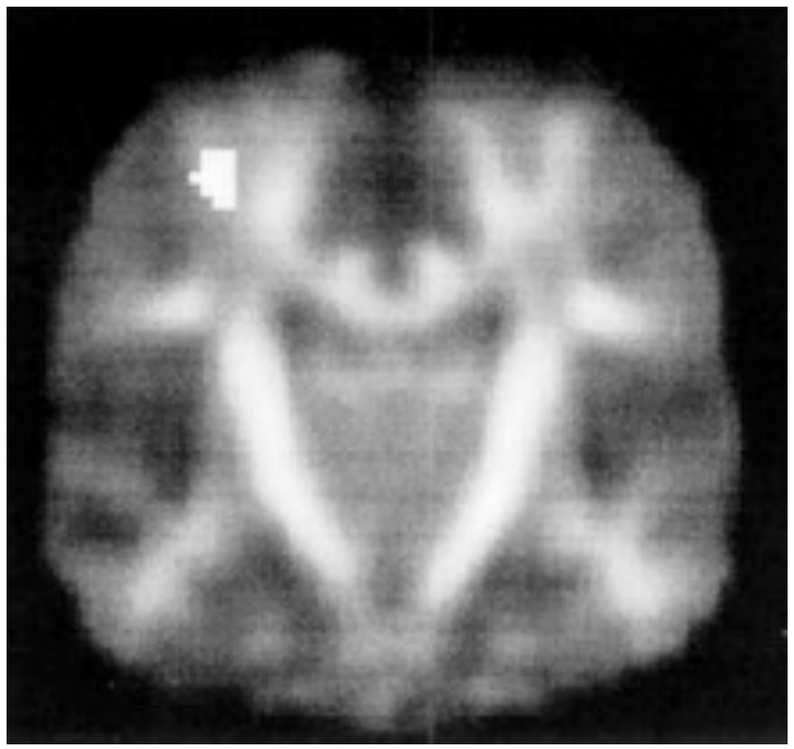
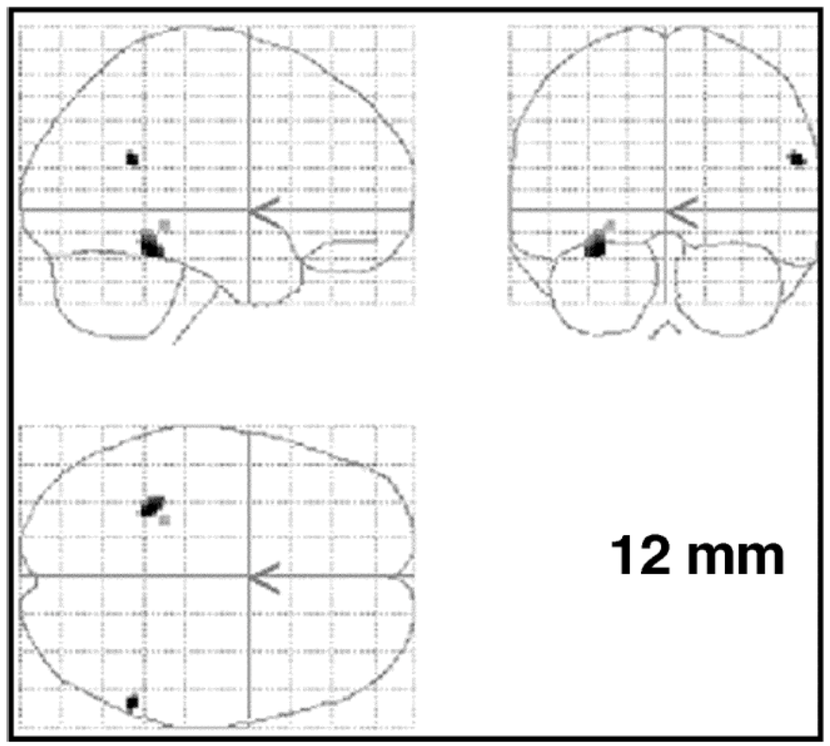


Büchel 2004

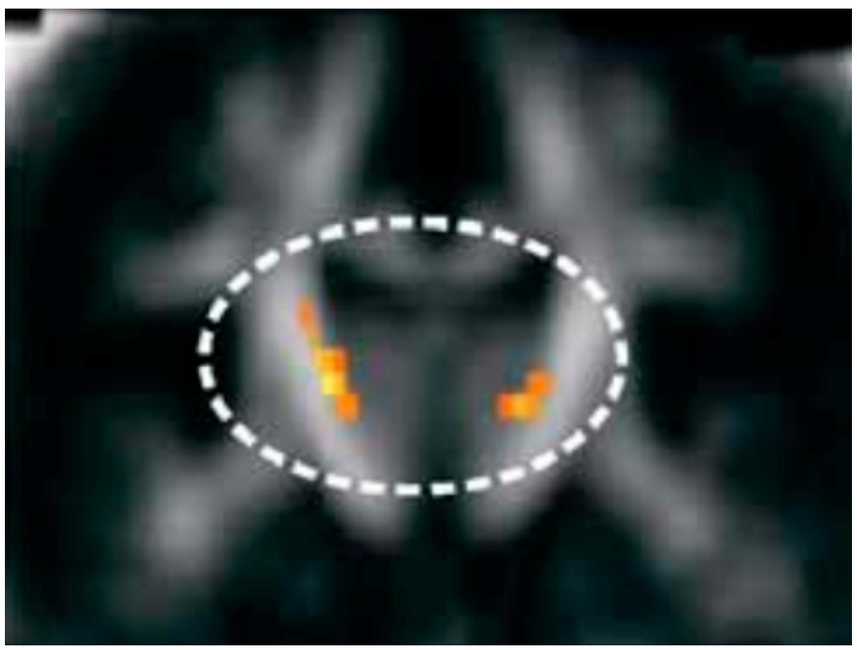
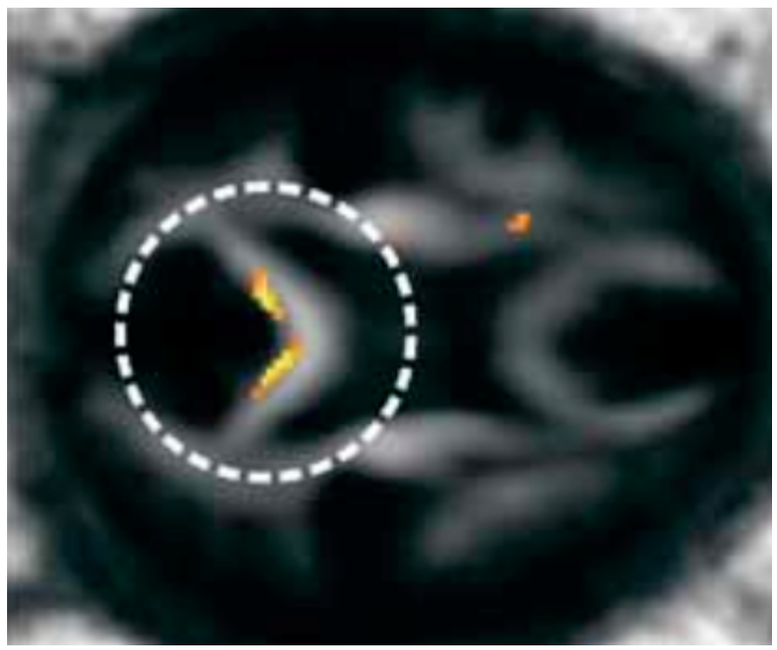
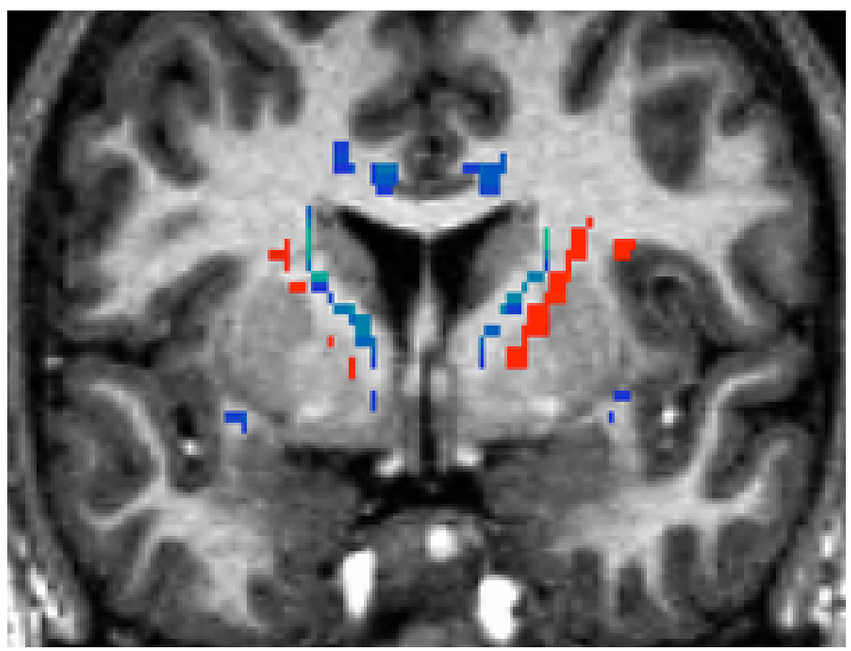


Jones 2005

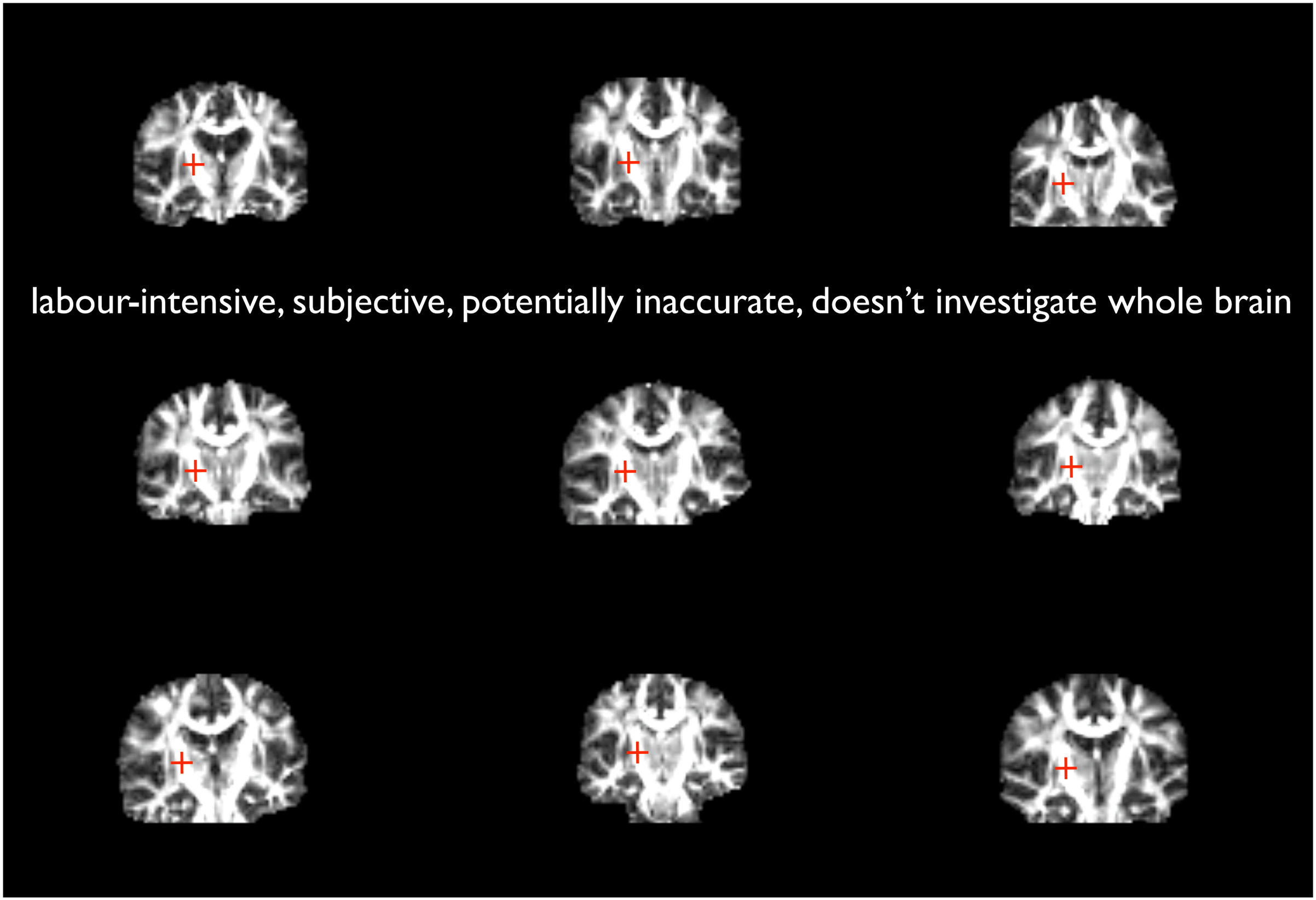
VBM-style Analysis of FA

- Strengths
  - Fully automated & quick
  - Investigates whole brain

- Problems [Bookstein 2001, Davatzikos 2004, Jones 2005]
  - Alignment difficult; smallest systematic shifts between groups can be incorrectly interpreted as FA change
  - Needs smoothing to help with registration problems
  - No objective way to choose smoothing extent

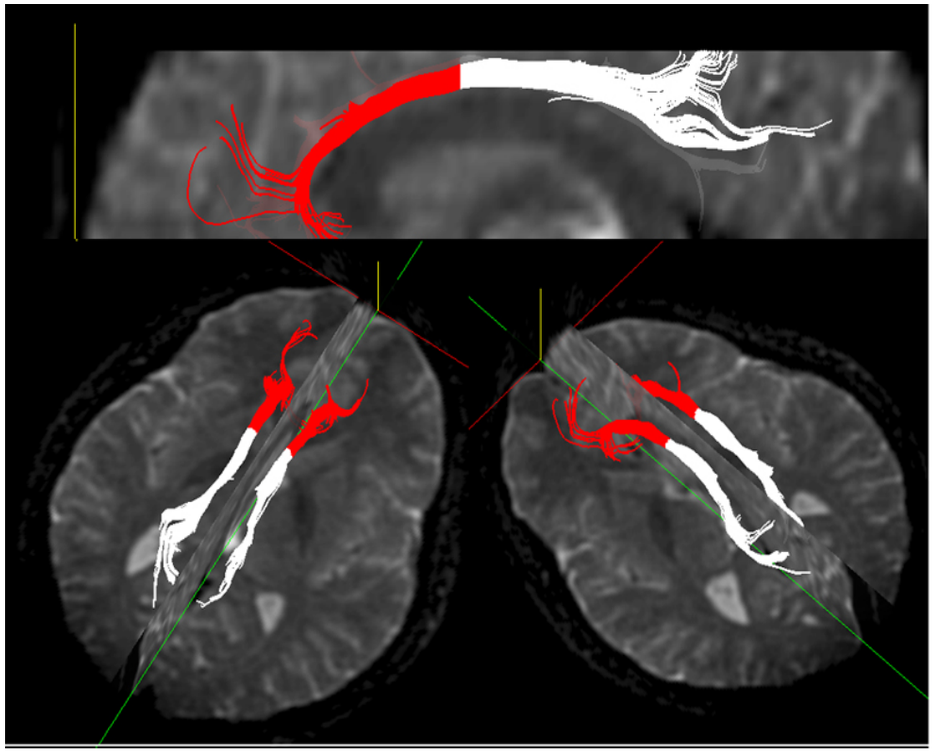




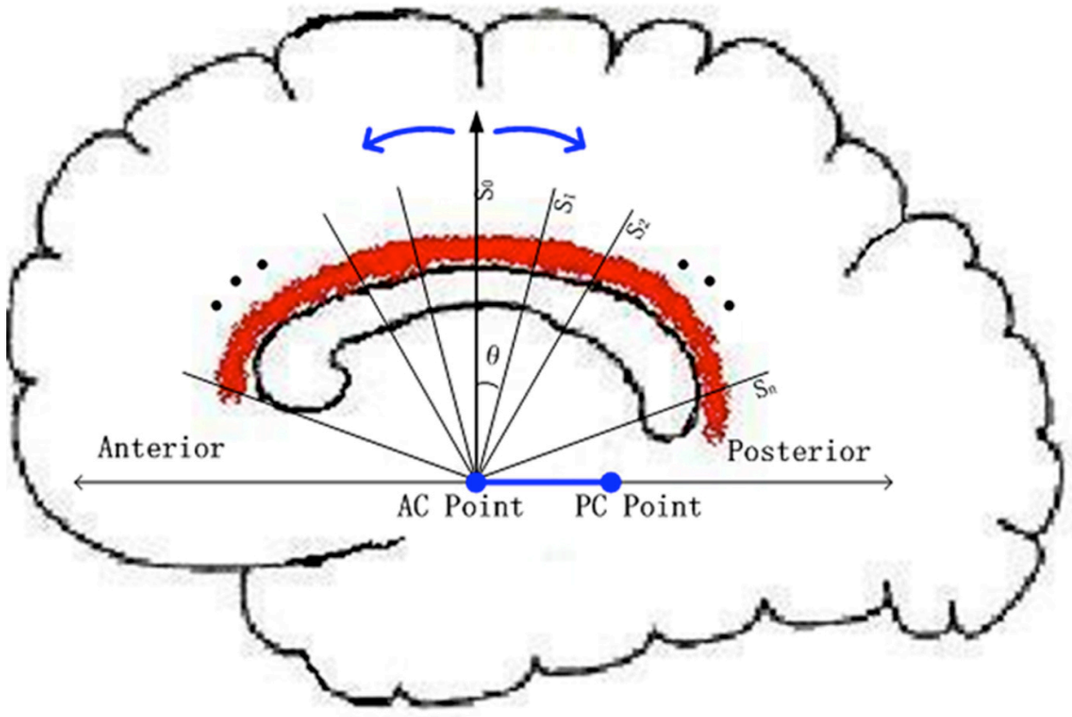
Hand-placed voxel/ROI-based FA Comparison



labour-intensive, subjective, potentially inaccurate, doesn't investigate whole brain

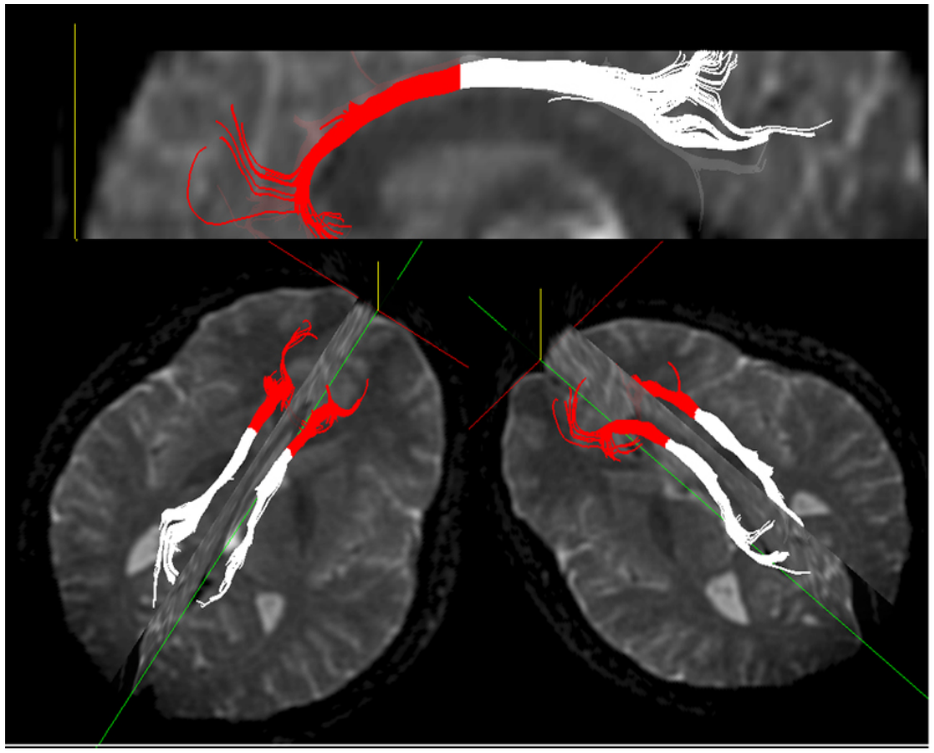
Tractography-Based FA Comparison

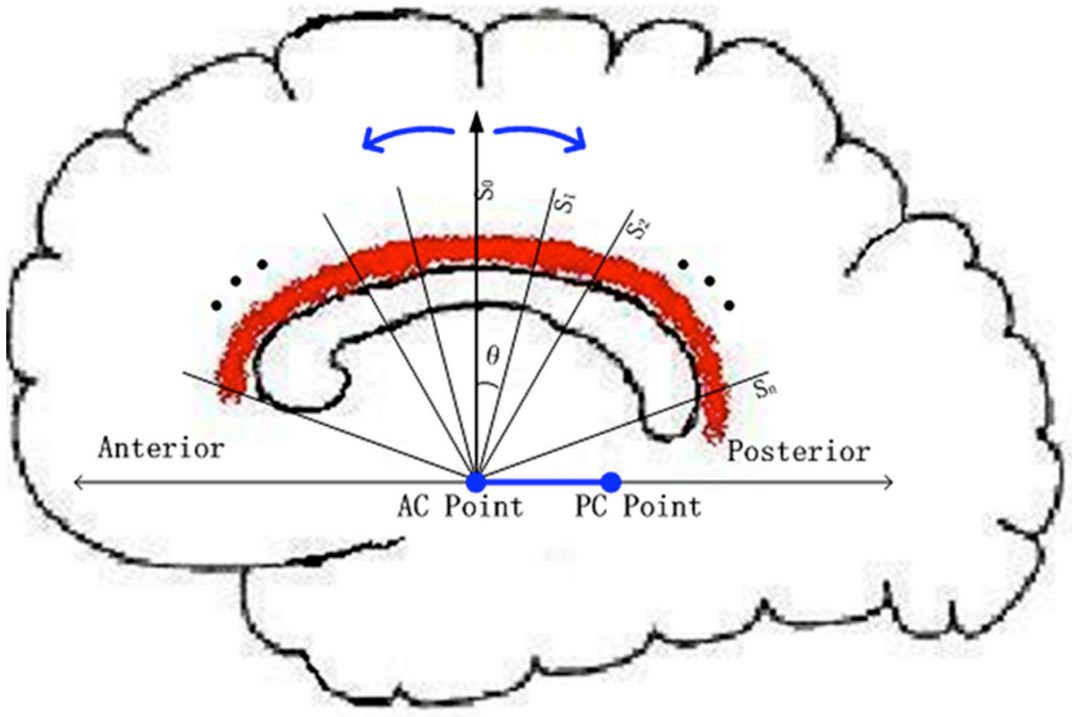




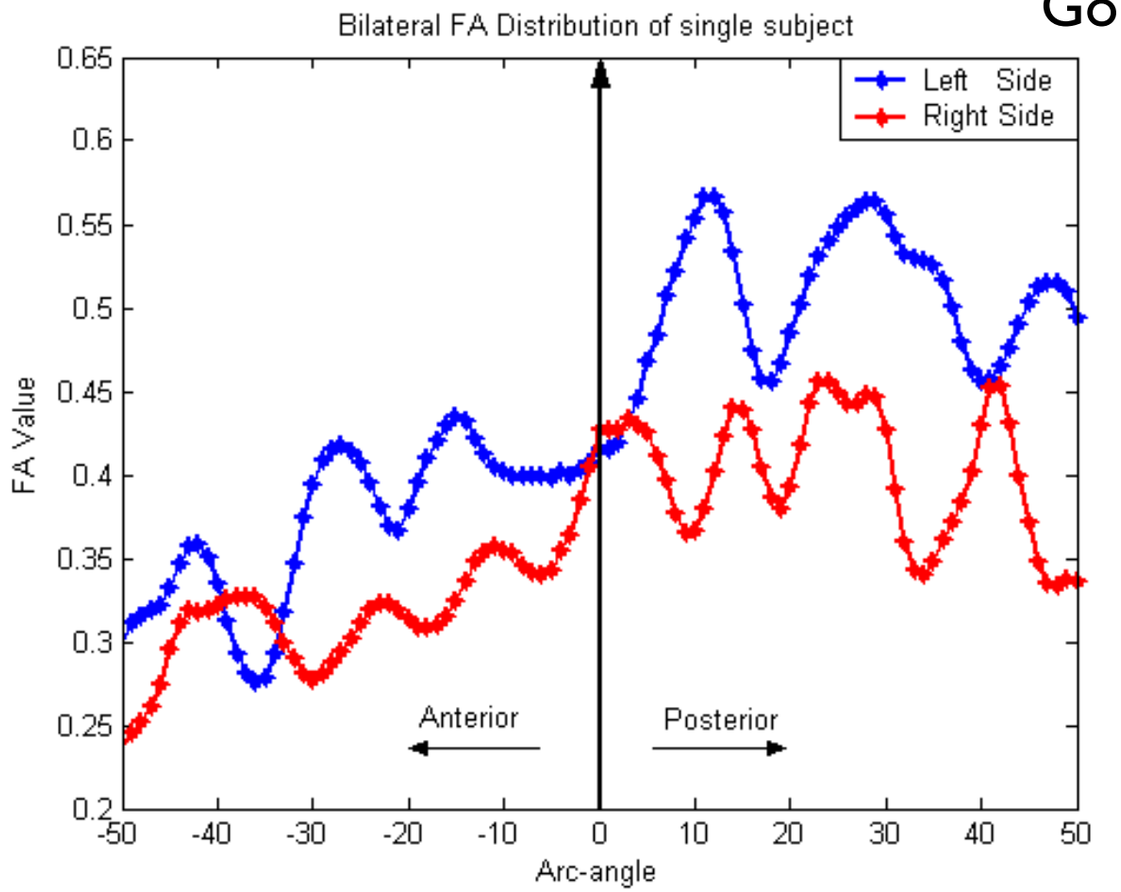
- Method [Gong 2005, Corouge 2006]
  - Define a given tract in all subjects
  - Parameterise FA along tract
  - Compare between subjects
- Strength: correspondence issue hopefully resolved
- Problems
  - Currently requires manual intervention to specify tract
  - Hence doesn't investigate whole brain
  - Projection of FA onto tract needs careful thought

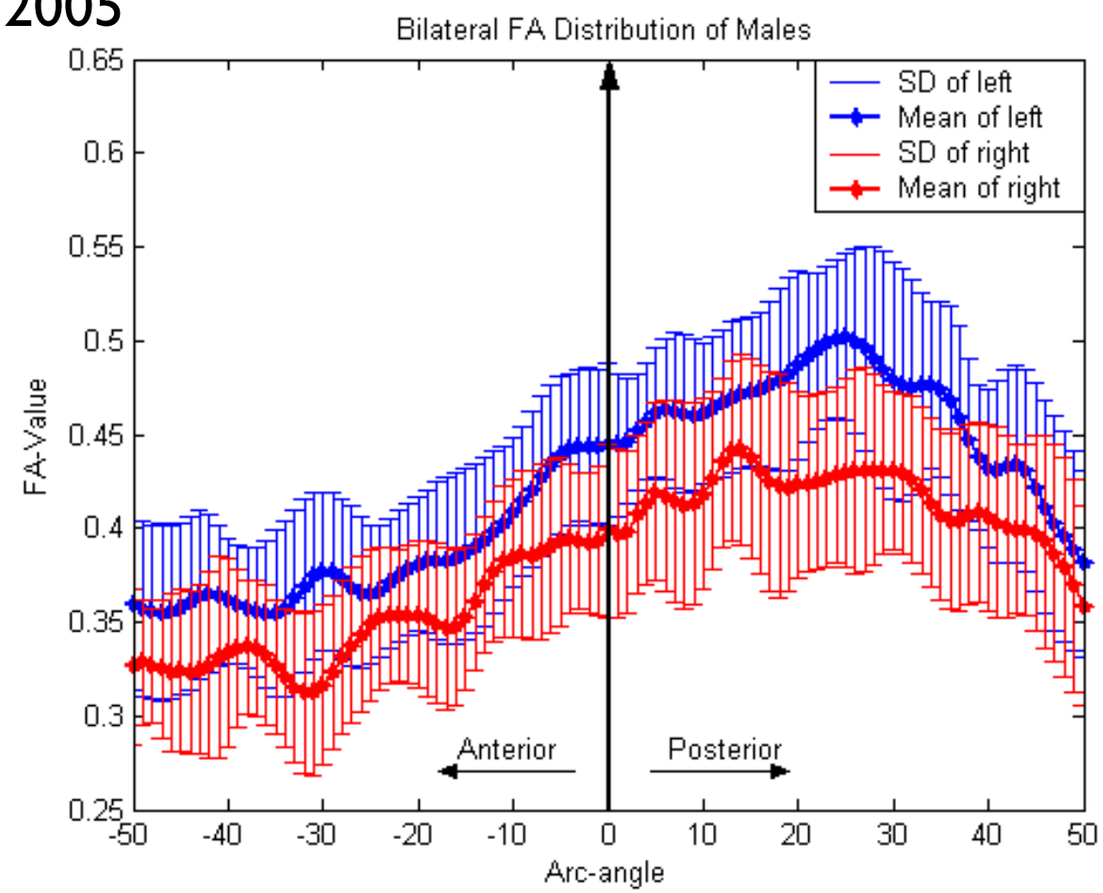
Tractography-Based FA Comparison



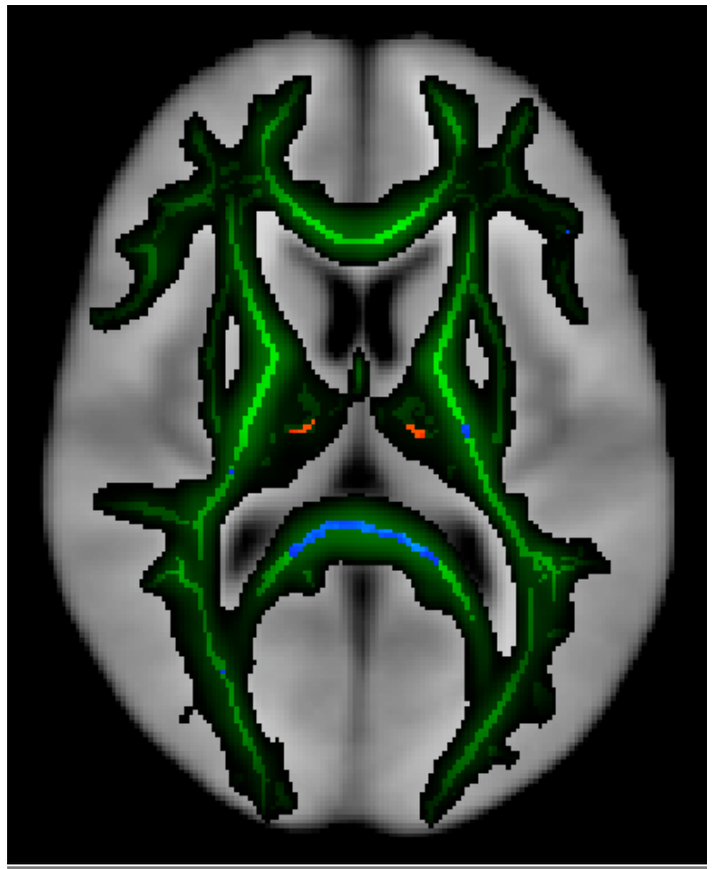


Gong 2005





TBSS : Tract-Based Spatial Statisics



- Need: robust “voxelwise” cross-subject stats on DTI
- Problem: alignment issues confound valid local stats
- TBSS: solve alignment using alignment-invariant features:
- Compare FA taken from tract centres (via skeletonisation)

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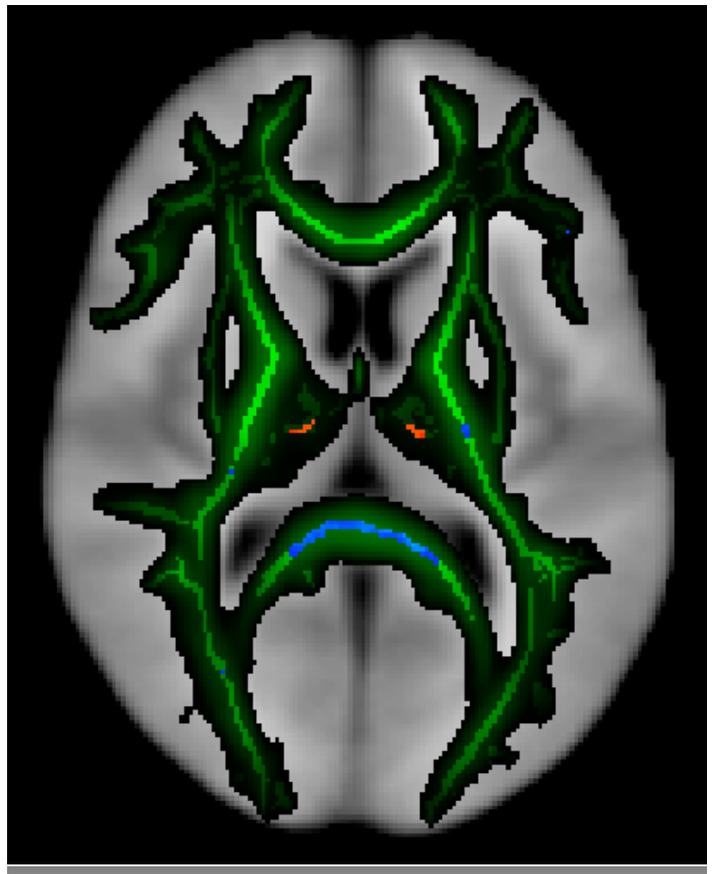

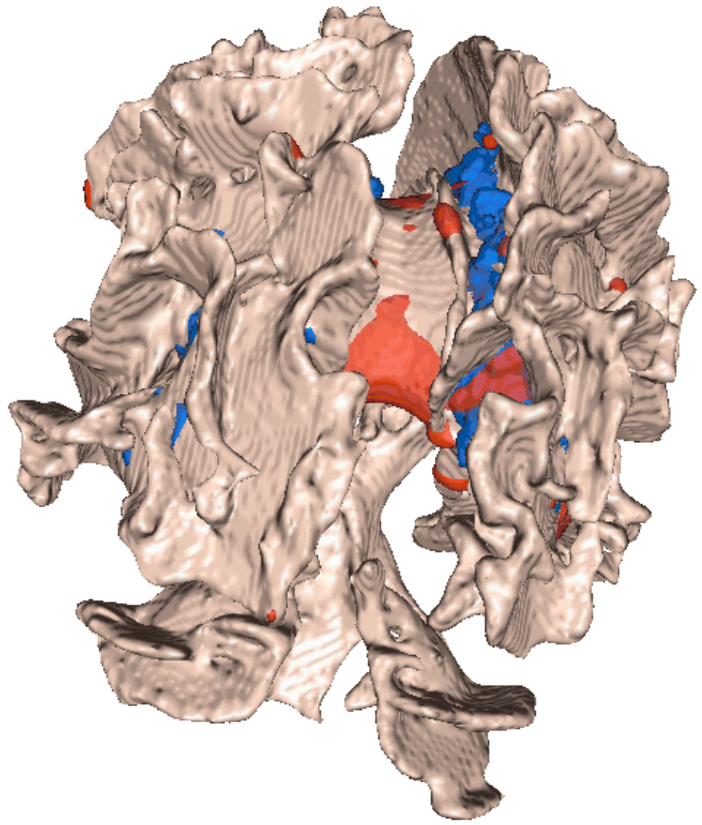

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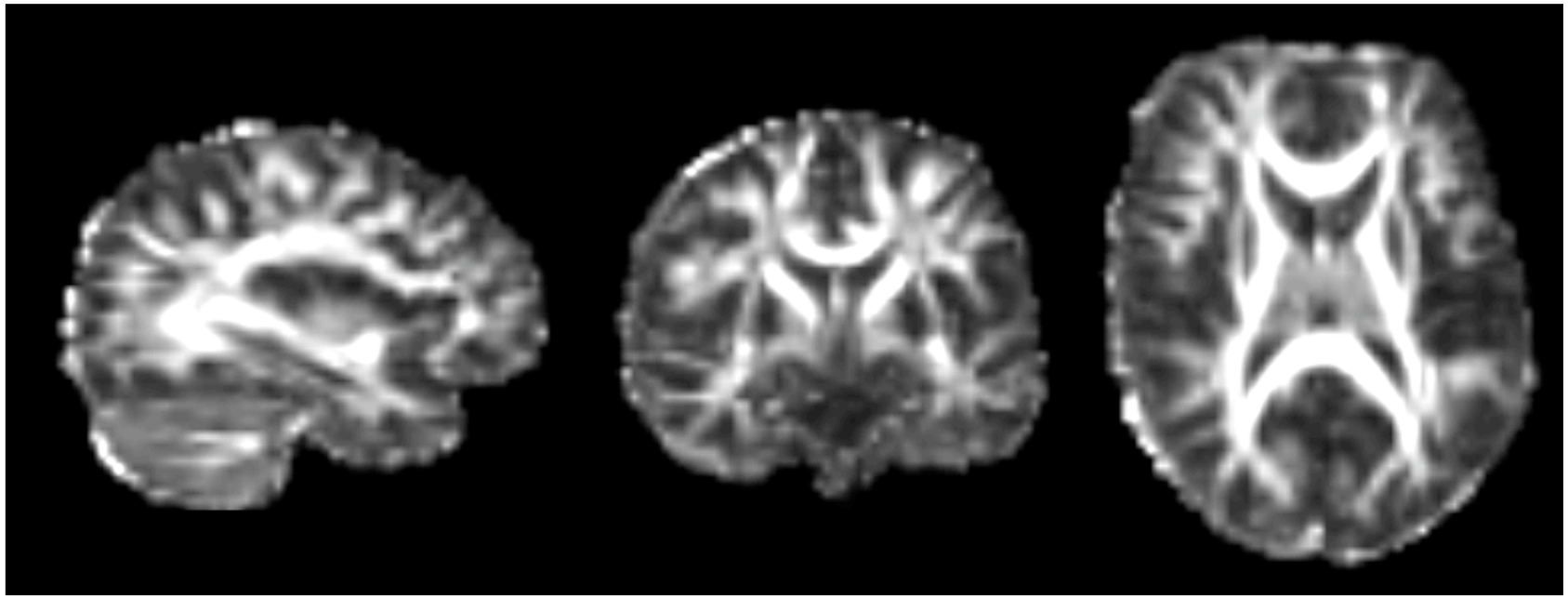
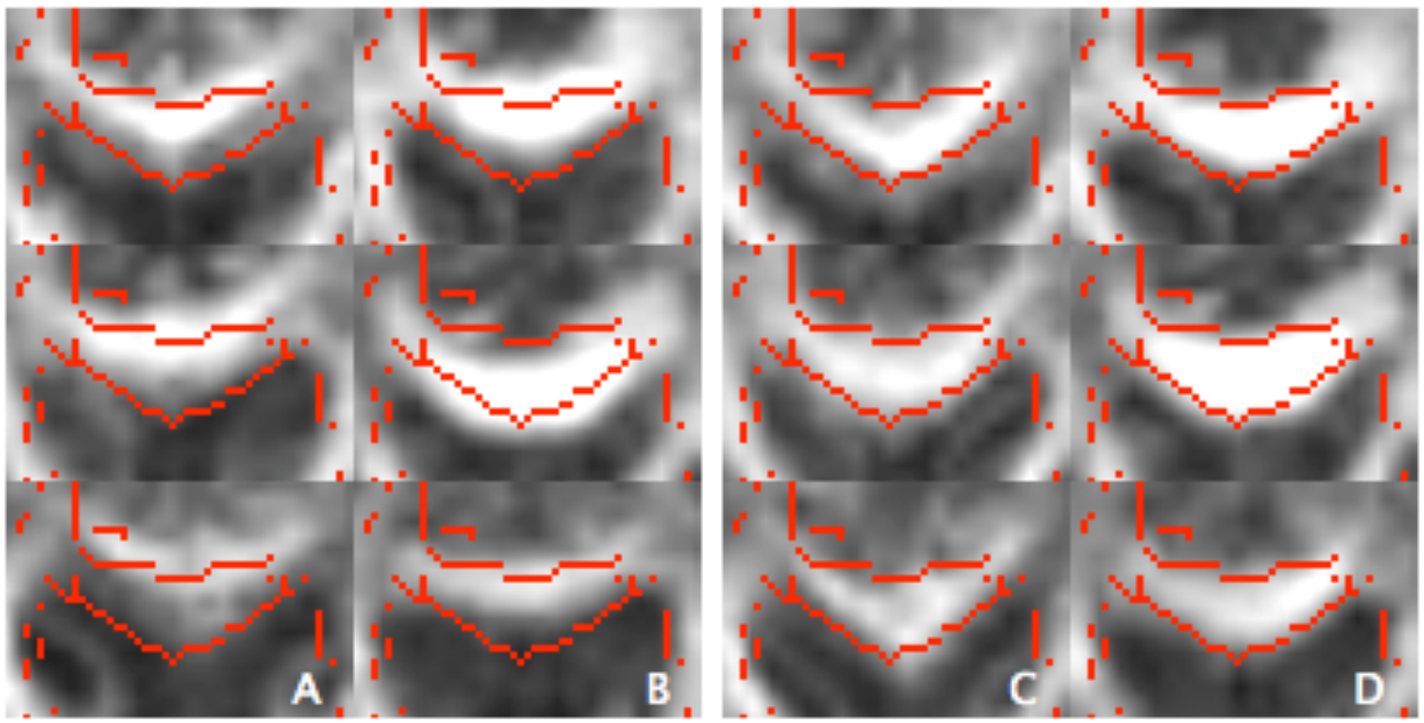
1. Use medium-DoF nonlinear reg to pre-align all subjects' FA

(nonlinear reg: FNIRT)





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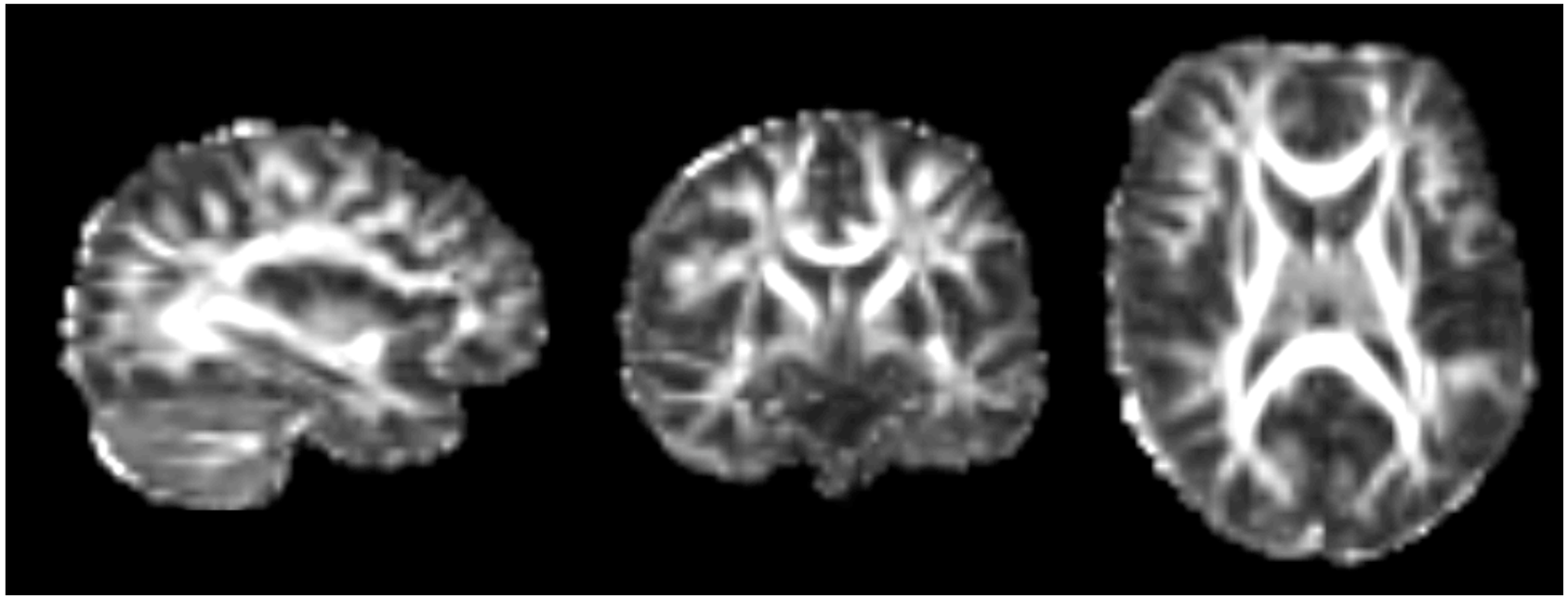
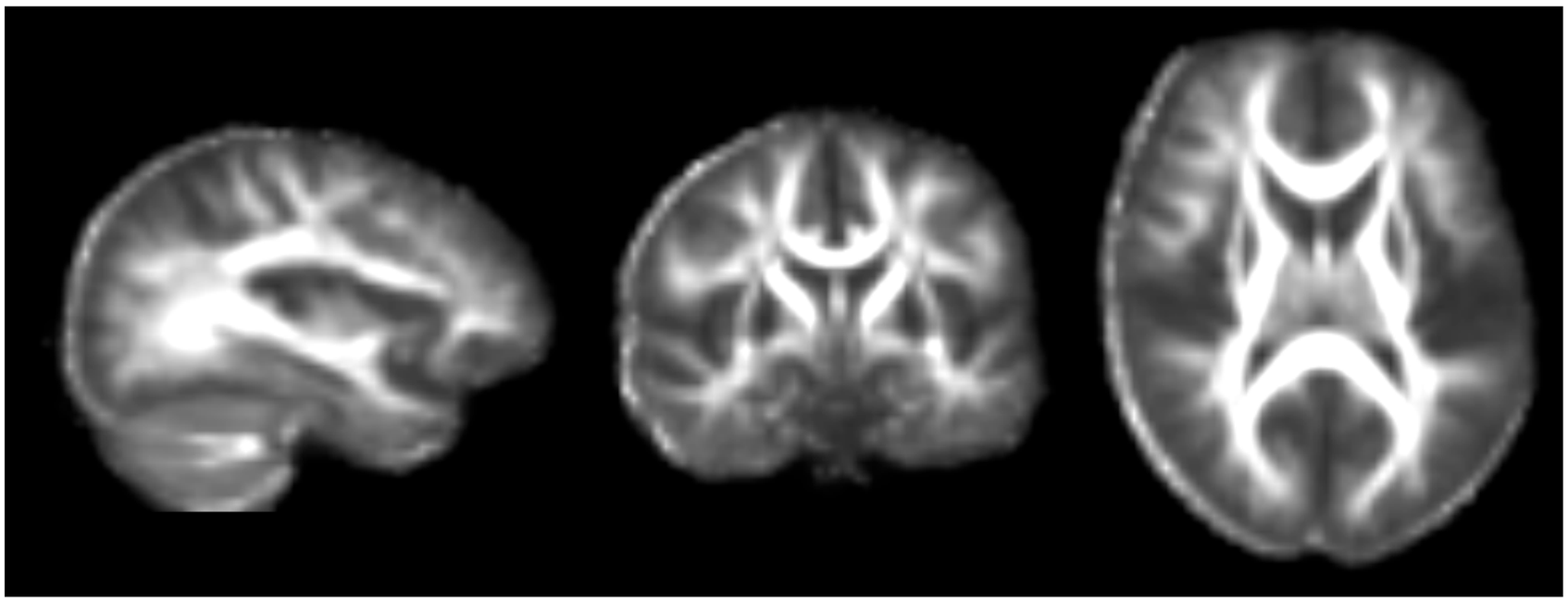
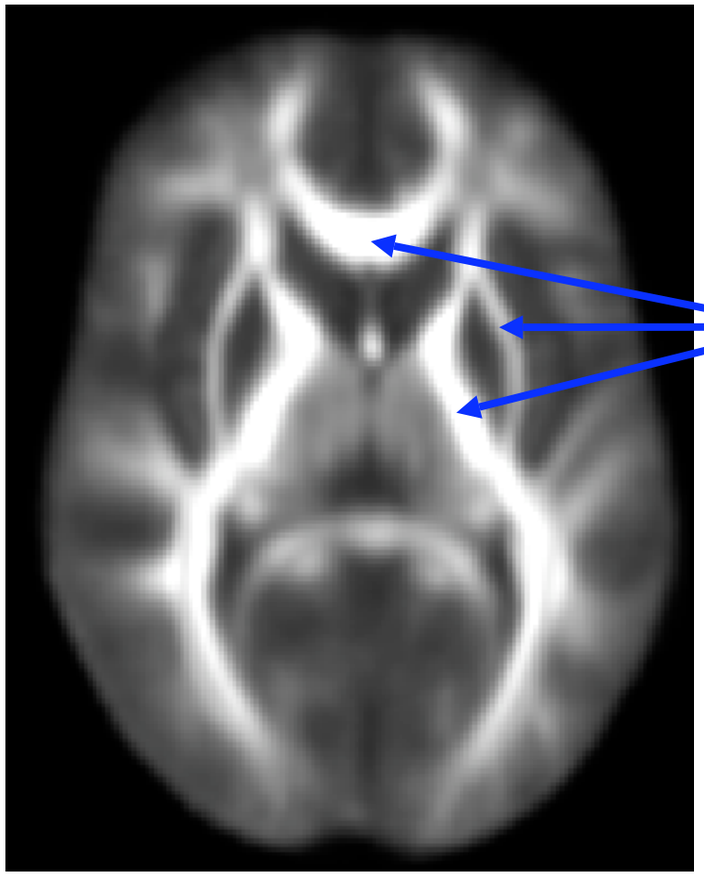
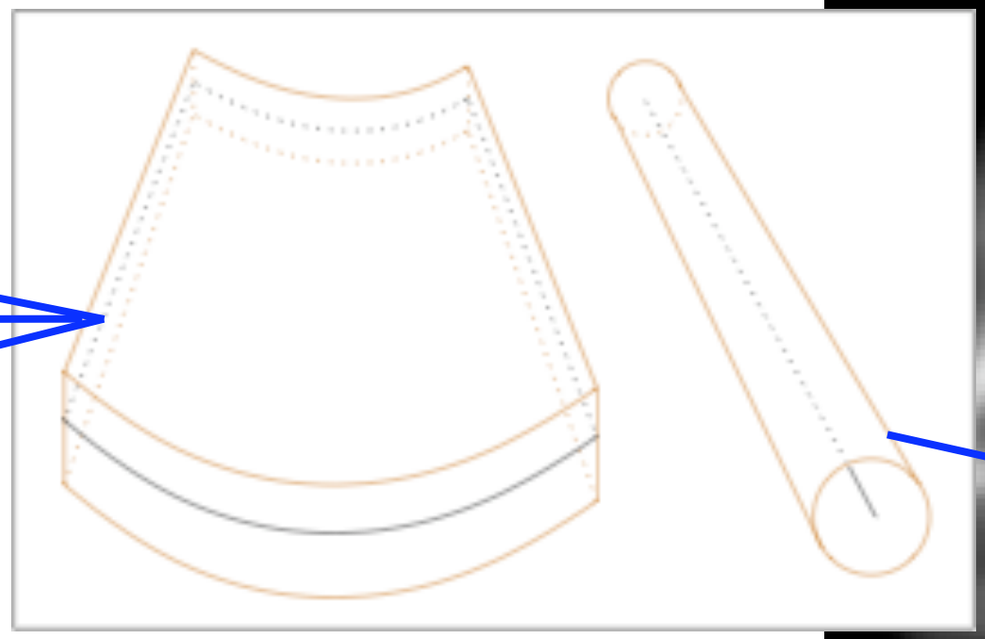


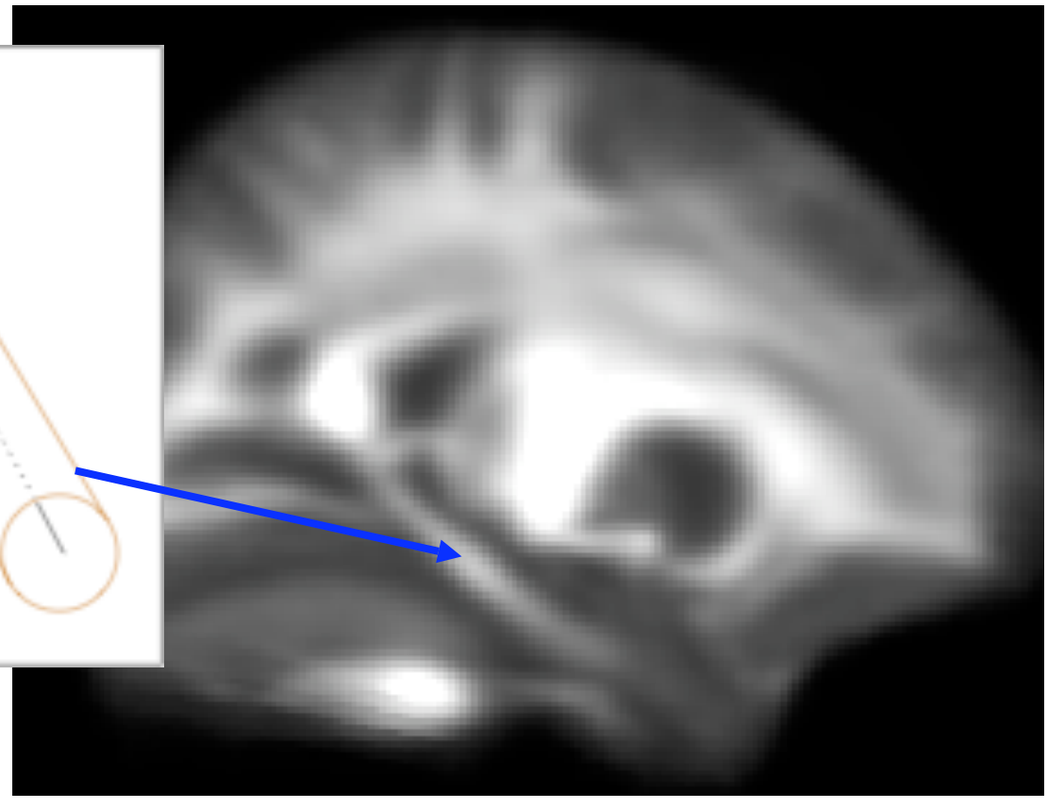
2. Create mean FA image (no smoothing)



2. “Skeletonise” Mean FA







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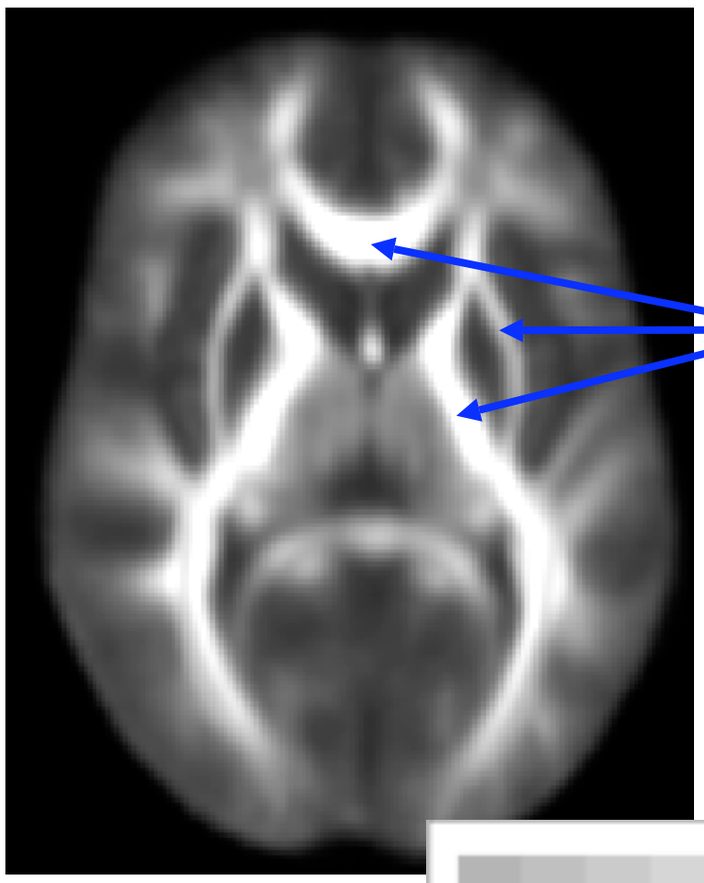
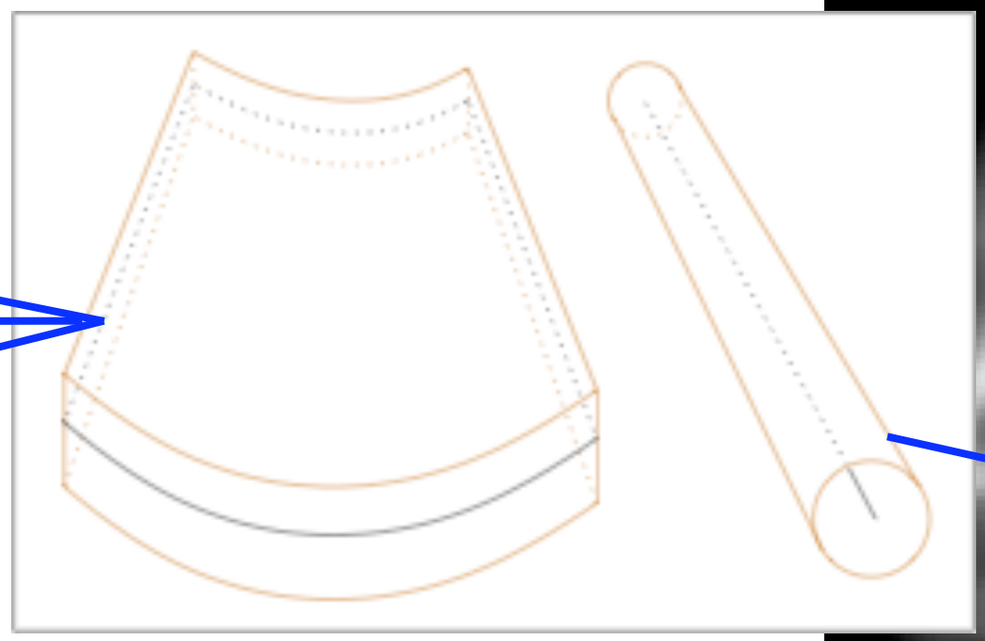
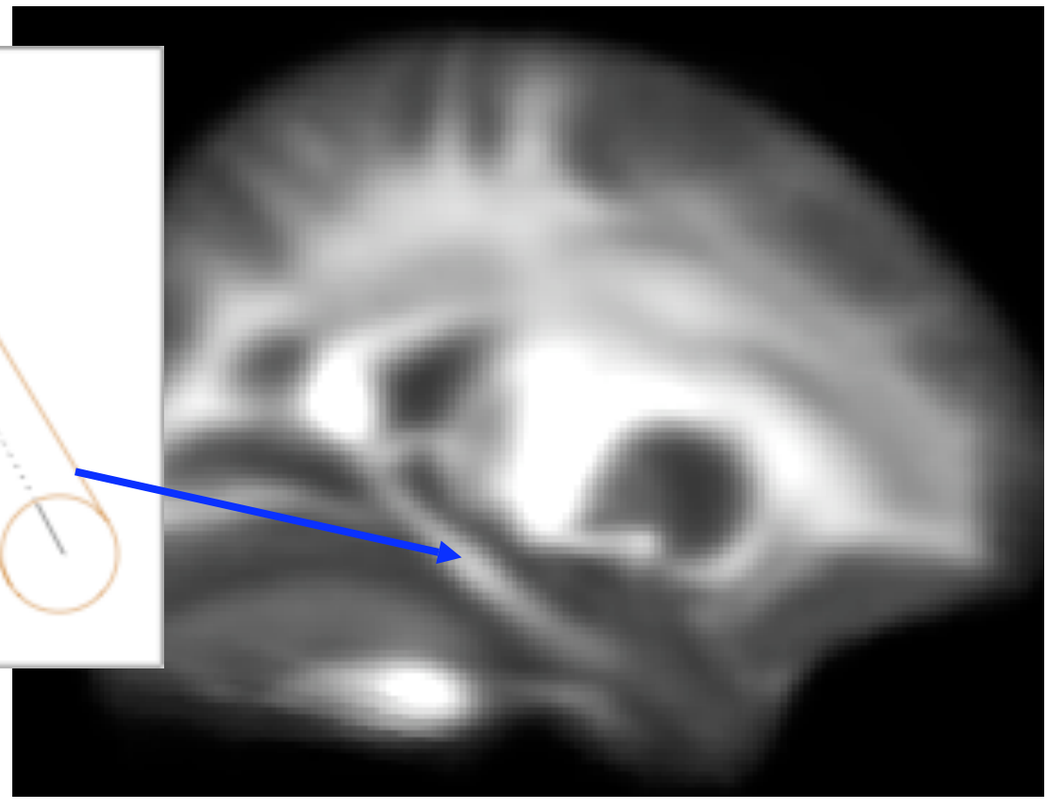
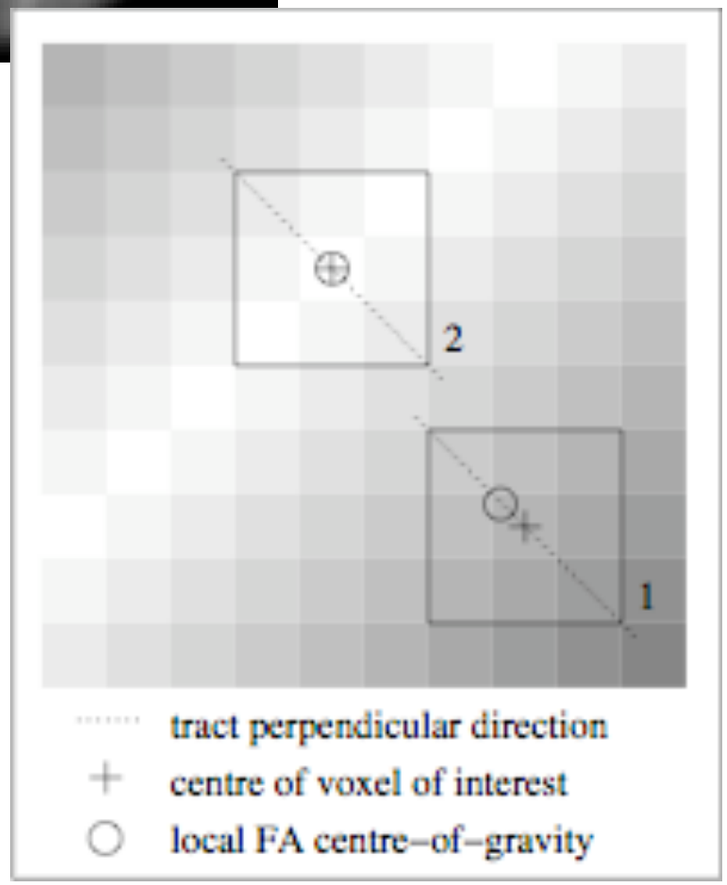


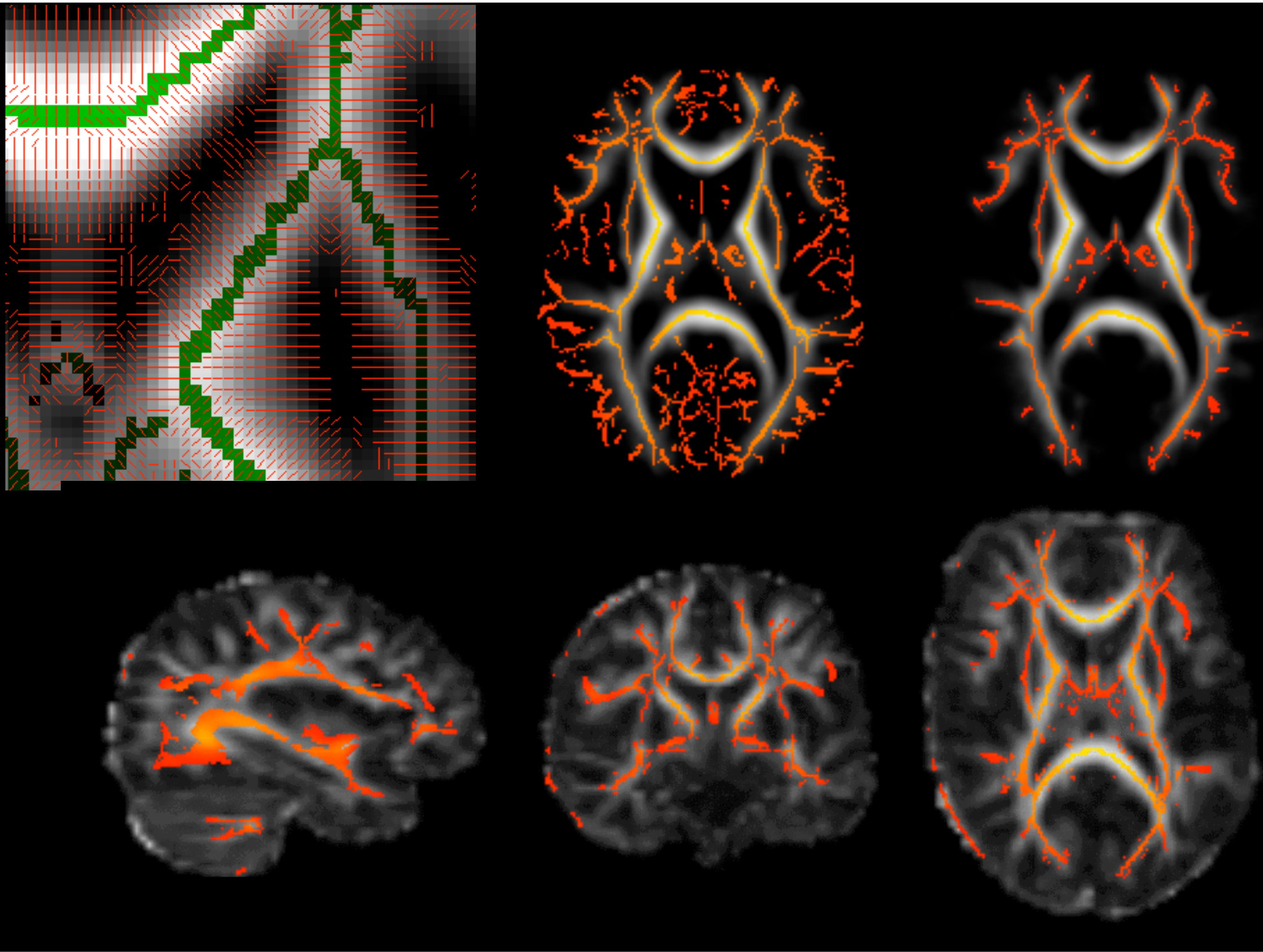






3. Threshold Mean FA Skeleton

giving "objective" tract map



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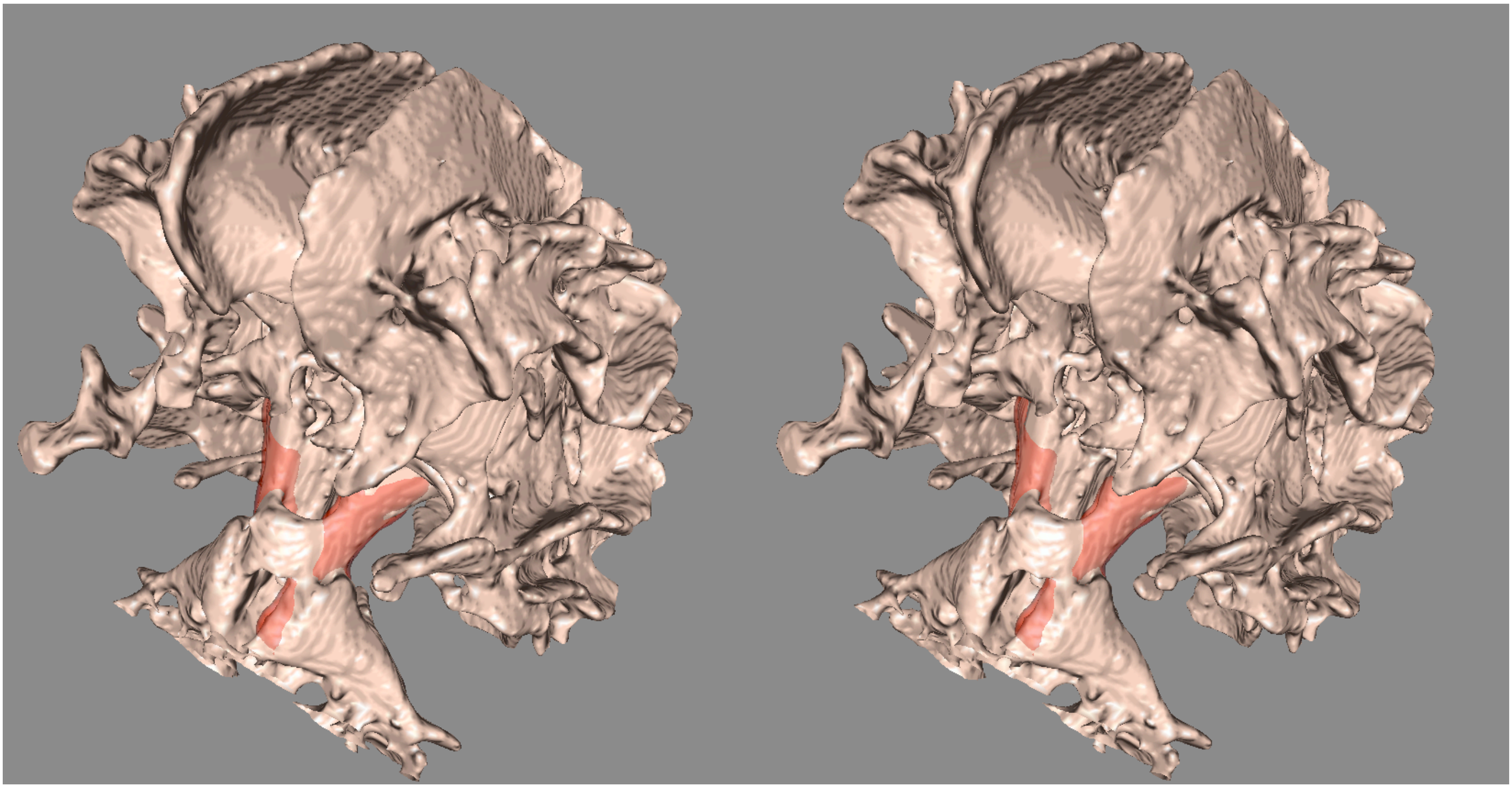

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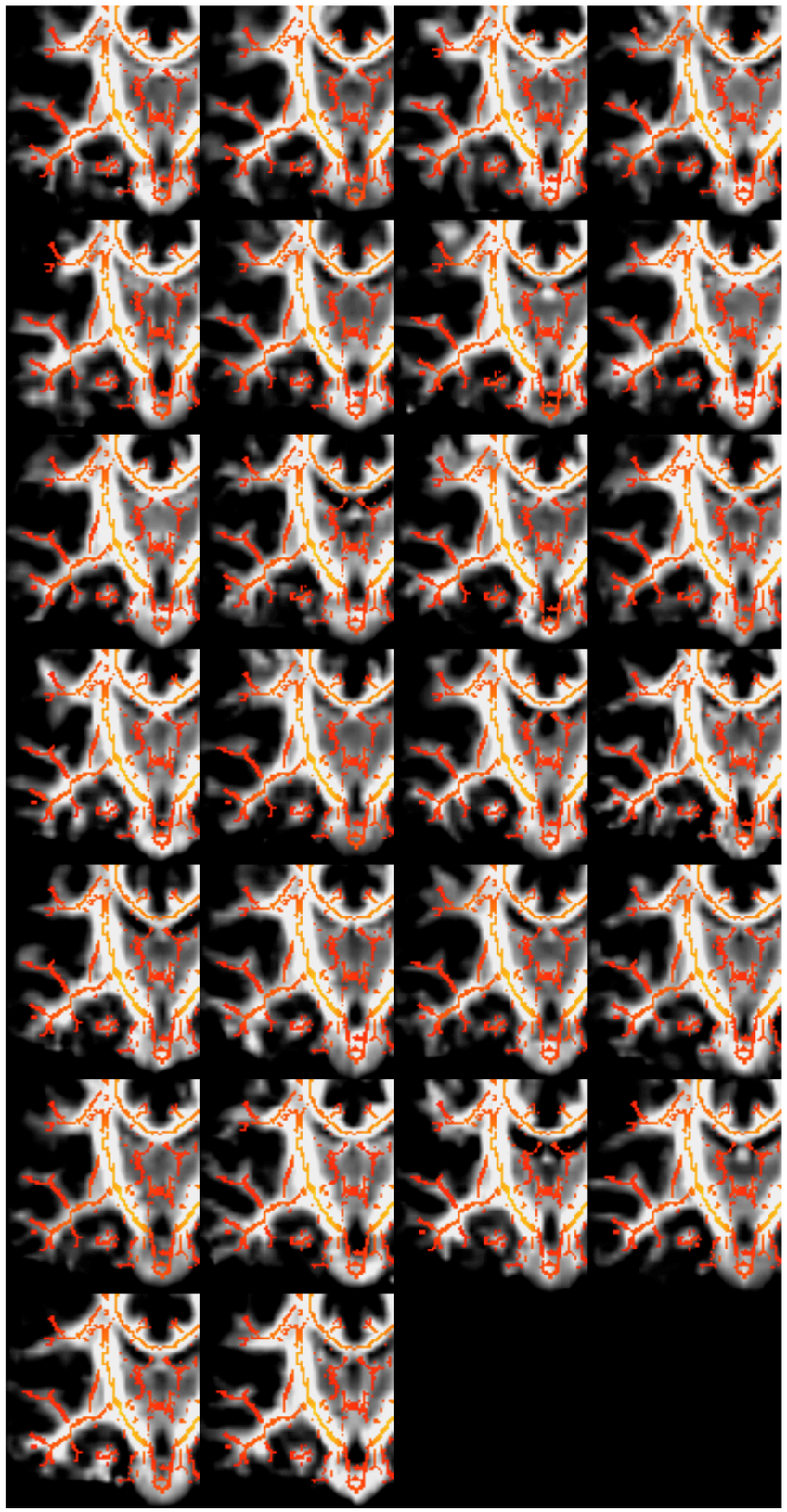
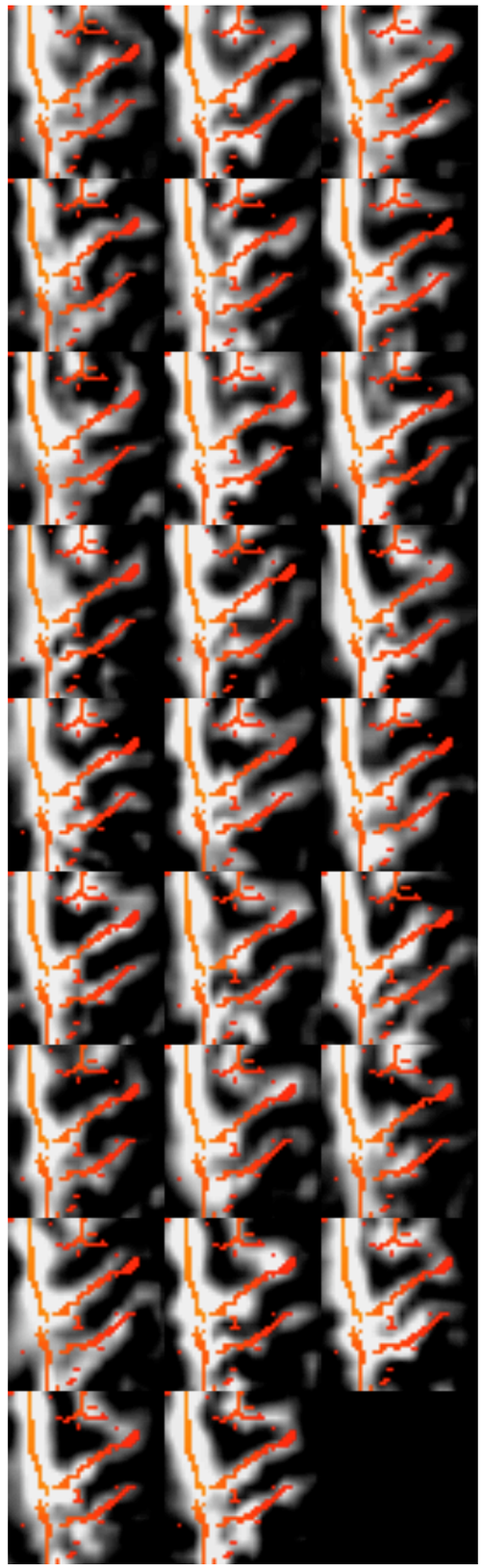
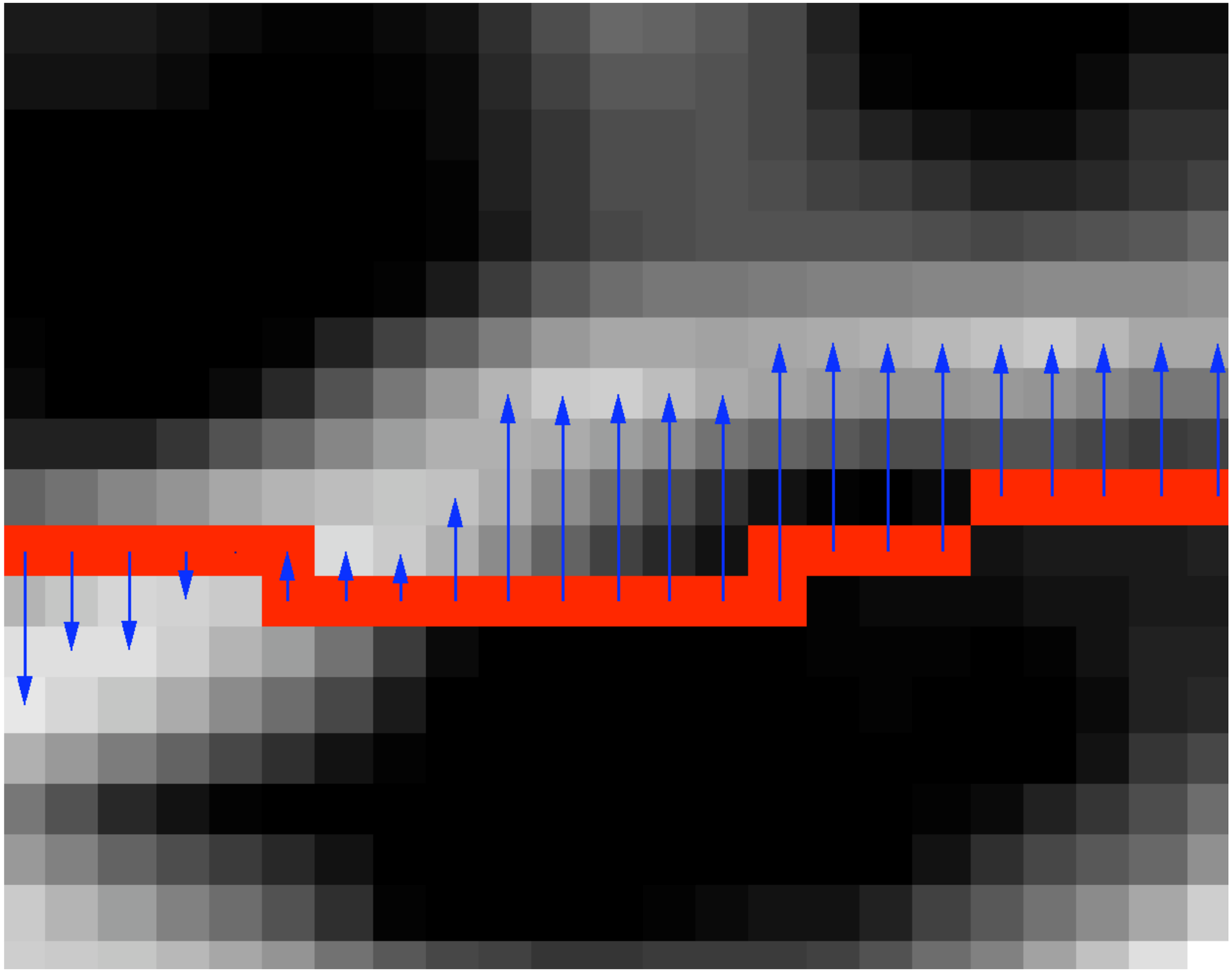




4. For each subject's warped FA, fill each point on the mean-space skeleton with nearest maximum FA value (i.e., from the centre of the subject's nearby tract)



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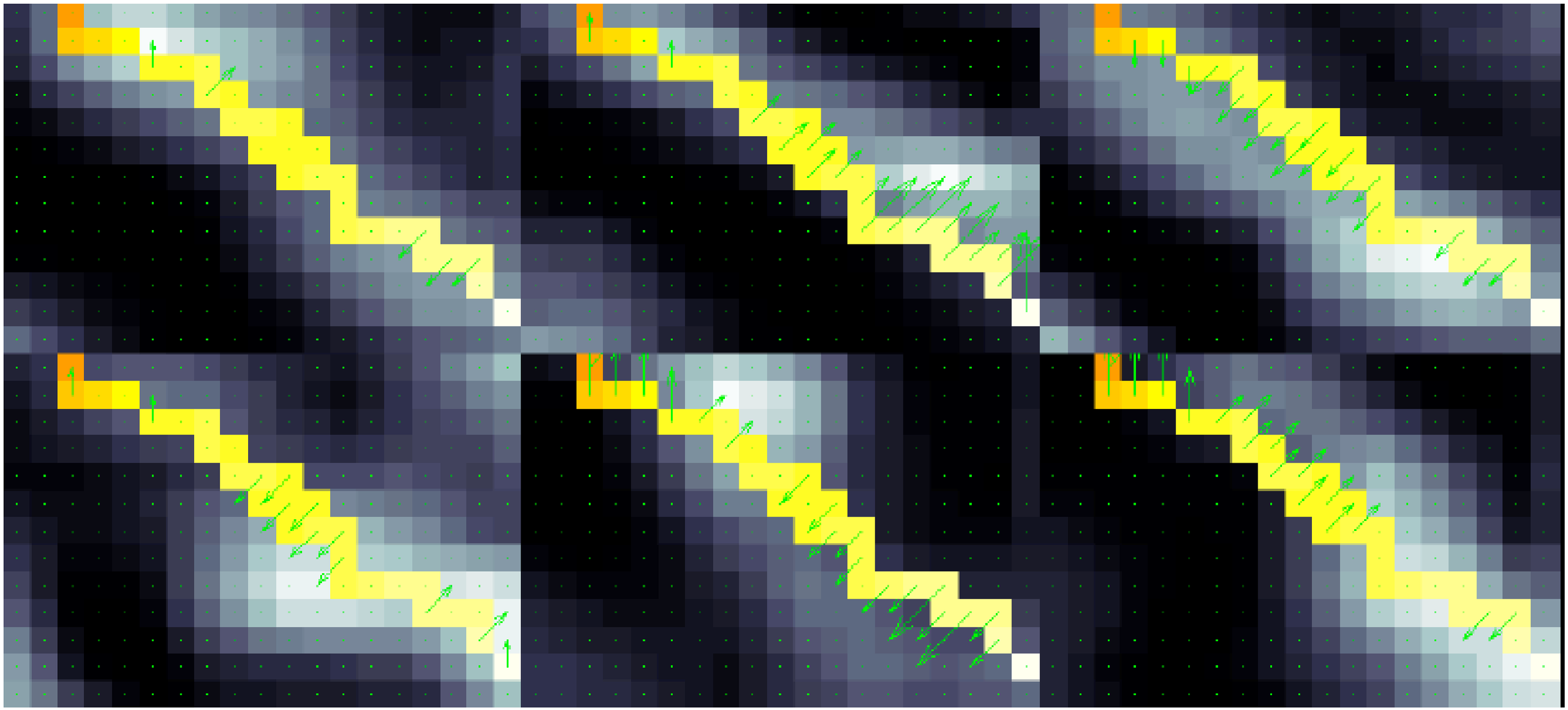


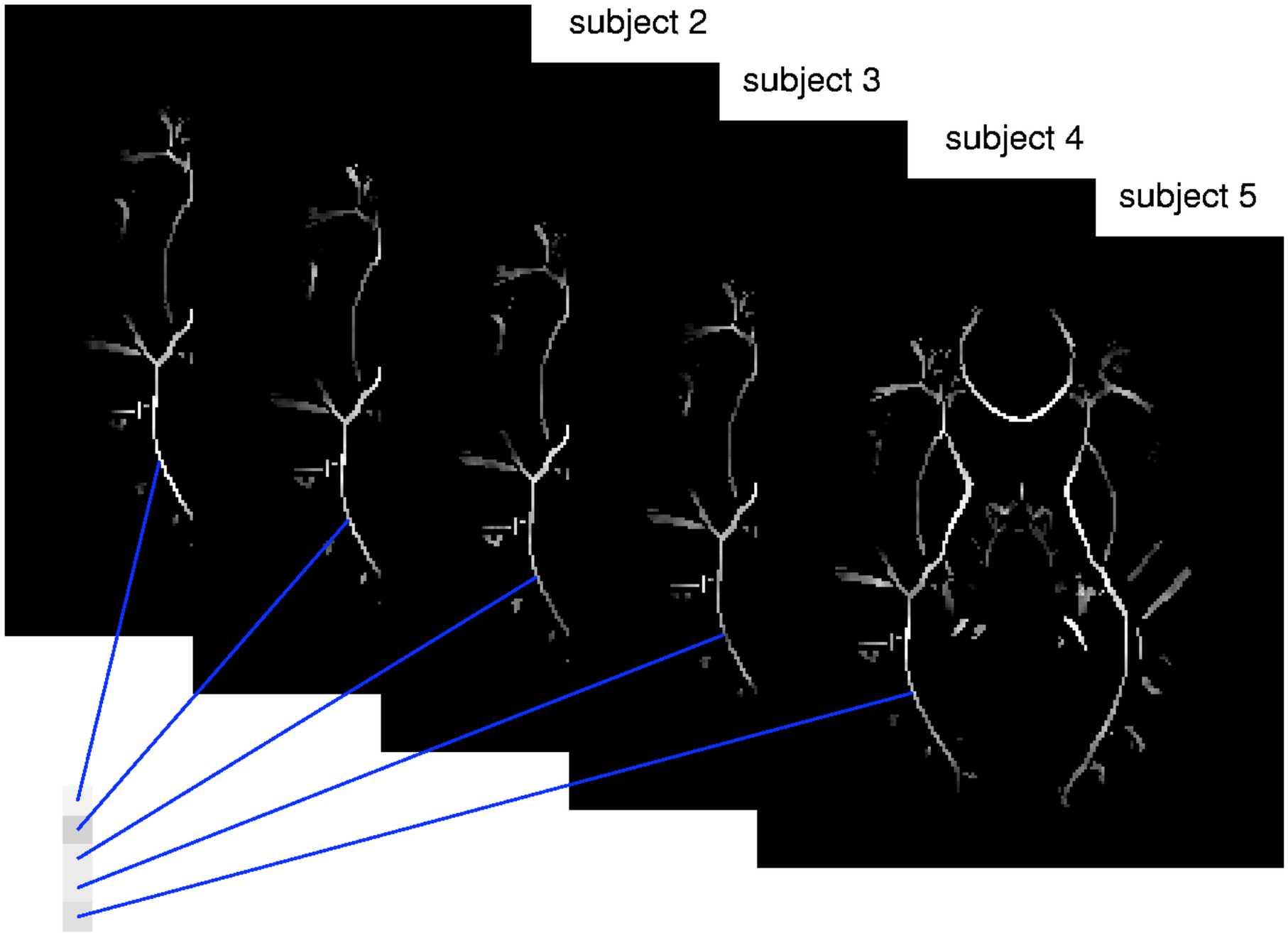
subject 1

subject 2

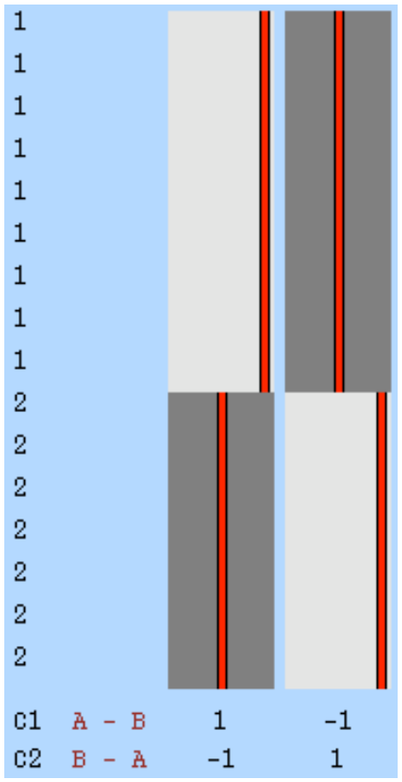
subject 3

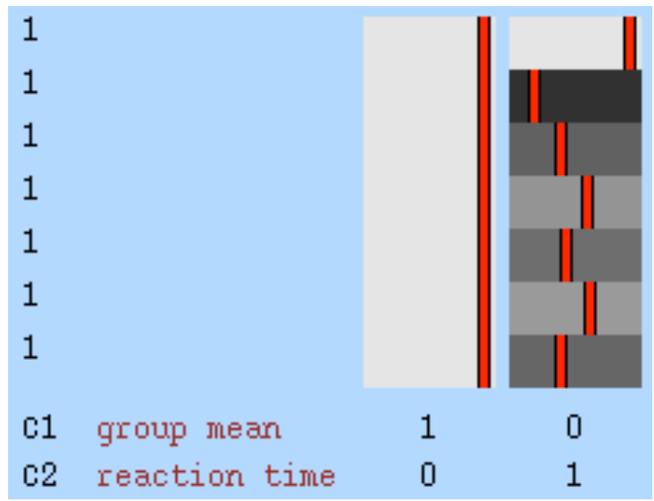
subject 4

subject 5

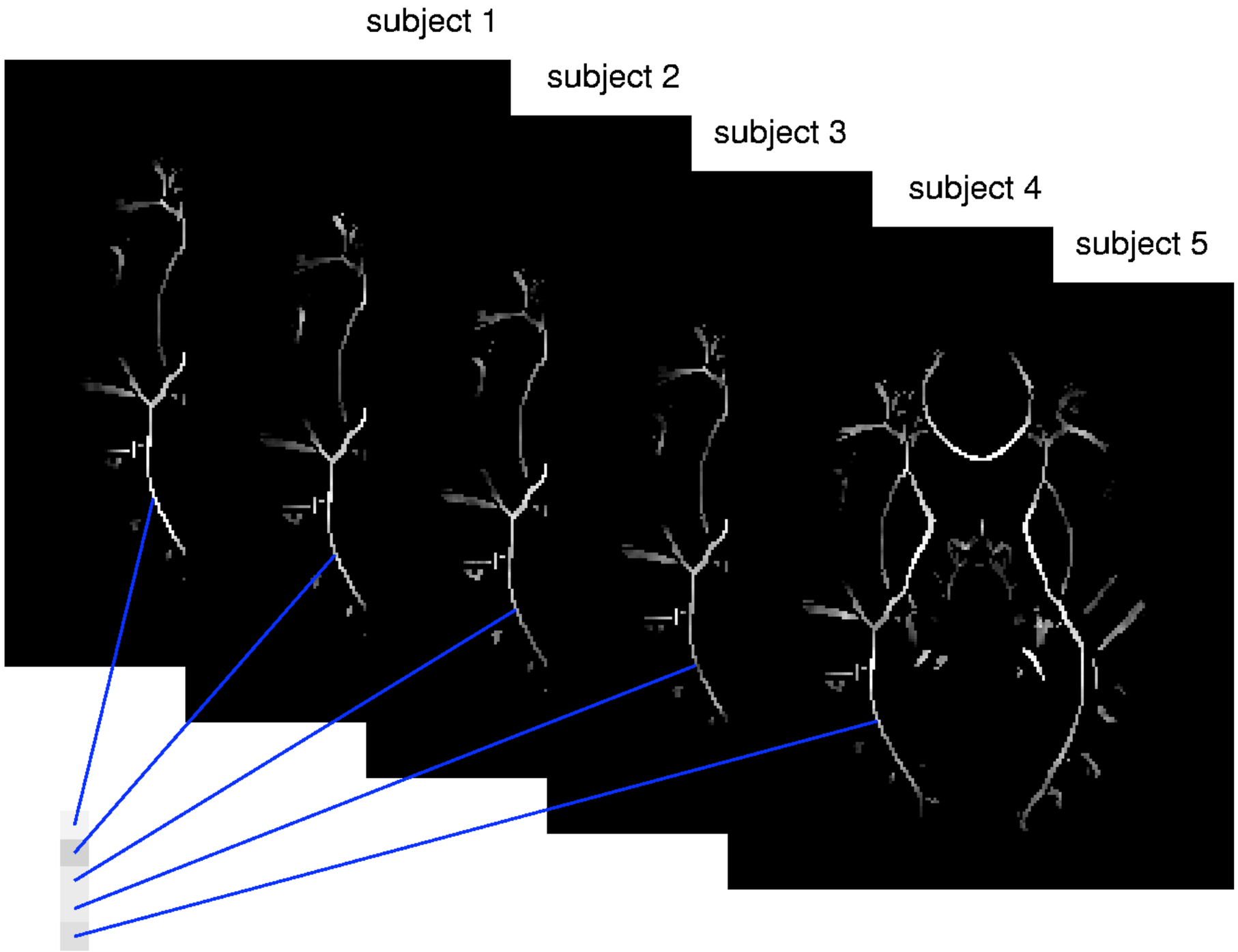


one skeleton voxel's data vector (to be fed into GLM)





5. Do cross-subject voxelwise stats on skeleton-projected FA



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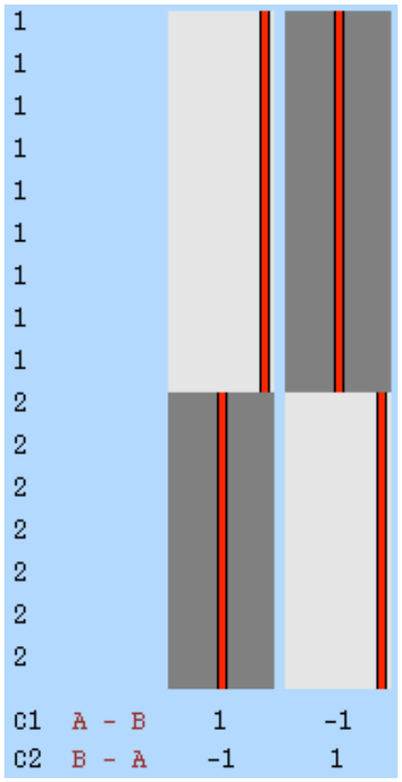
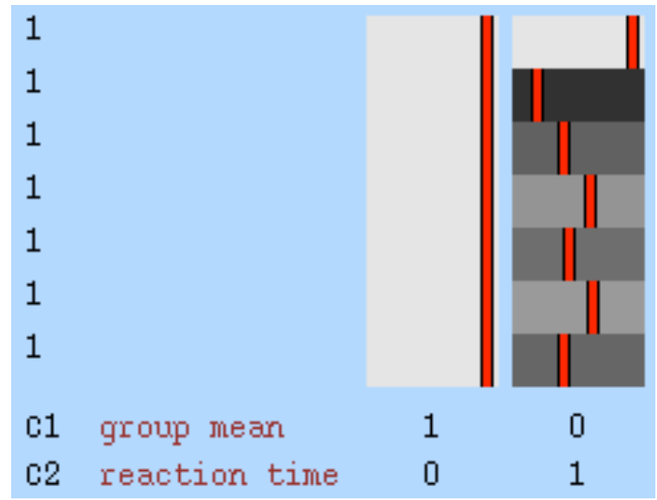
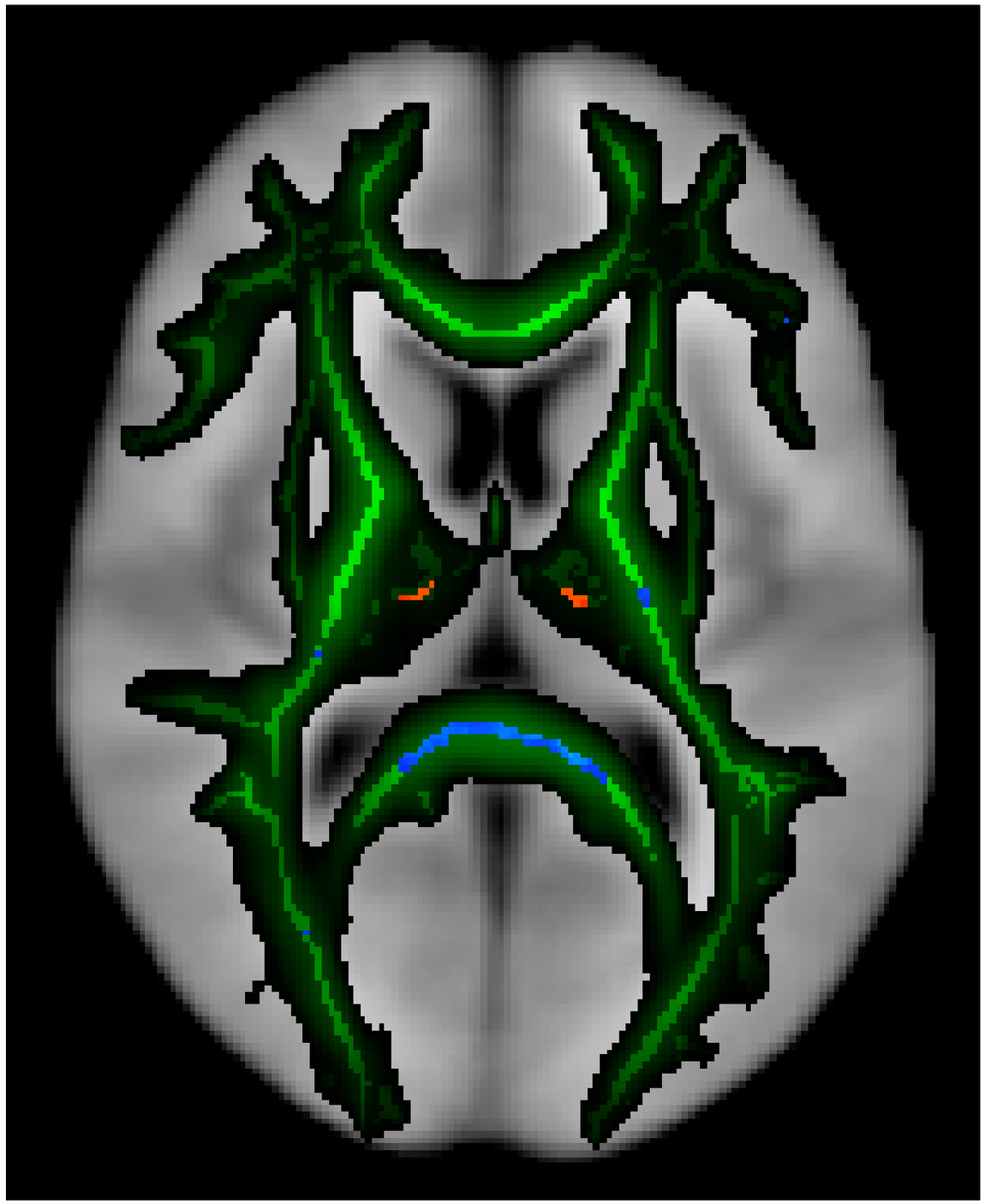
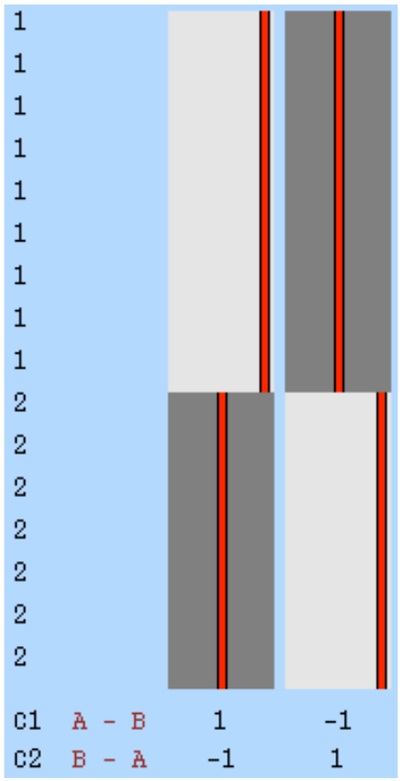
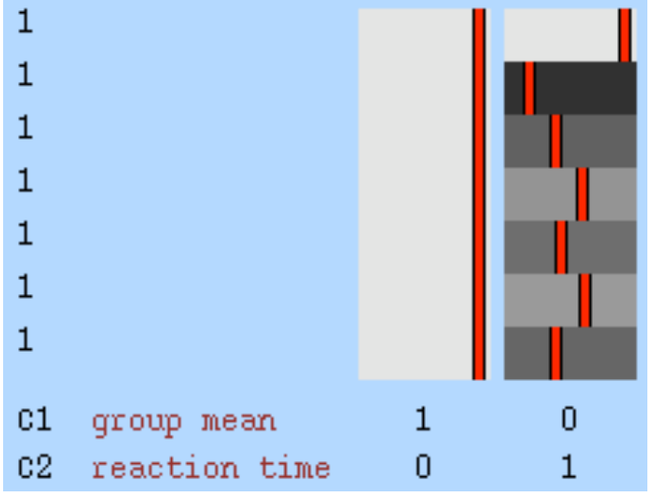




5. Do cross-subject voxelwise stats on skeleton-projected FA
6. Threshold, (e.g., permutation testing, including multiple comparison correction)

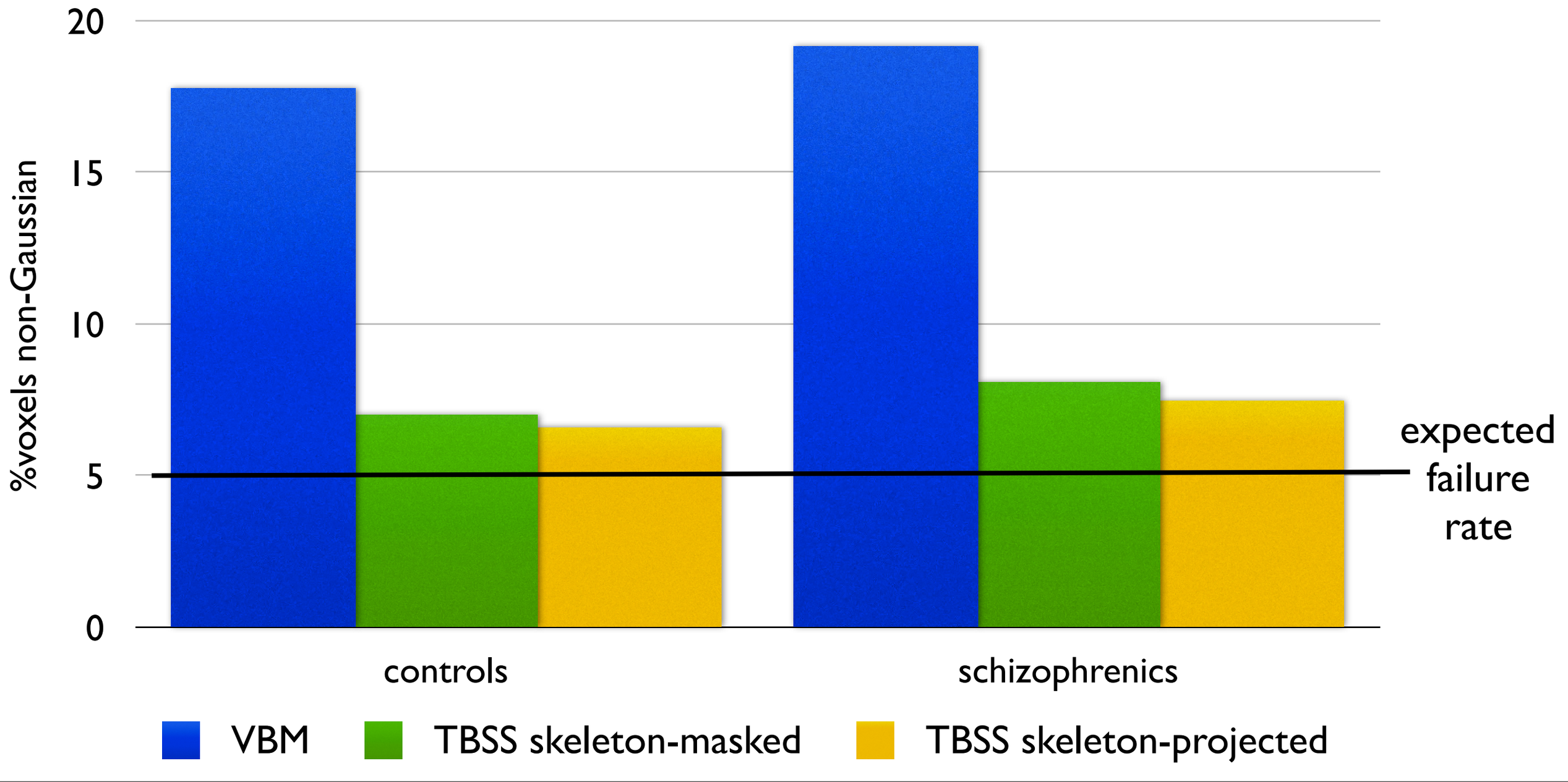






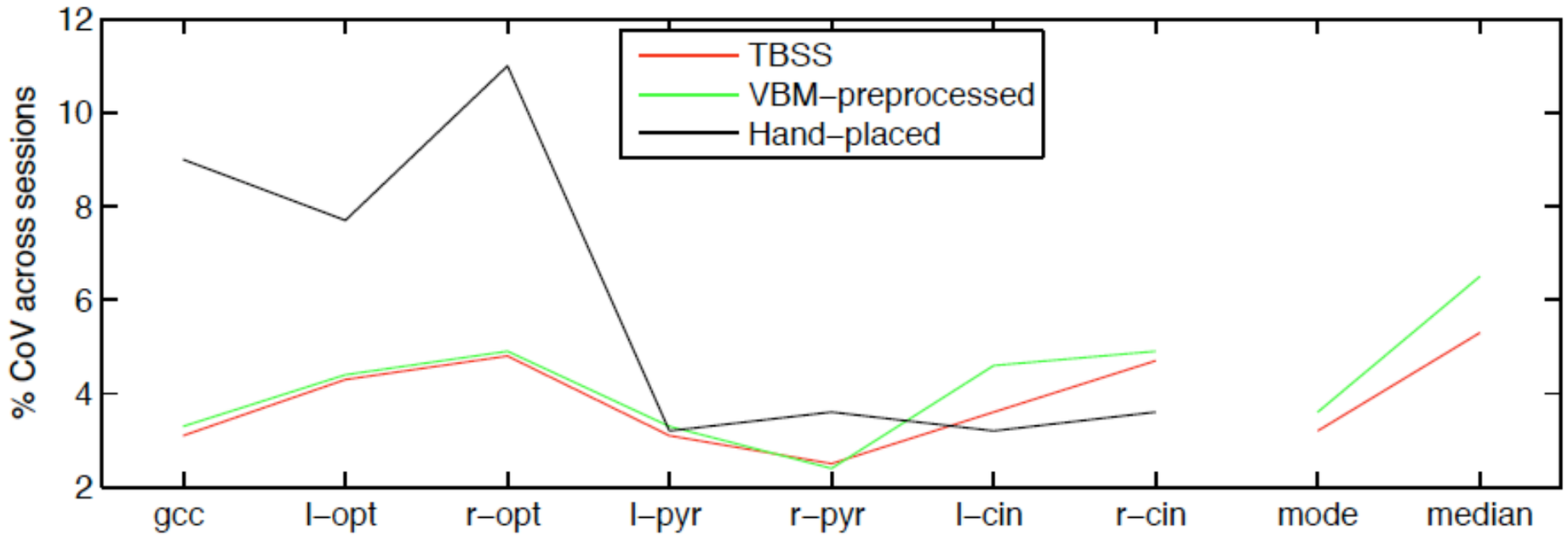
Testing for Gaussianity

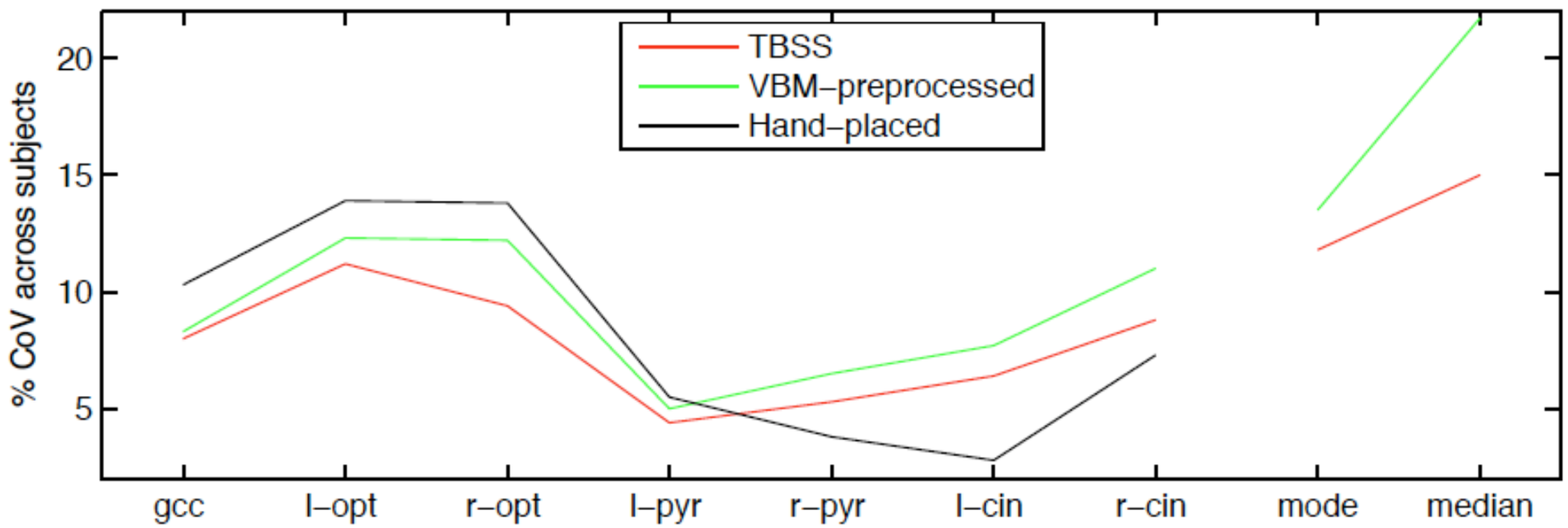
- 36 controls & 33 schizophrenics (Mackay)
- Test each voxel across subjects for Gaussianity using Lilliefors at 5%
- No smoothing with any preprocessing method



Repeatability Tests

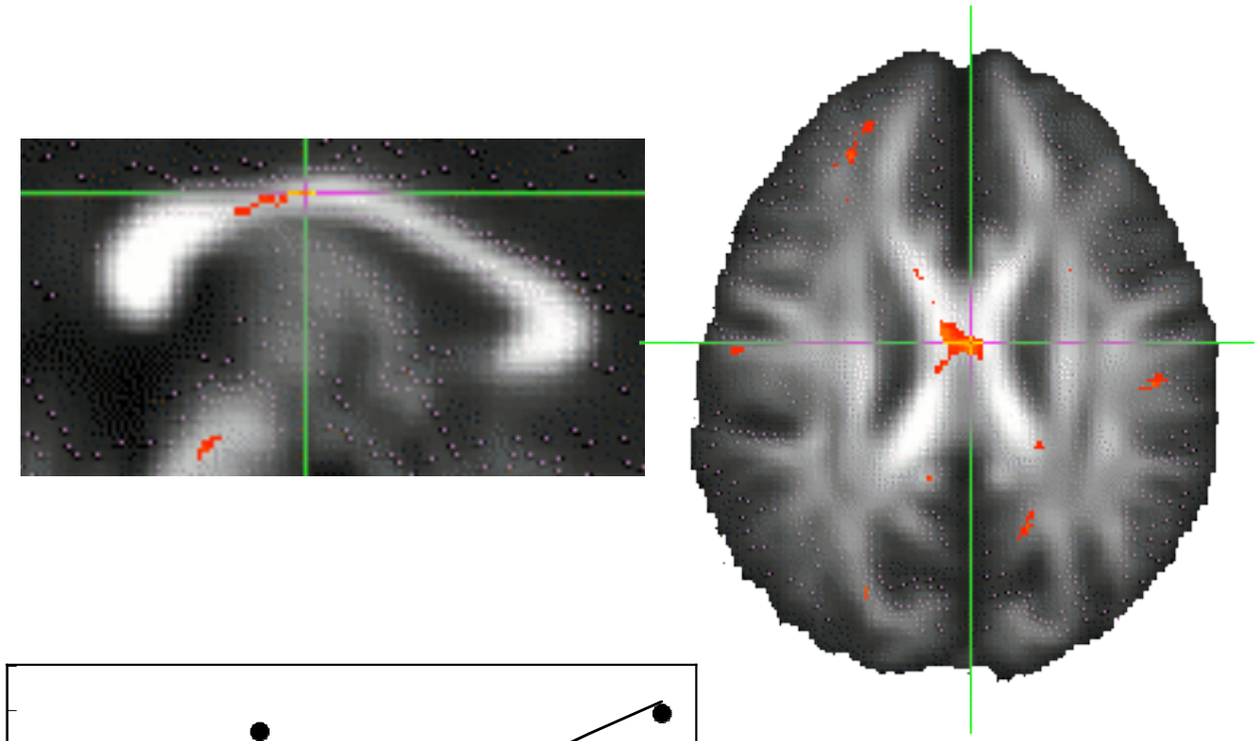
- 8 controls scanned twice each
- Measure %CoV across sessions & subjects
- Test hand-placed points and global mode & median

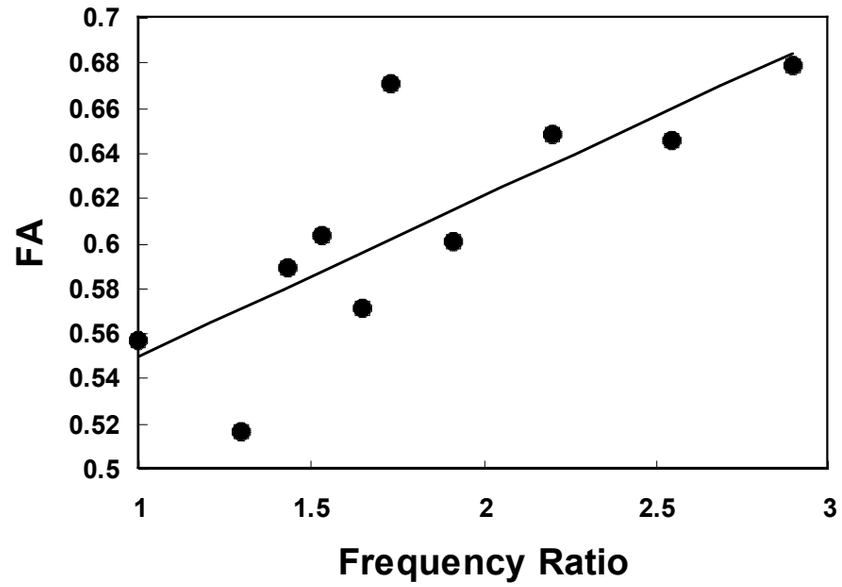




Differences in healthy controls

Normal variation in bimanual co-ordination skill



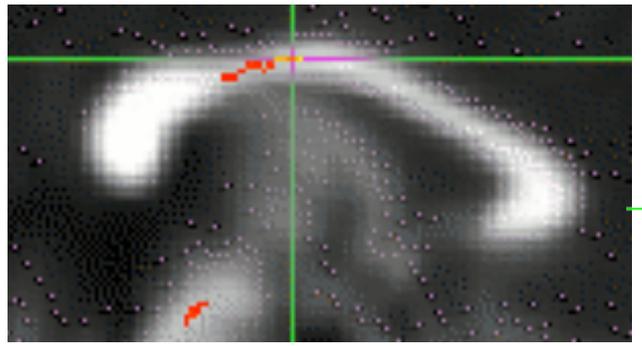


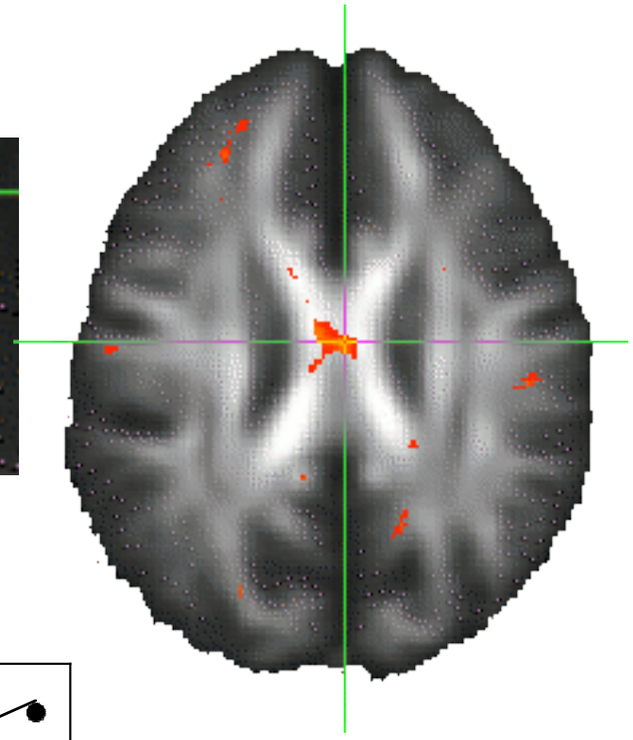
Johansen-Berg et al, OHBM, 2006

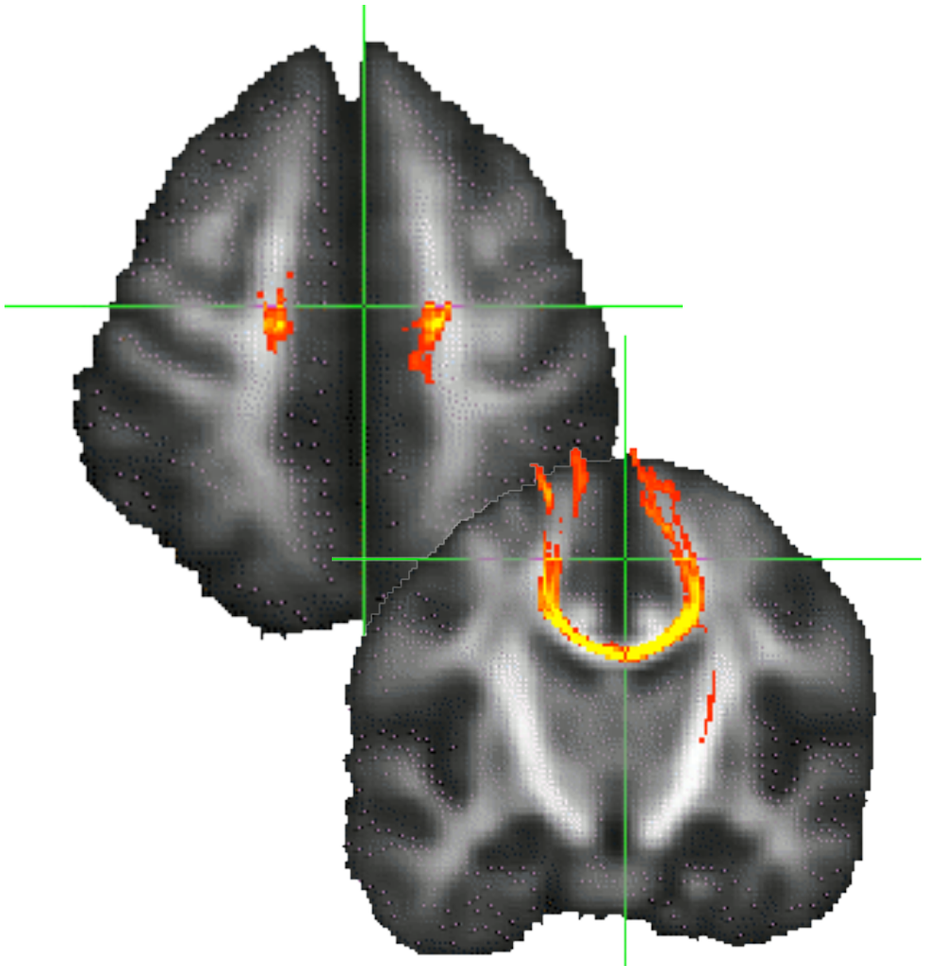
- Inter-individual variation in FA along a specific motor pathway is related to variation in motor skill
- Experience-dependent structural changes?

Differences in healthy controls

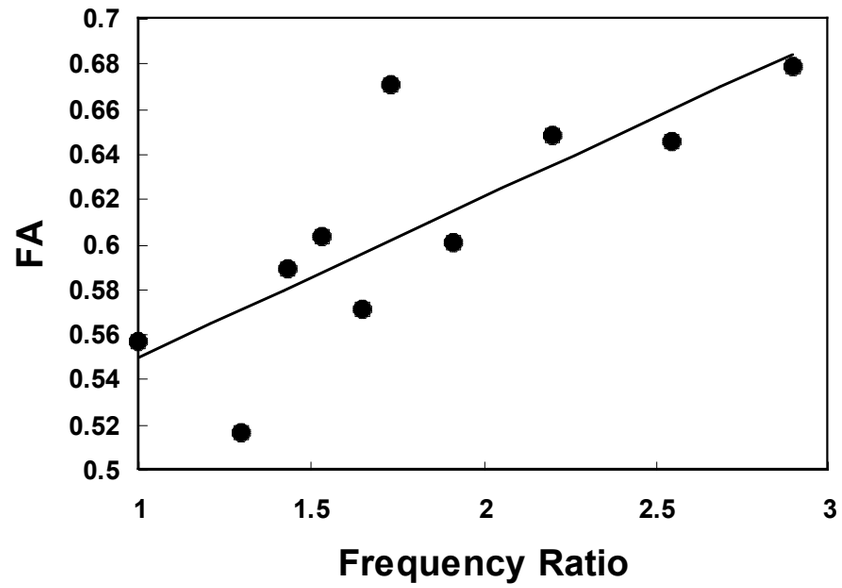
Normal variation in bimanual co-ordination skill







Johansen-Berg et al, OHBM, 2006

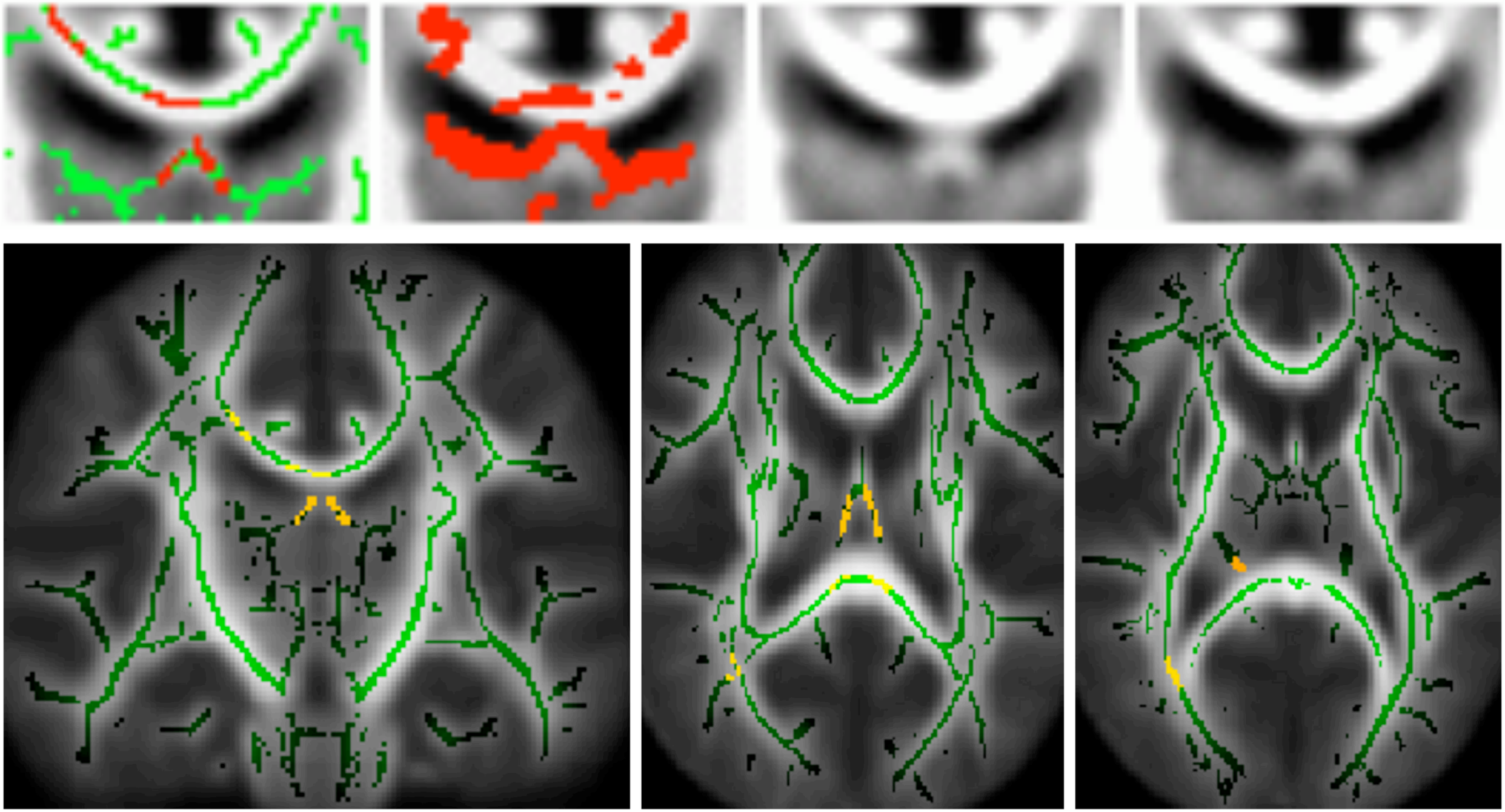


- Inter-individual variation in FA along a specific motor pathway is related to variation in motor skill
- Experience-dependent structural changes?

Schizophrenia (Mackay)

TBSS & VBM show reduced FA in corpus callosum & fornix
VBM shows spurious result in thalamus due to increased ventricles in schiz.

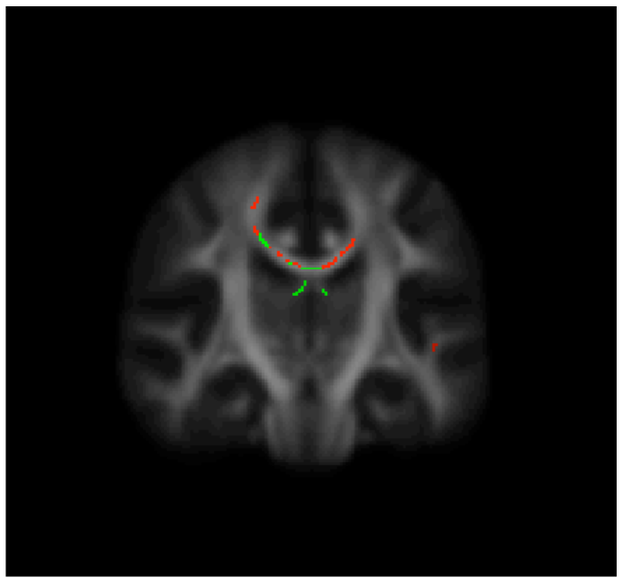
TBSS | VBM | mean FA (controls) | mean FA (schiz.)

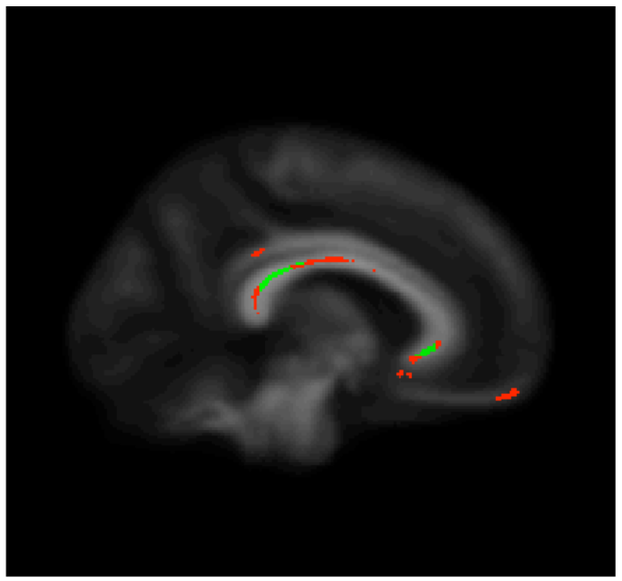


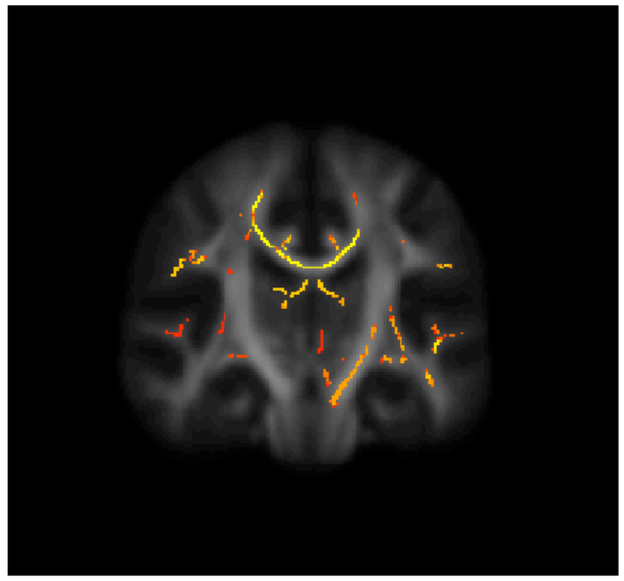
TFCE for TBS

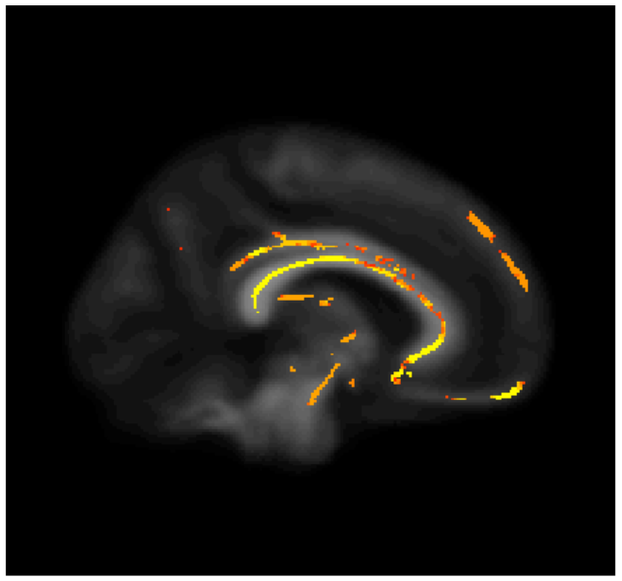
controls > schizophrenics

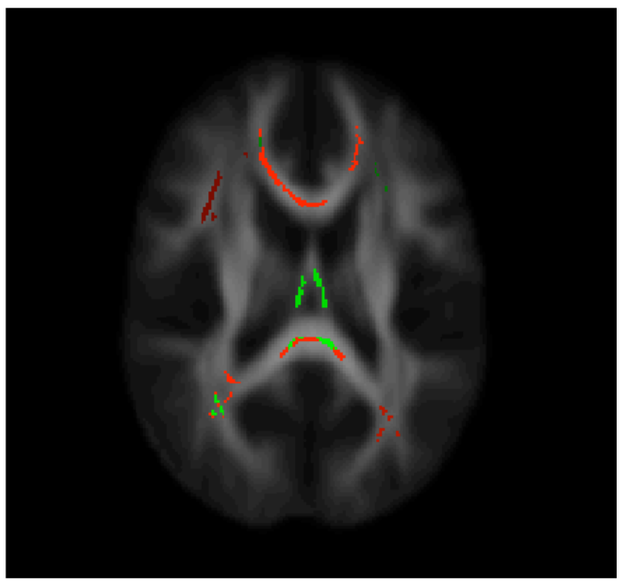
p<0.05 corrected for multiple comparisons across space, using randomise



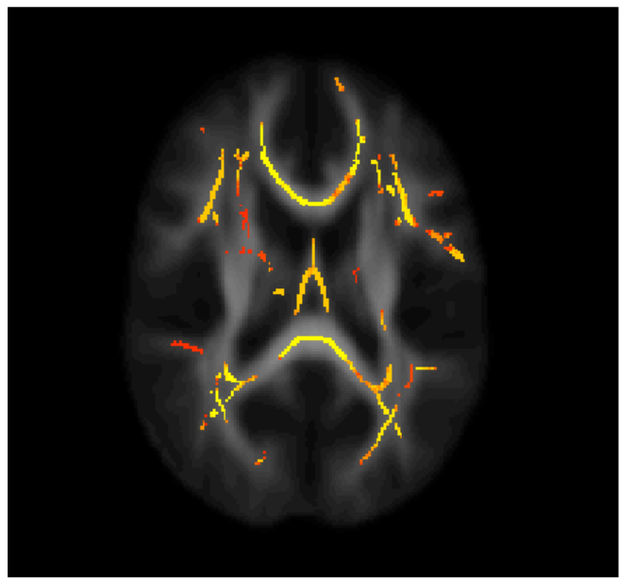








cluster-based:
cluster-forming
threshold =
2 or 3



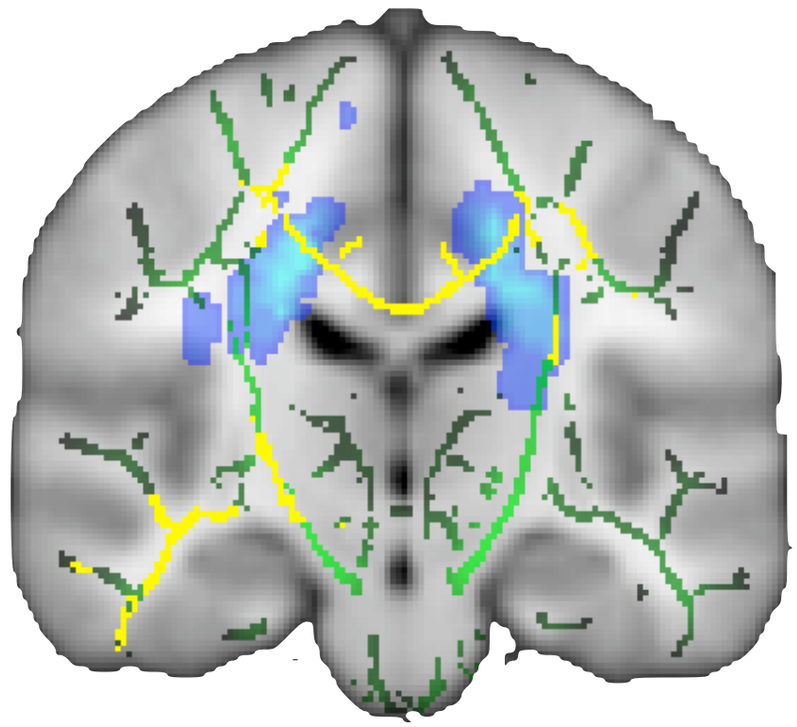
TFCE

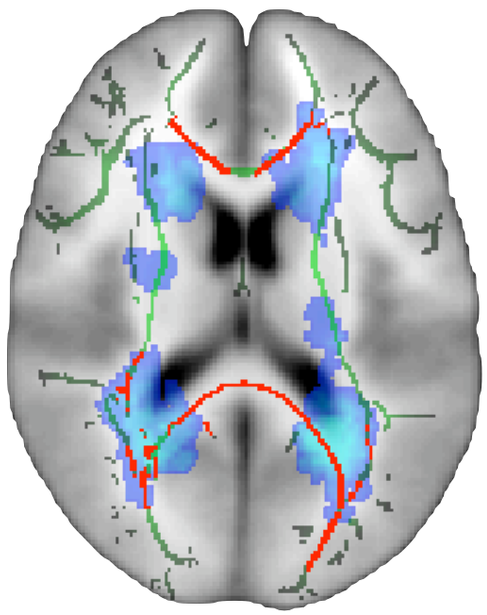
Multiple Sclerosis (Cader, Johansen-Berg & Matthews)

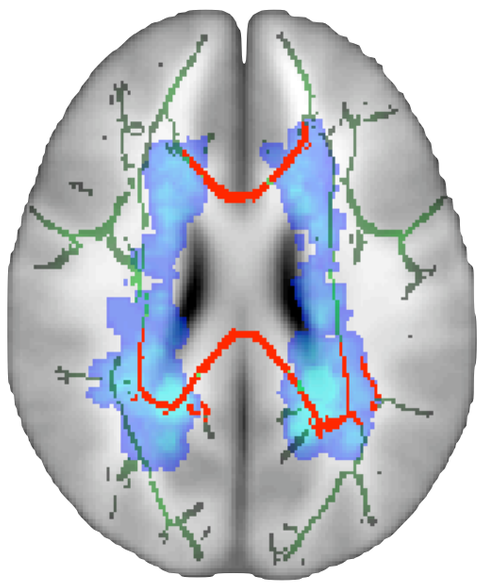
- 15 MS patients

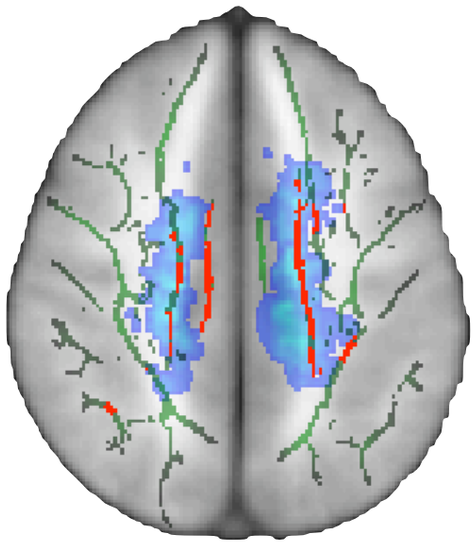
- Yellow = -ve corr. FA vs EDSS

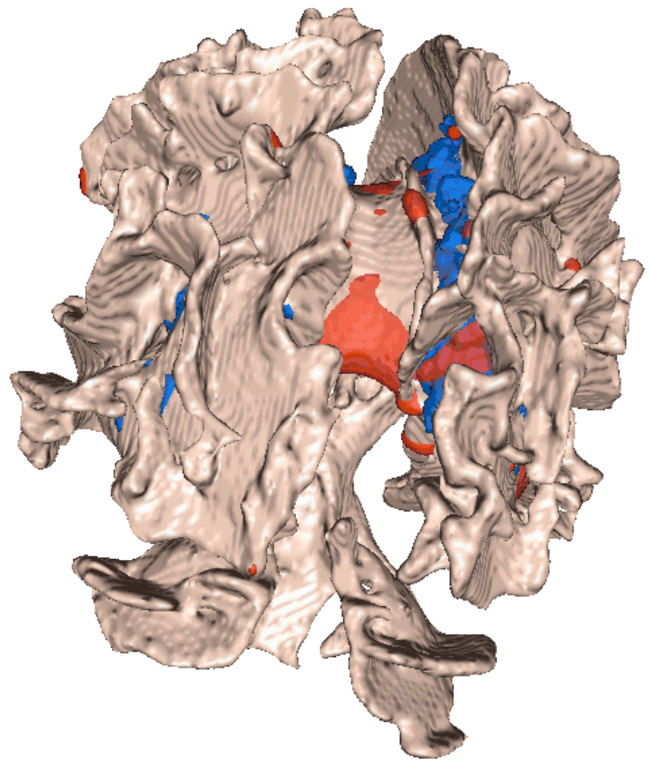
- Blue = group lesion probability (50%)
- Red = -ve corr. FA vs lesion volume
  Note reduced FA away from lesions



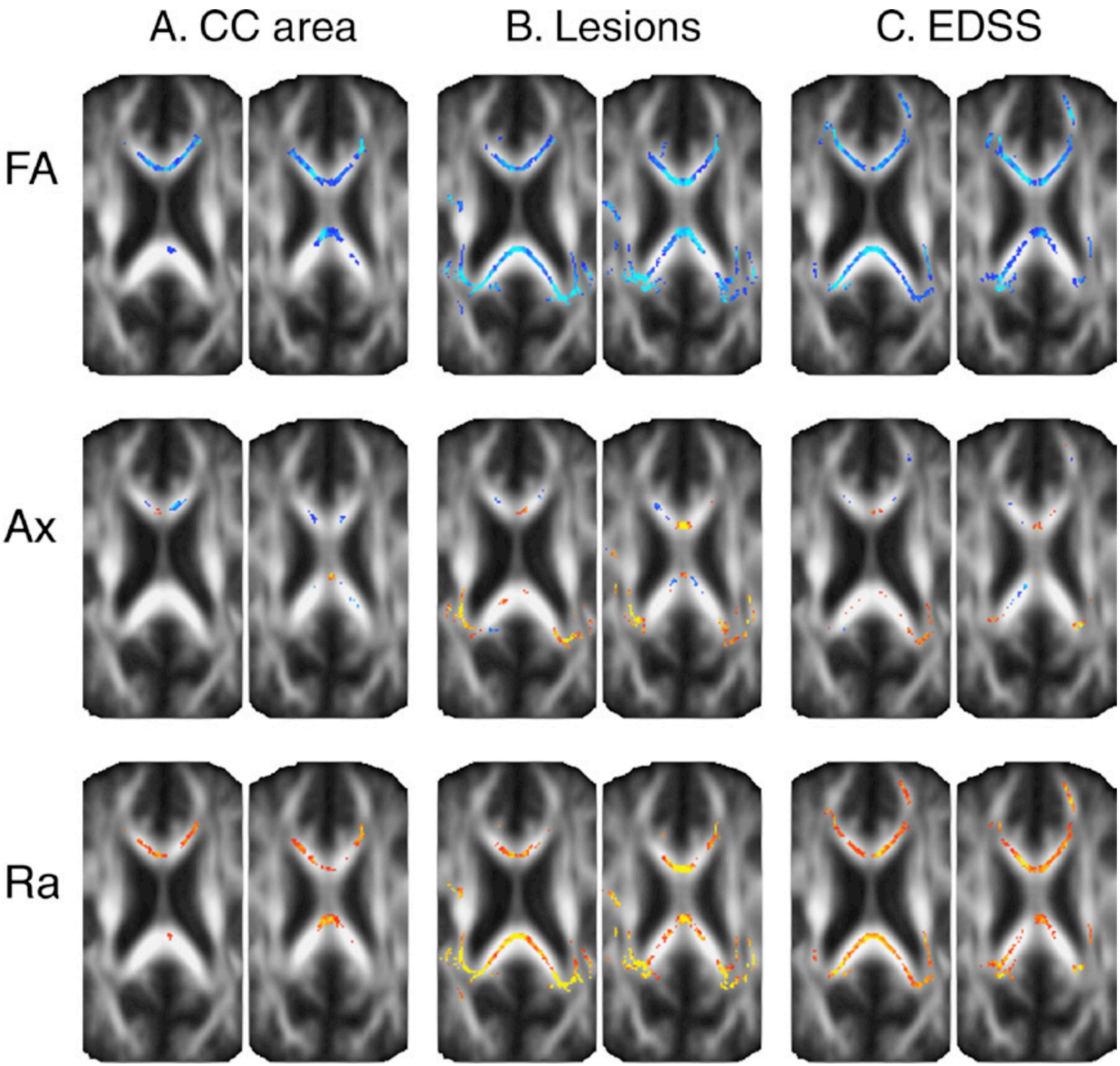






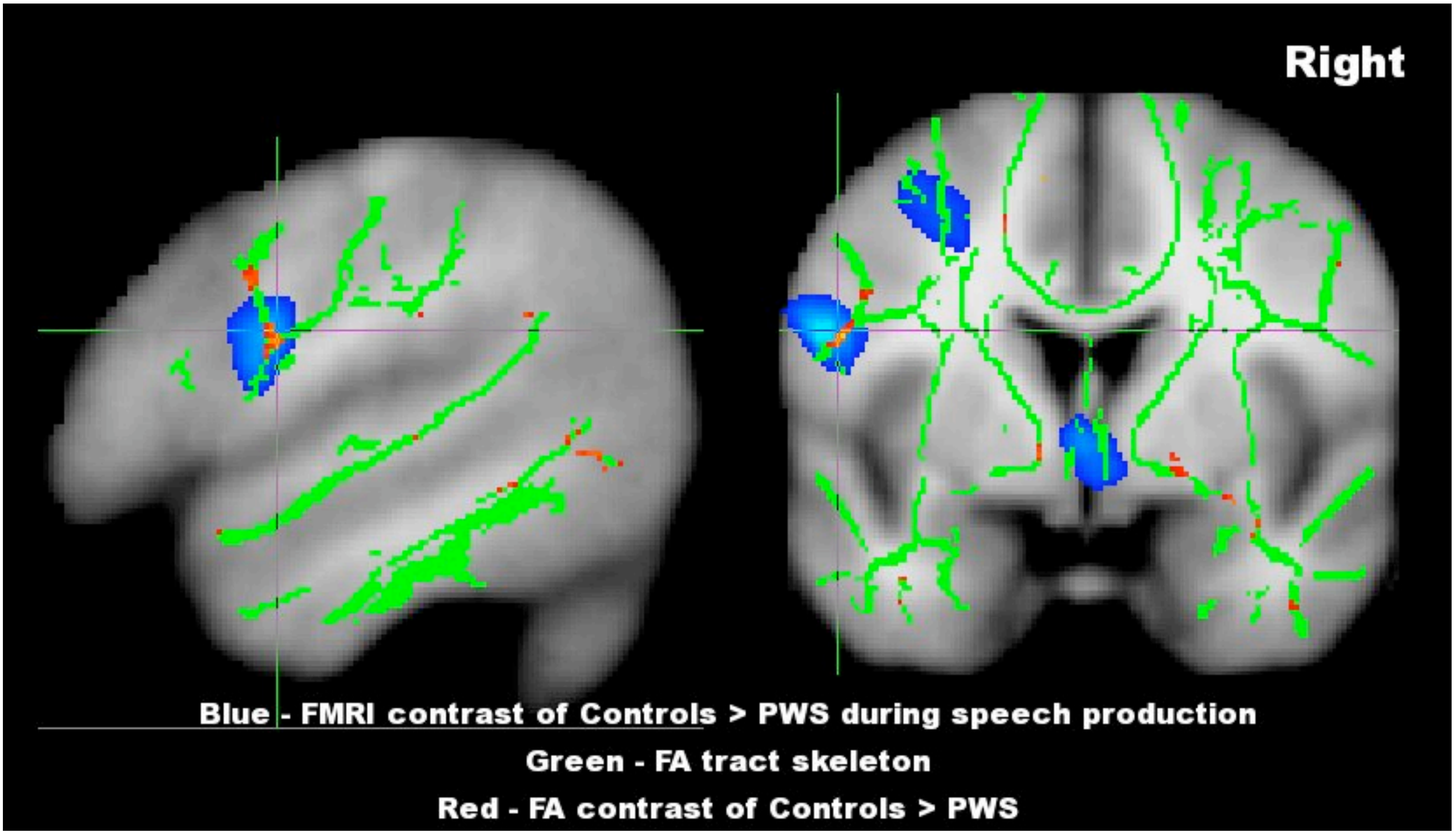


Multiple Sclerosis (Cader, Johansen-Berg & Matthews)



Lower FA in Stutterers in ventral-premotor

(Watkins)



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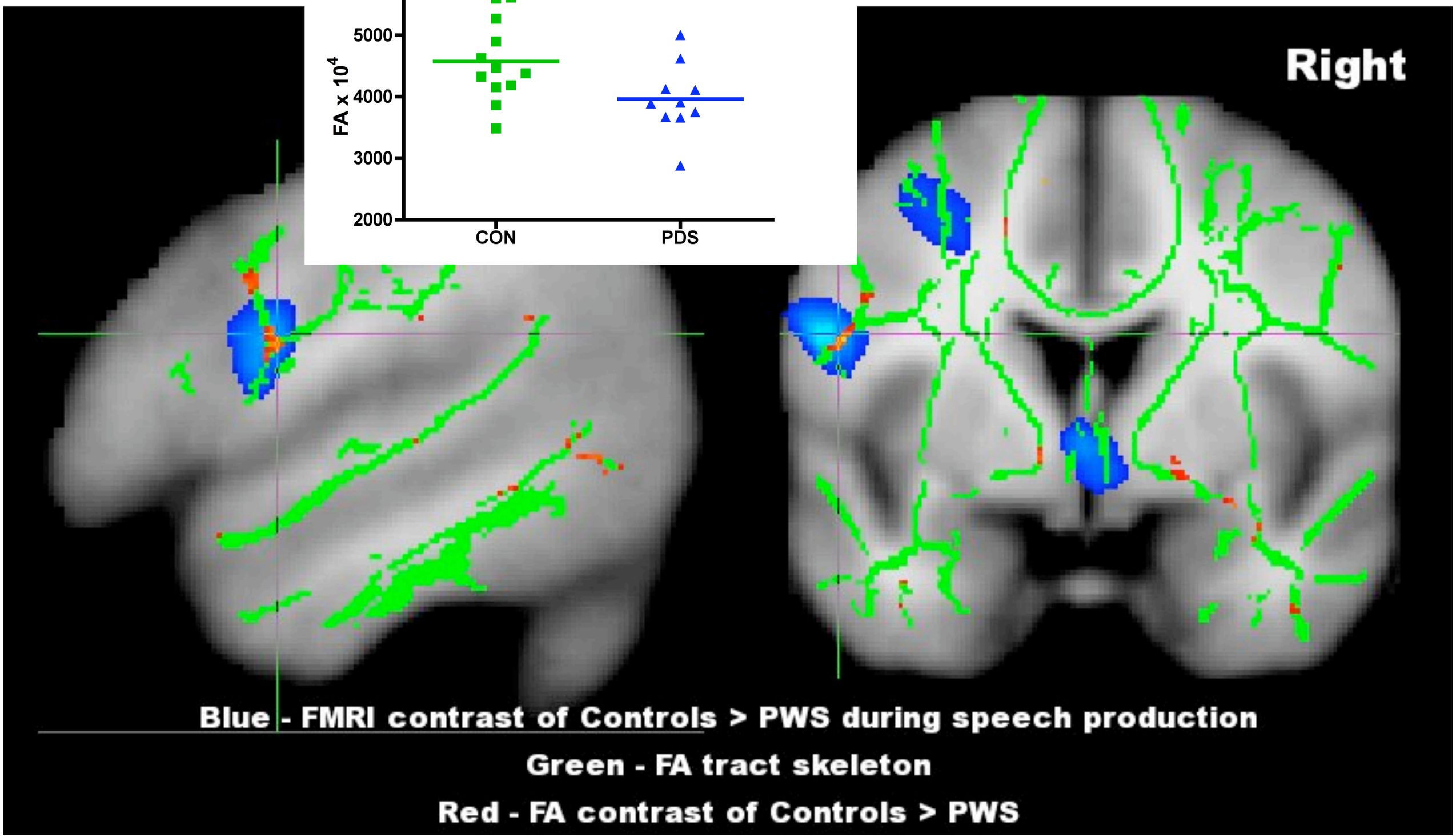
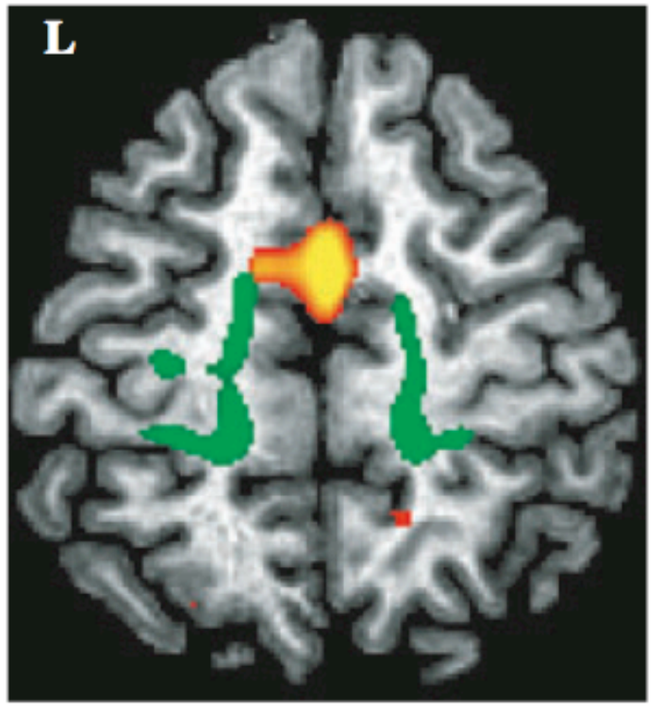
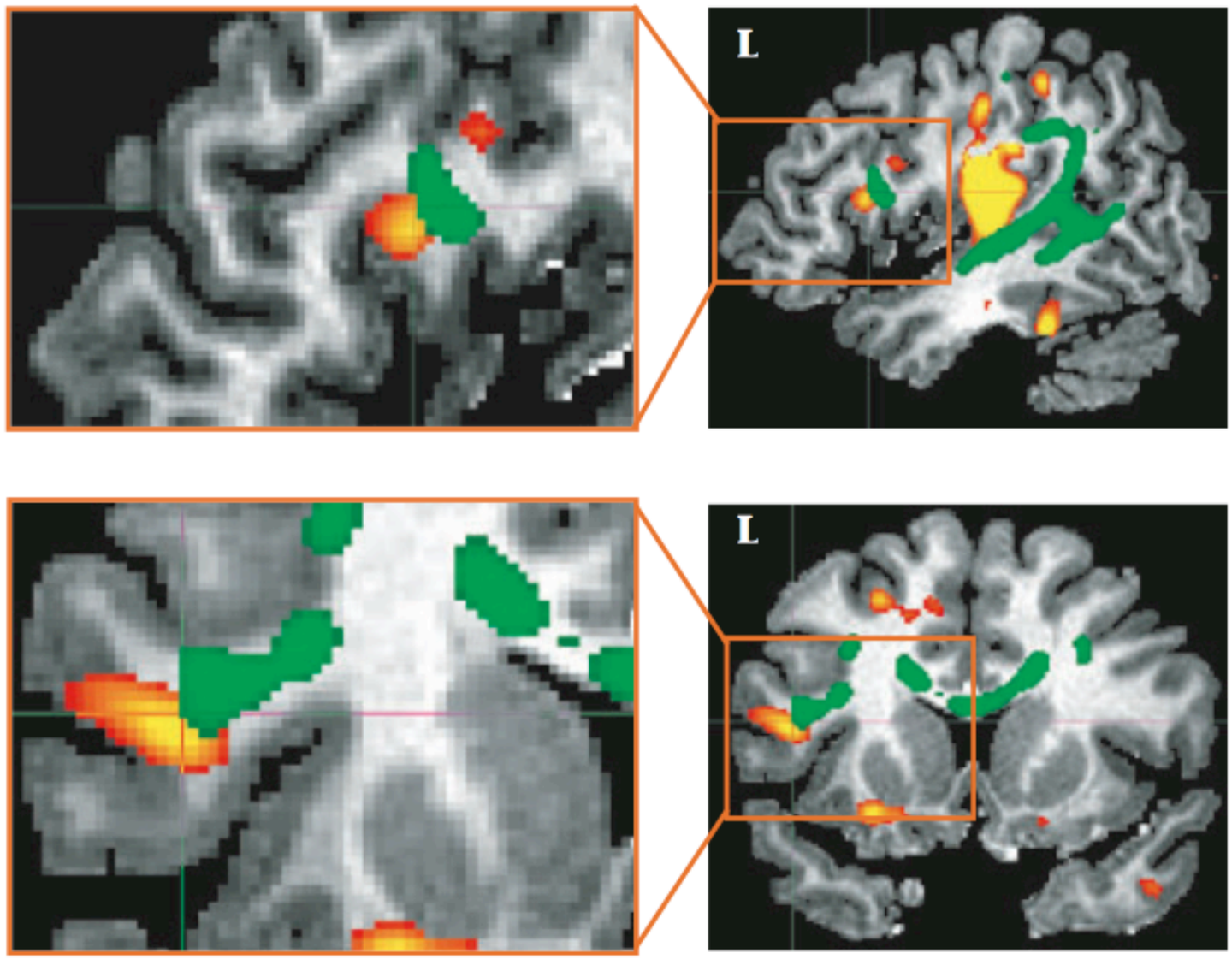


TBSS & FSL-VBM in adolescent-onset schizophrenia Douaud & James, Brain 2007



FA reduction

GM reduction

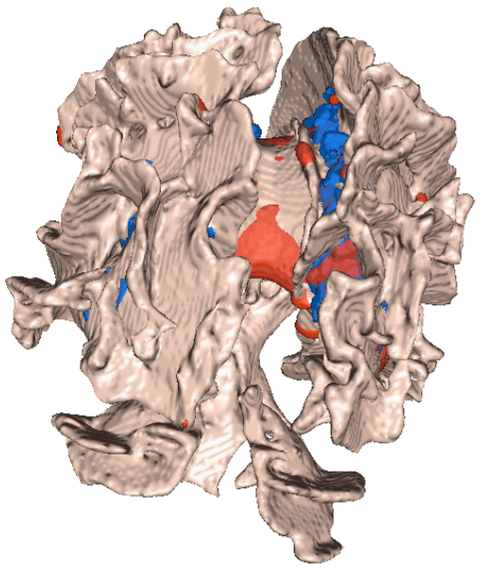


TBSS - Conclusions

- Attempting to solve correspondence/smoothing problems
- Less ambiguity of interpretation / spurious results than VBM
- Easier to test whole brain than ROI / tractography

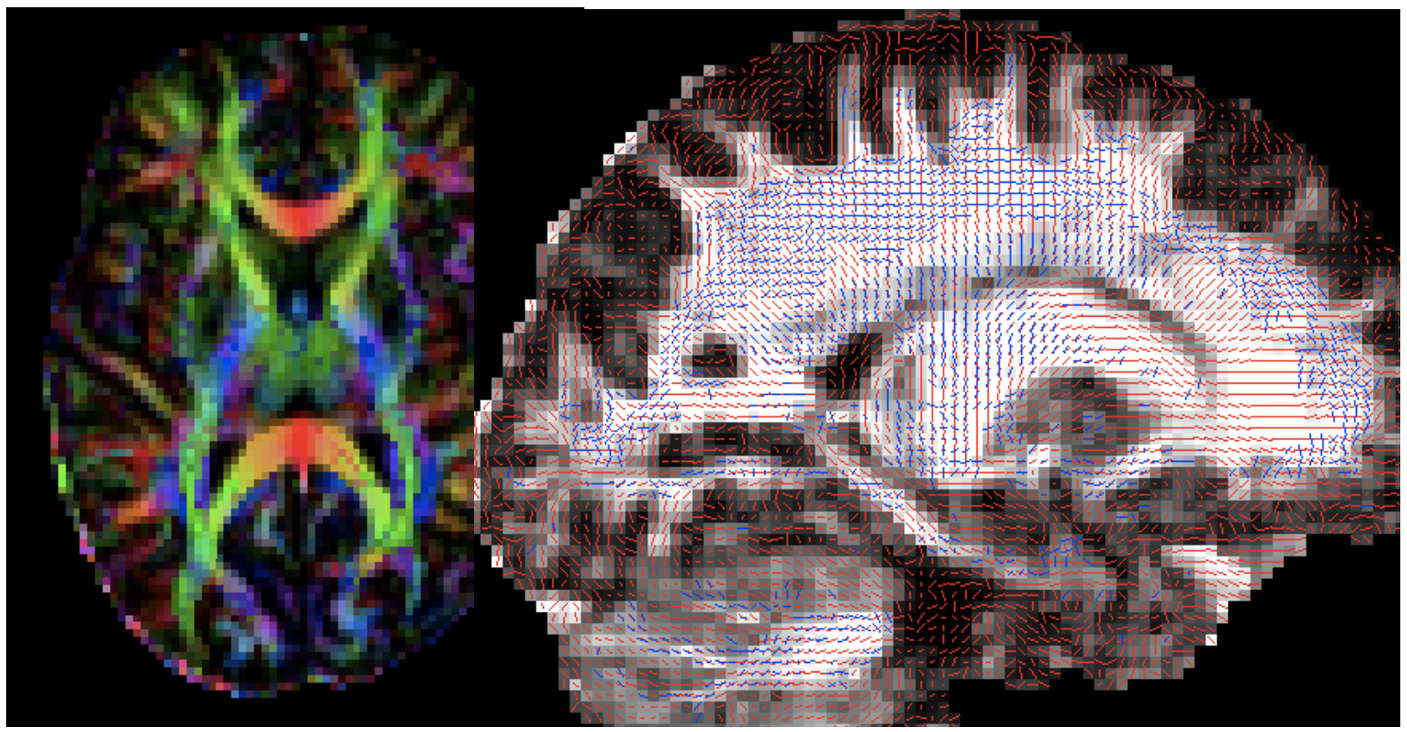
- Limitations & Dangers
  - Interpretation of partial volume tracts still an issue
  - Crossing tracts?

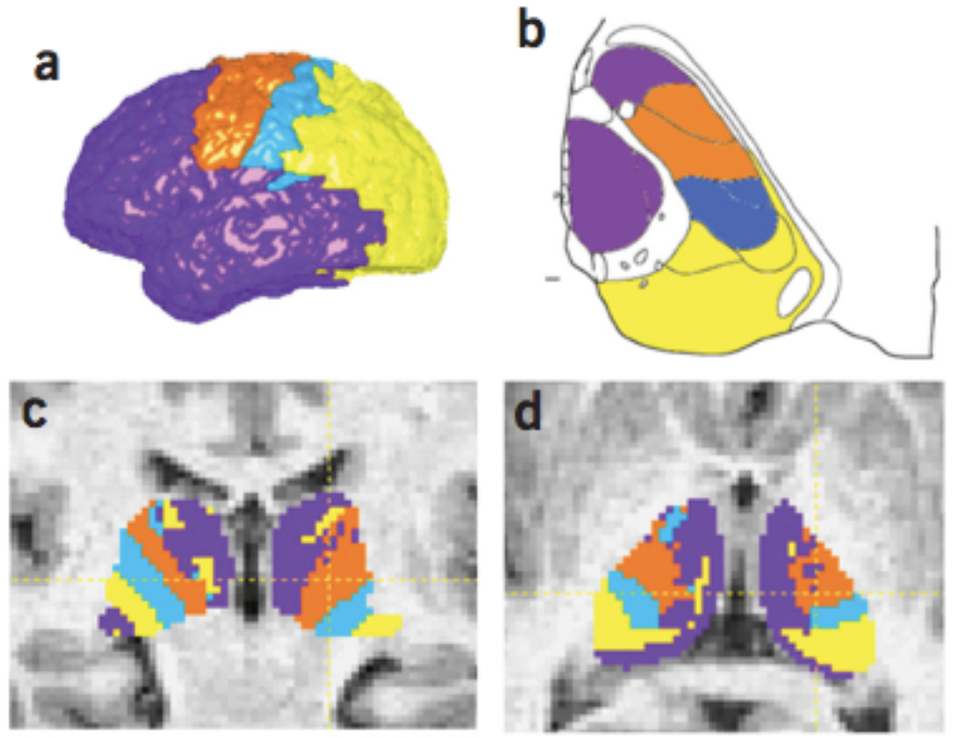
- Future work
  - Use full tensor (for registration and test statistic)
  - Use other test statistics (MD, PDD, width)
  - Multivariate stats (across voxels and/or different diffusion measures) & discriminant (ICA, SVM)



FMRIB Diffusion Toolbox

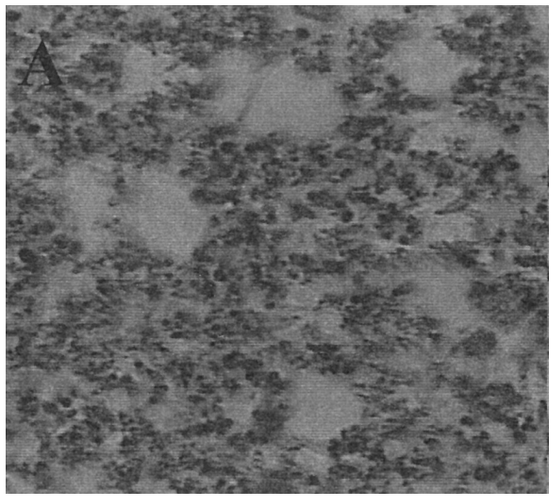
- DTI model fit
- Eddy current correction
- Voxel-Based diffusion analysis (TBSS)
- BEDPOSTX modelling crossing fibres
- PROBTRACKX propagating uncertainty in tractography





Connectivity - Why do we care?

- Clinical measurements
  - White matter (dys)connectivity is thought to form the substrate for many different neurological and psychiatric disorders.

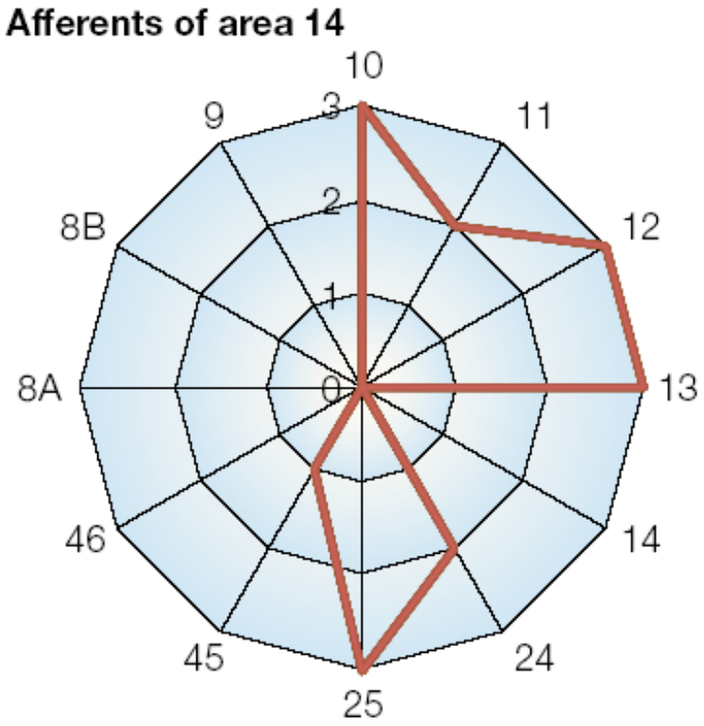


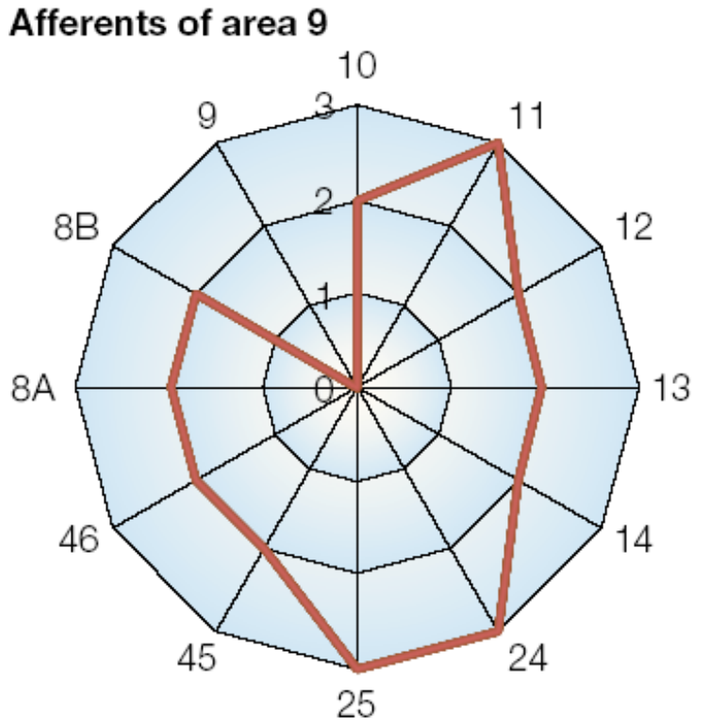
Evangelou et al. 2000

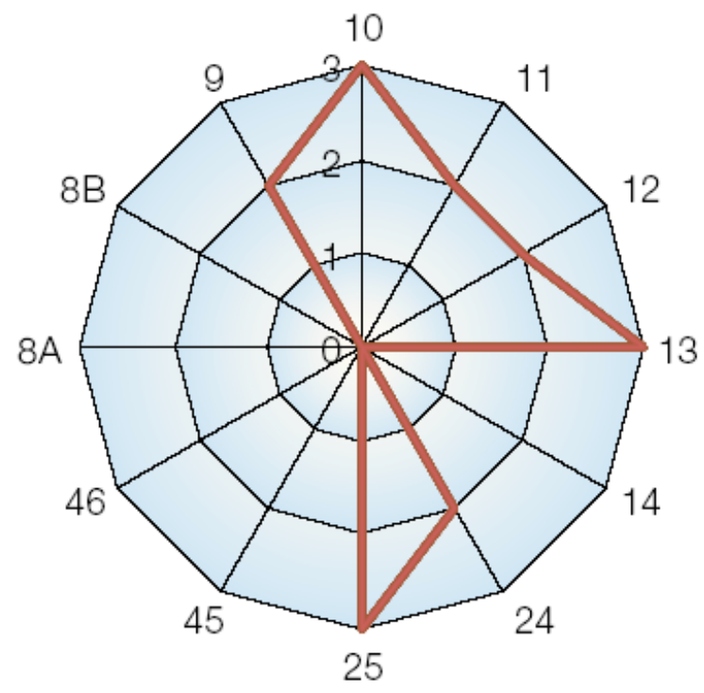
E.g. axonal degeneration/ demyelination in MS.

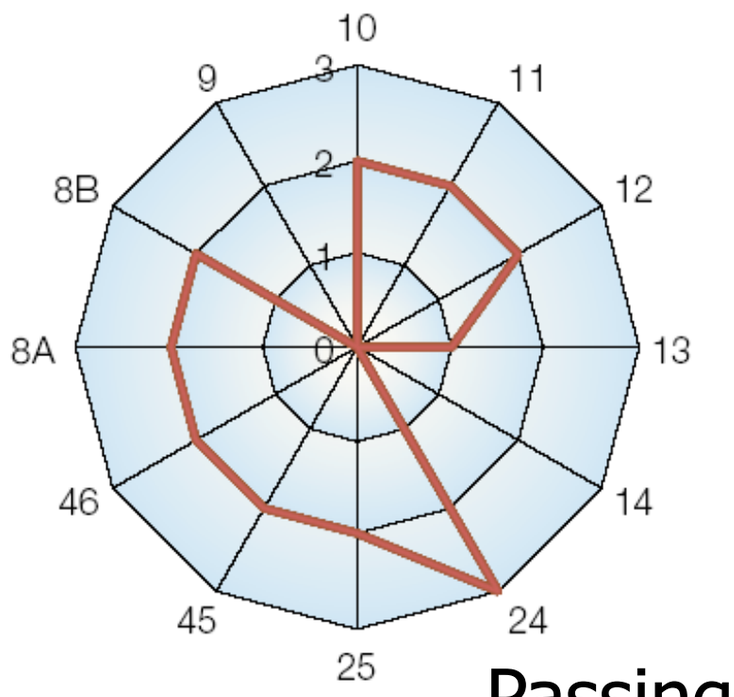
  - Diffusion tractography allows in-vivo measurements specific to different connections.

Basic Science - Connections constrain function





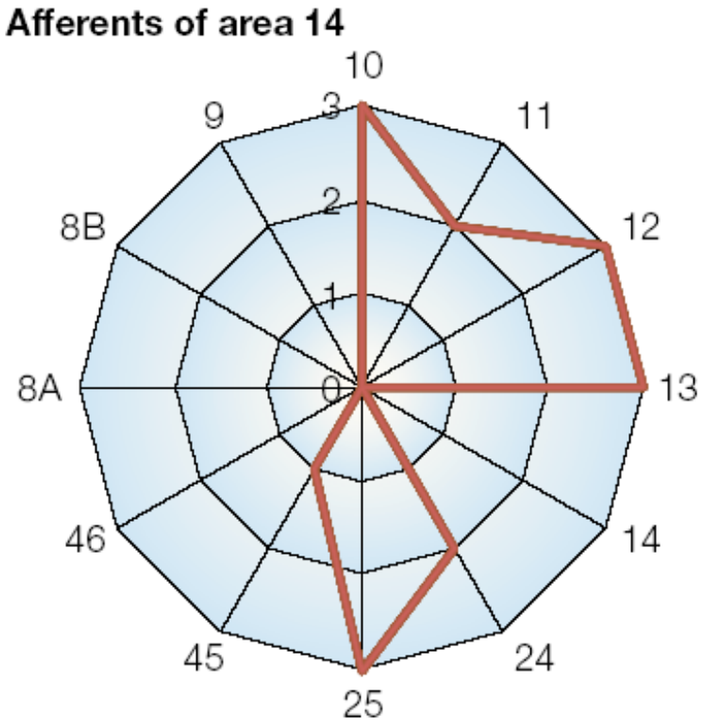


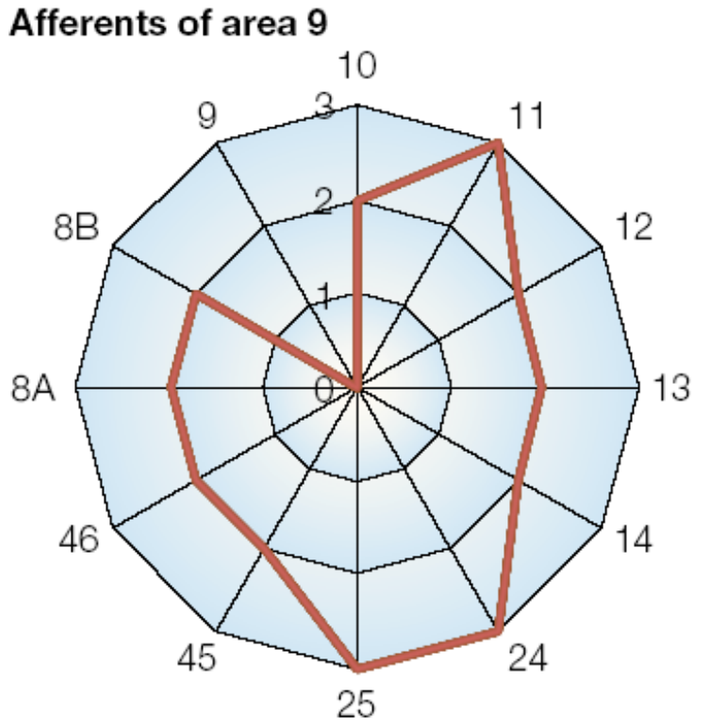


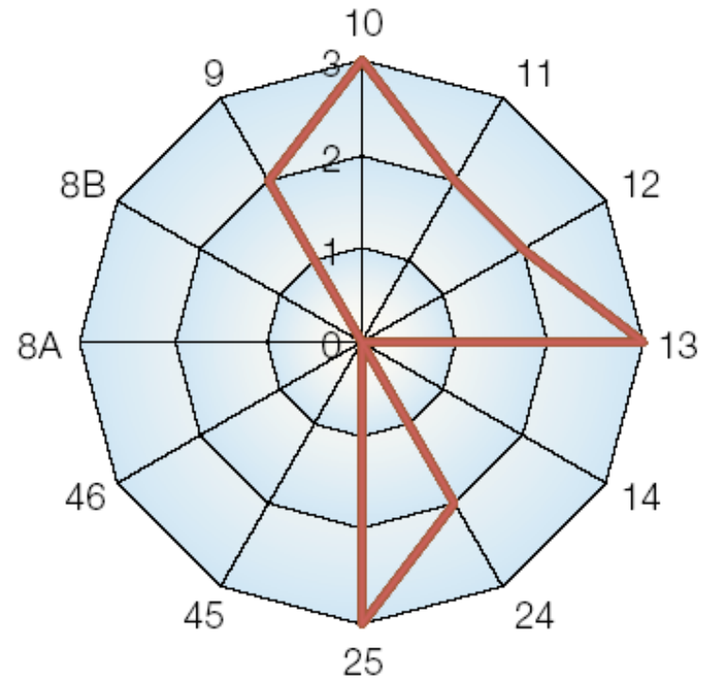
Different regions have distinct connectivity fingerprints

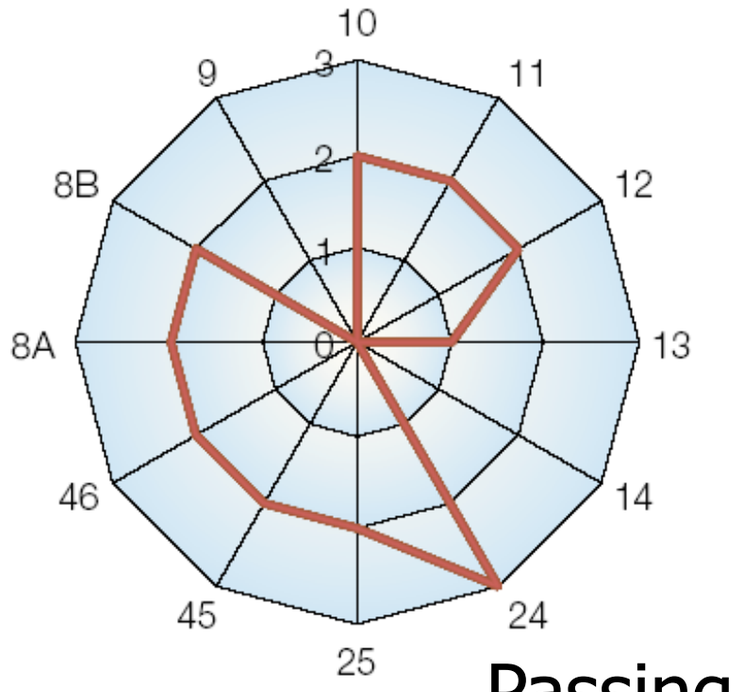
Passingham et al, NNR, 2003

Basic Science - Connections constrain function









Different regions have distinct connectivity fingerprints

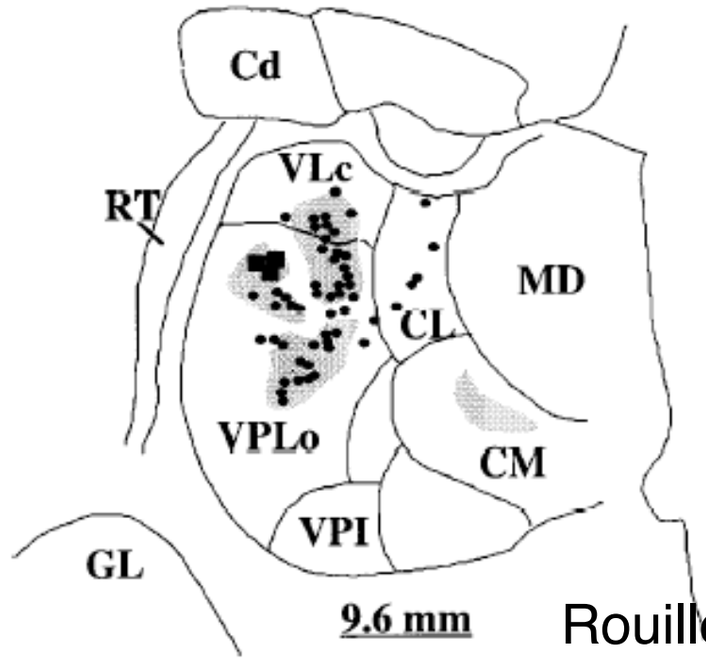
Understanding regional connectivity will be essential for our understanding of systems neuroscience.

Passingham et al, NNR, 2003

Investigating connectivity

Investigating connectivity

- Tracer studies in non-human animals



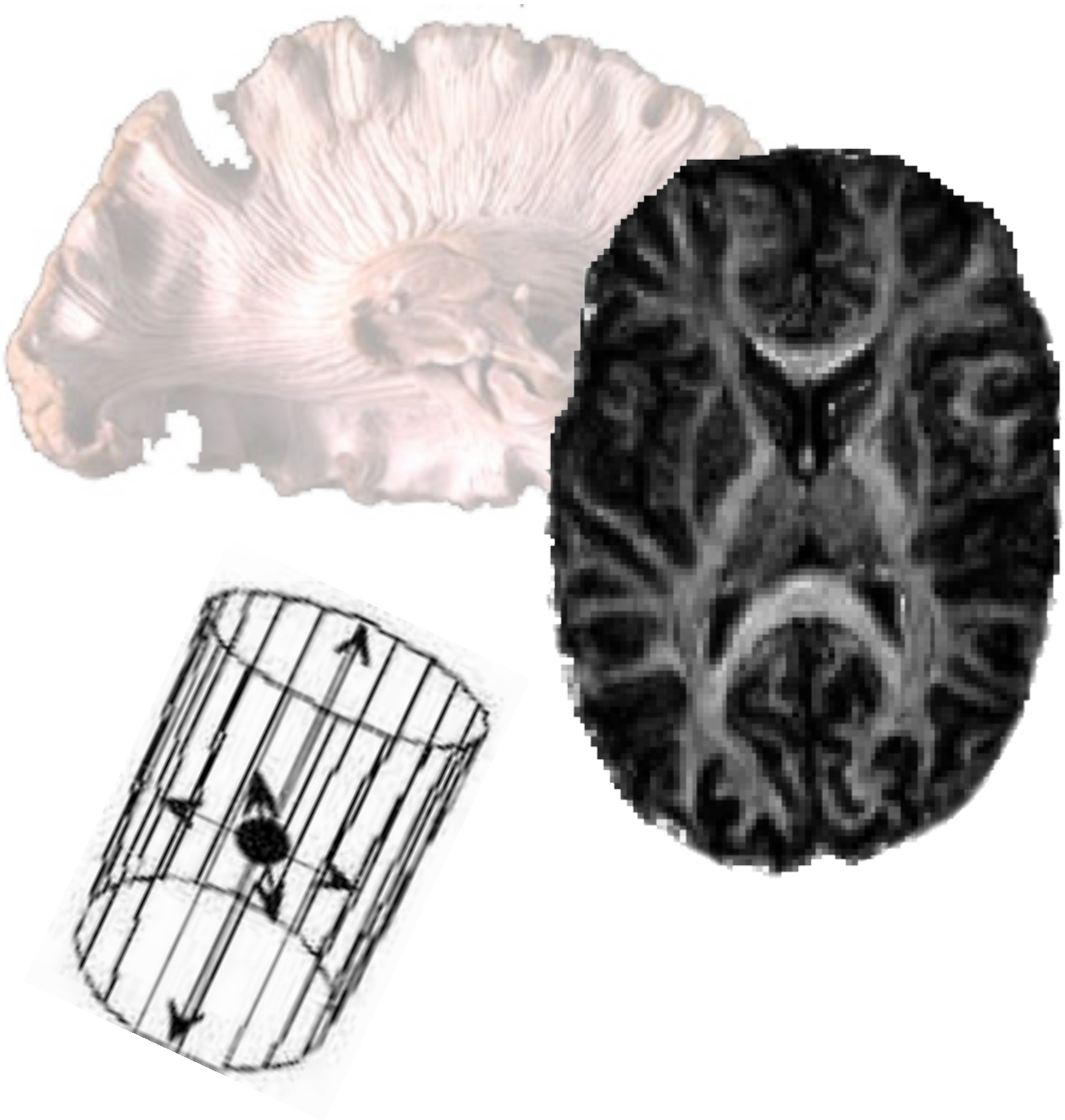
Rouiller et al, 1998

Post-mortem

- In human
  - Post-mortem dissection reveals large tracts
  - Post-mortem histology shows degeneration after remote lesions

Investigating human brain connectivity

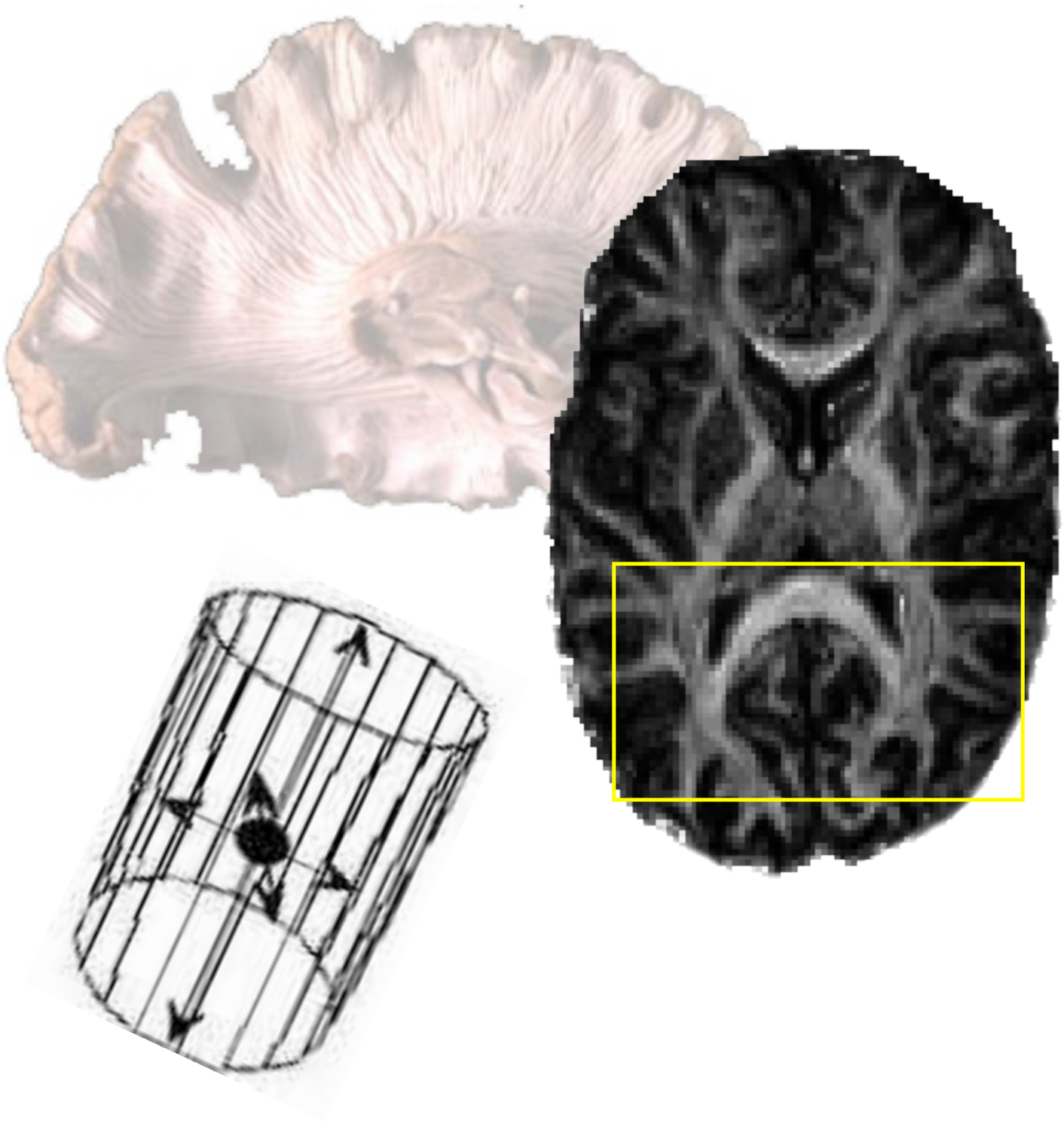
Investigating human brain connectivity



Diffusion-weighted MR imaging

- Fractional anisotropy
- Principal diffusion direction

Investigating human brain connectivity



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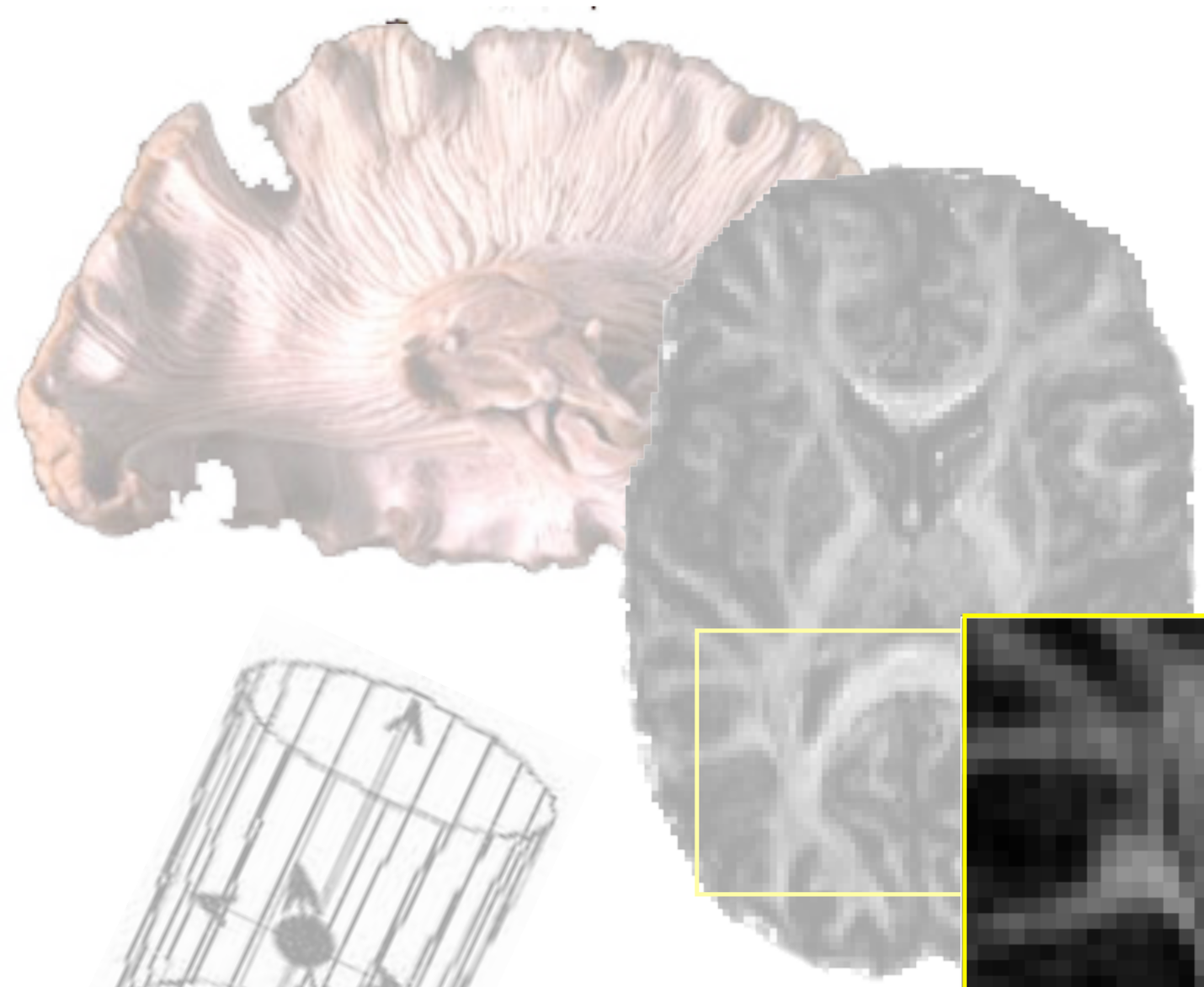

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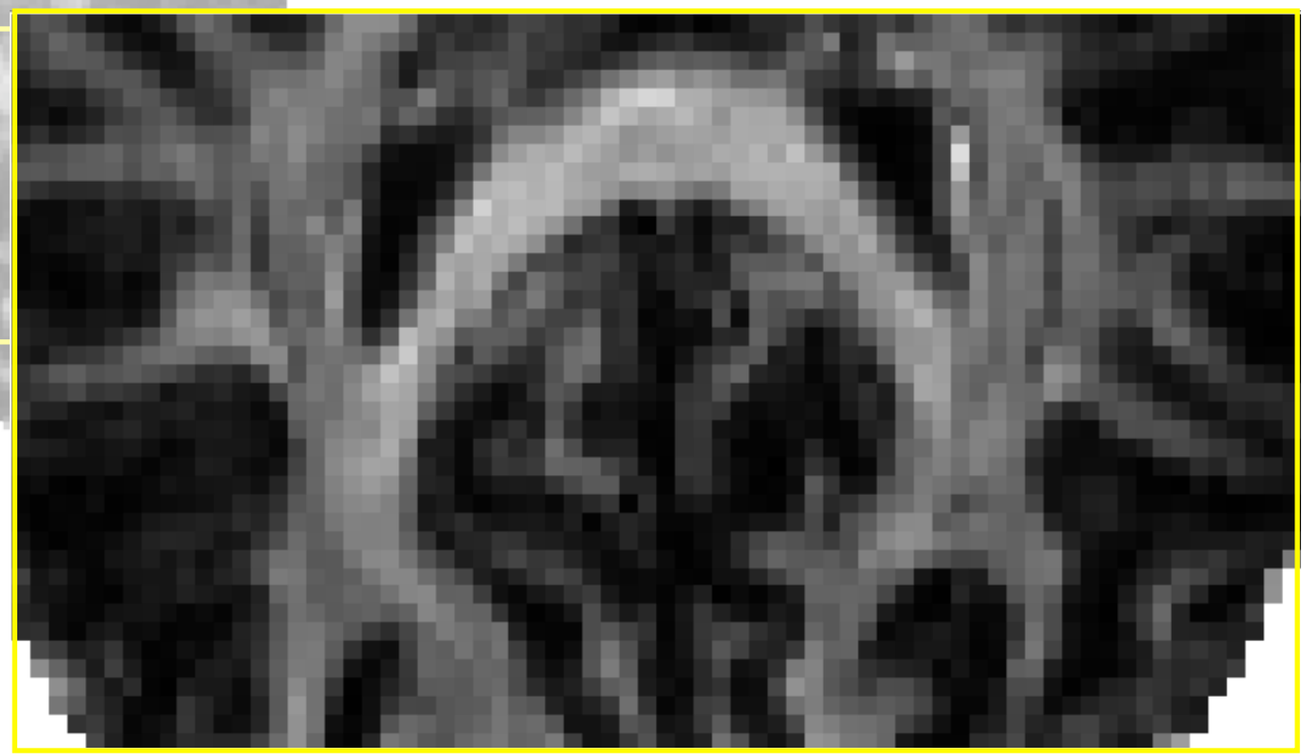
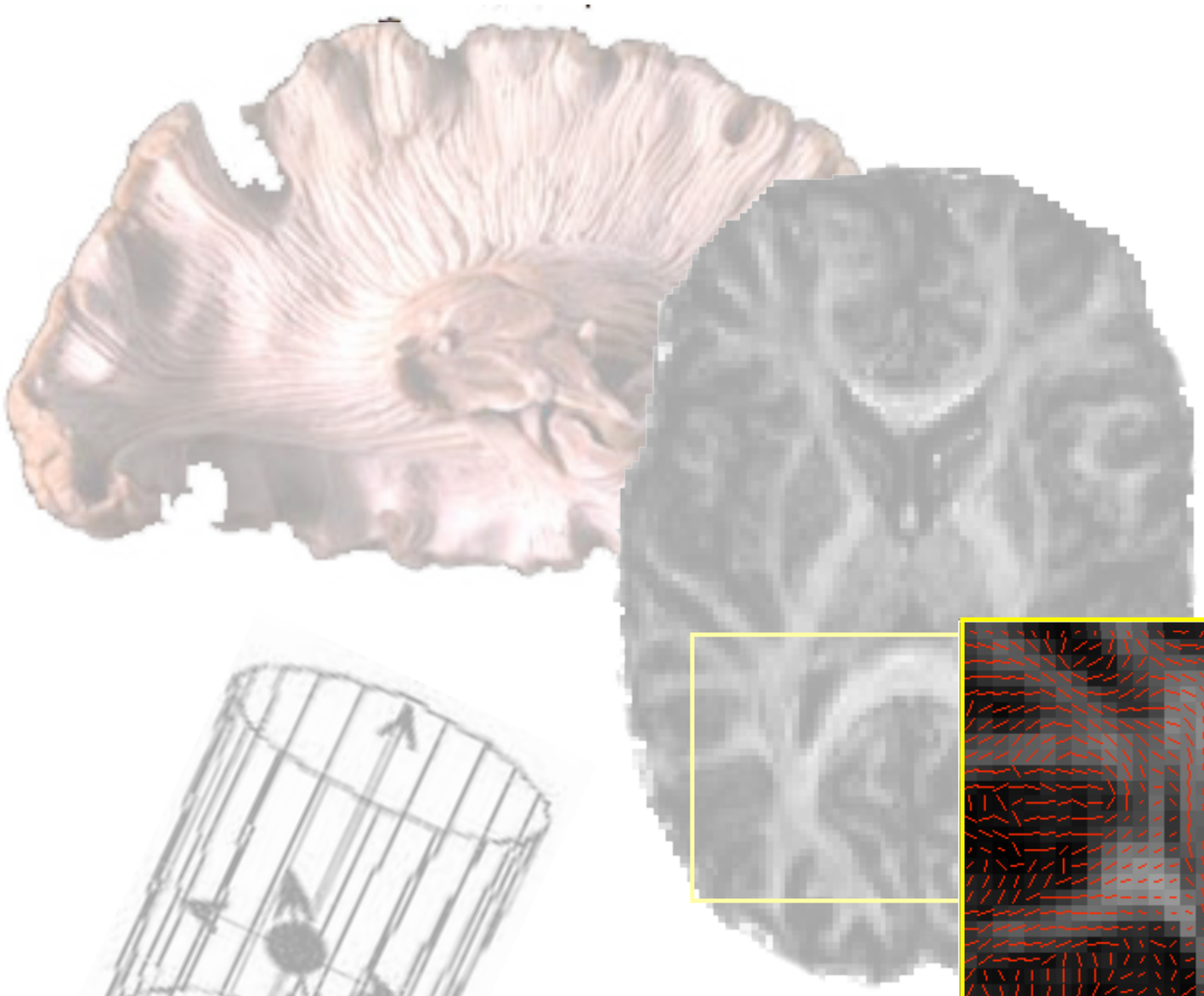


Investigating human brain connectivity



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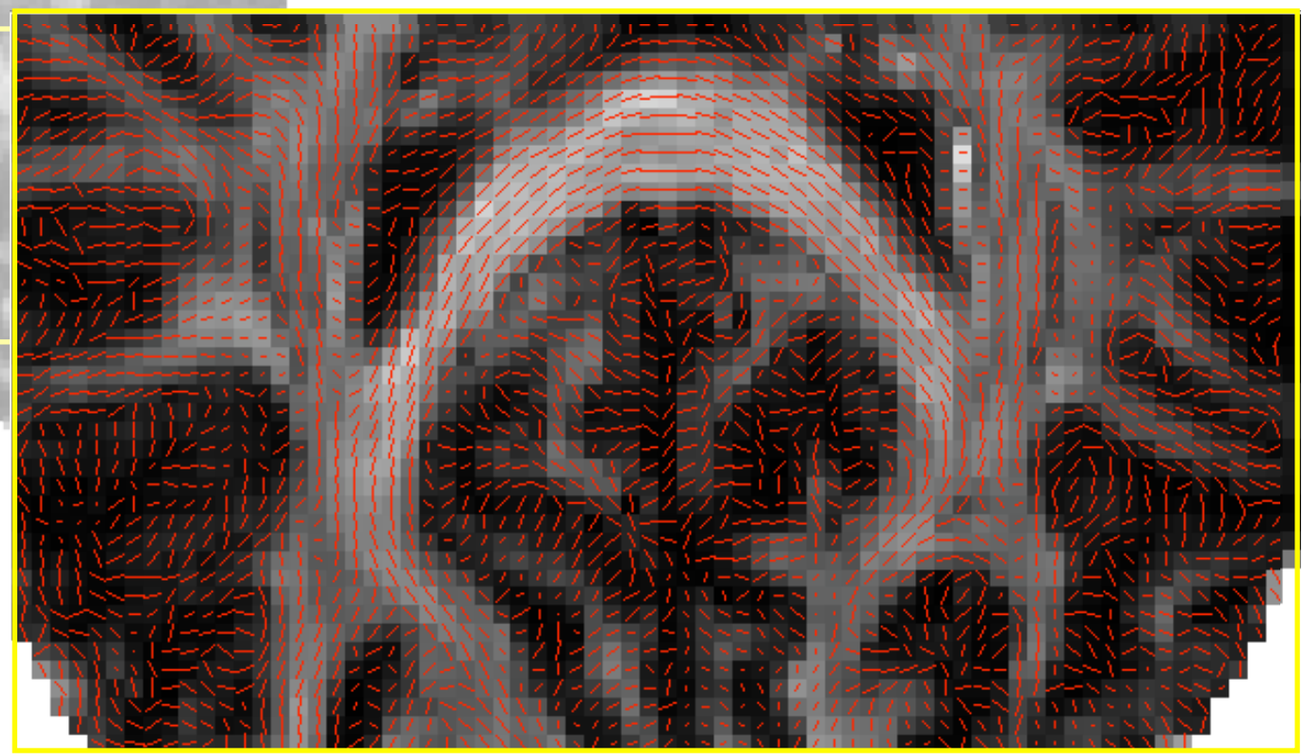

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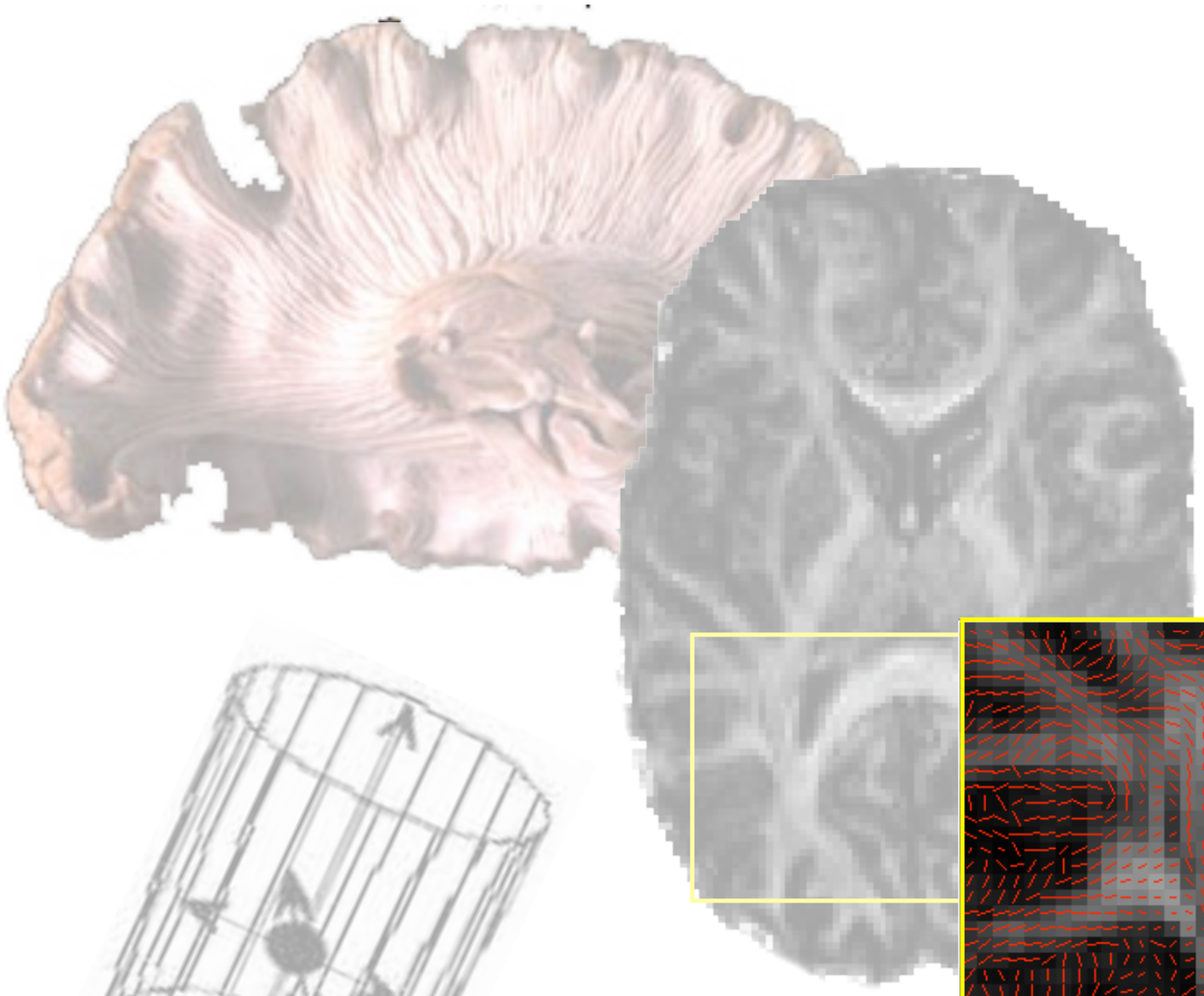

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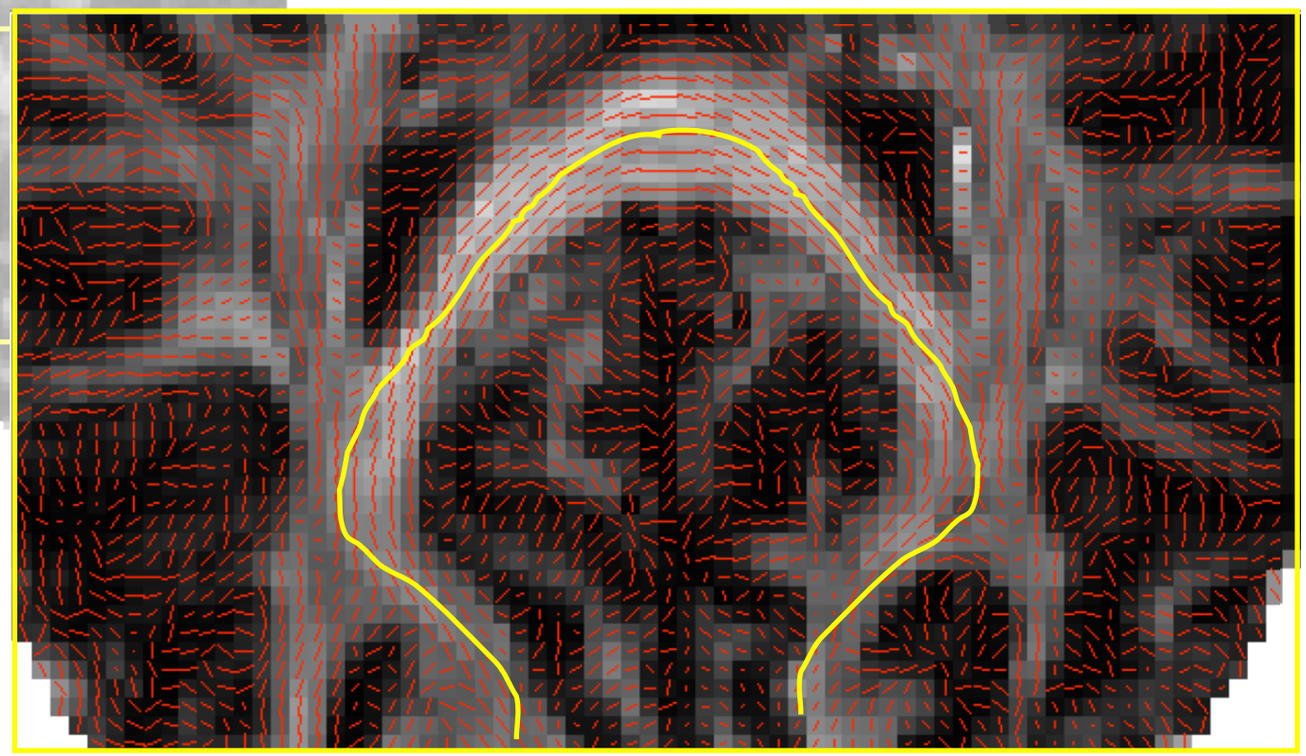
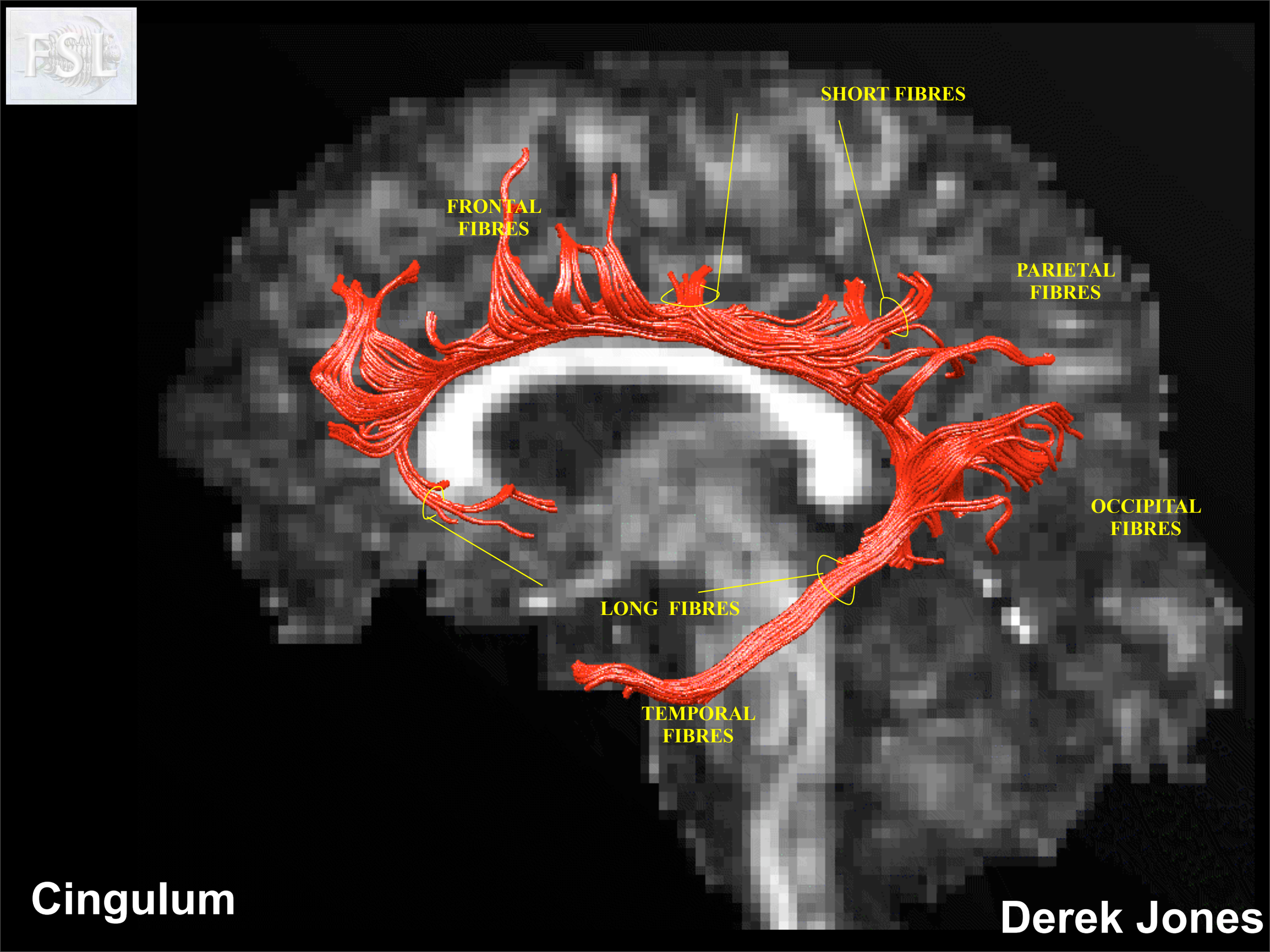


Streamline tractography can dissect major bundles

Cingulum

Derek Jones

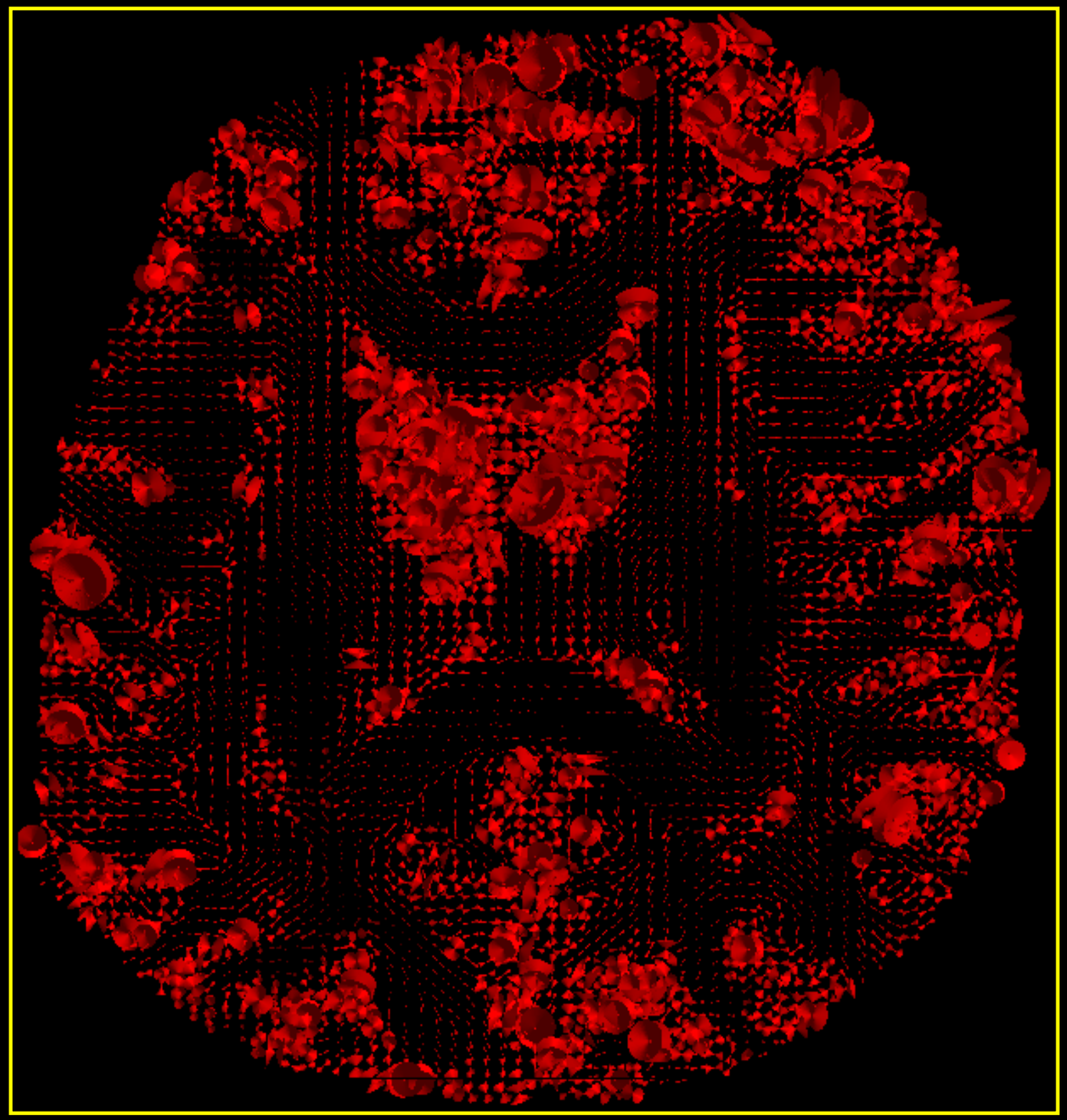


Cingulum

Derek Jones

But elsewhere...Uncertainty in fibre orientation.

Measured from repeated datasets



Derek Jones

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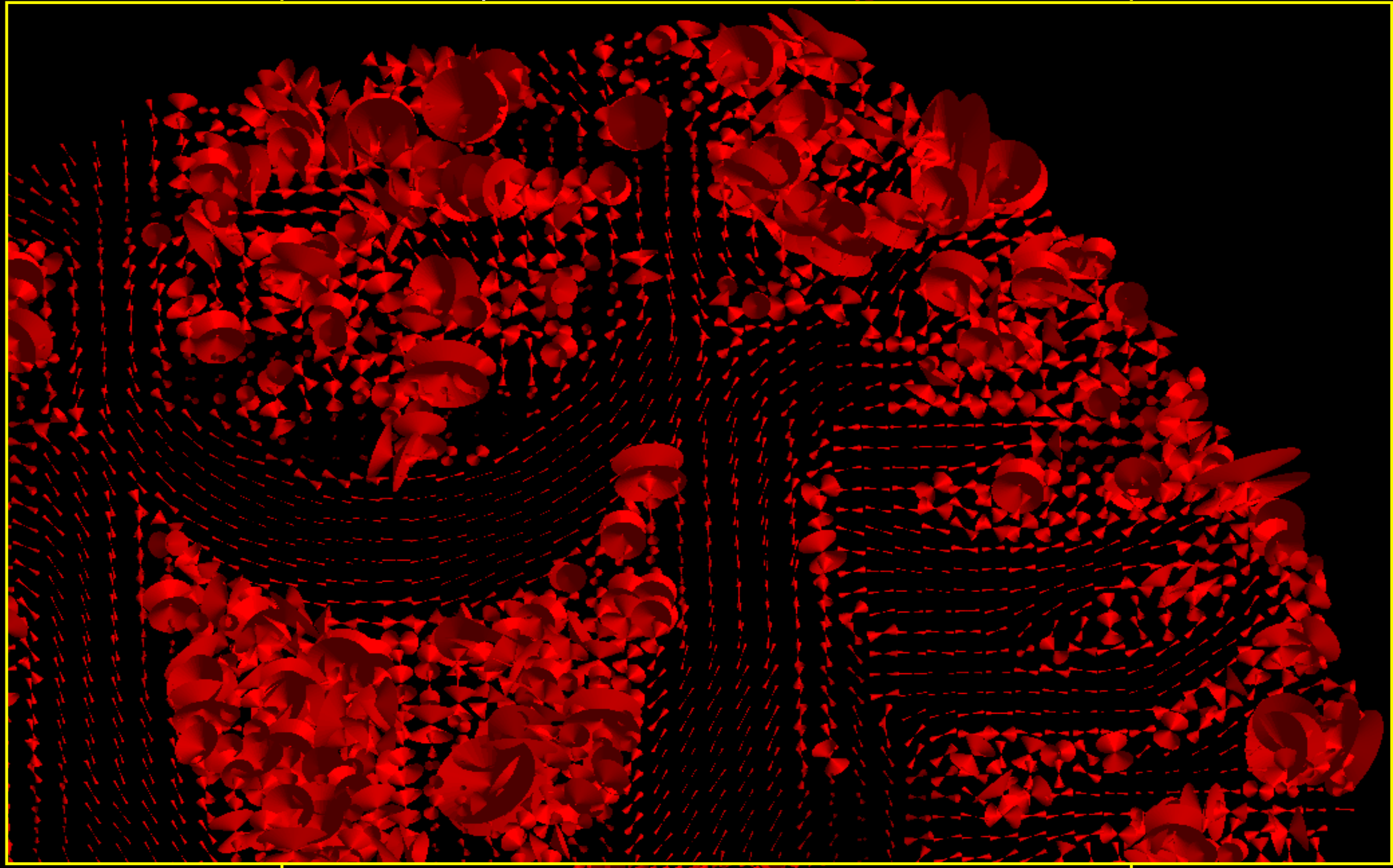

Derek Jones

So what can we do?

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- Remember ... a long time ago in the world of fMRI ...

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- We estimated two things:
  - A cope file (the parameters)
  - A varcope file (uncertainty in these parameters)

So what can we do?

- Remember ... a long time ago in the world of fMRI ...
- We estimated two things:
  - A cope file (the parameters)
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- We estimated our parameters, and their uncertainty from a single dataset.

So what can we do?

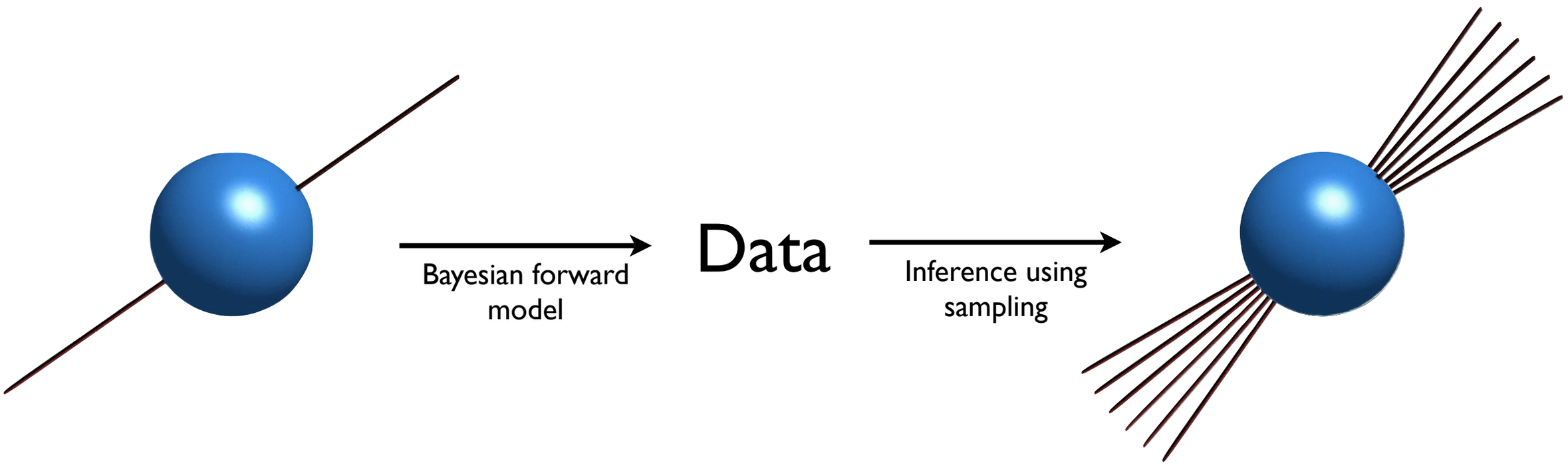
- Remember ... a long time ago in the world of fMRI ...

- We estimated two things:
  - A cope file (the parameters)
  - A varcope file (uncertainty in these parameters)

- We estimated our parameters, and their uncertainty from a single dataset.

- Can we do a similar thing with Diffusion parameters?

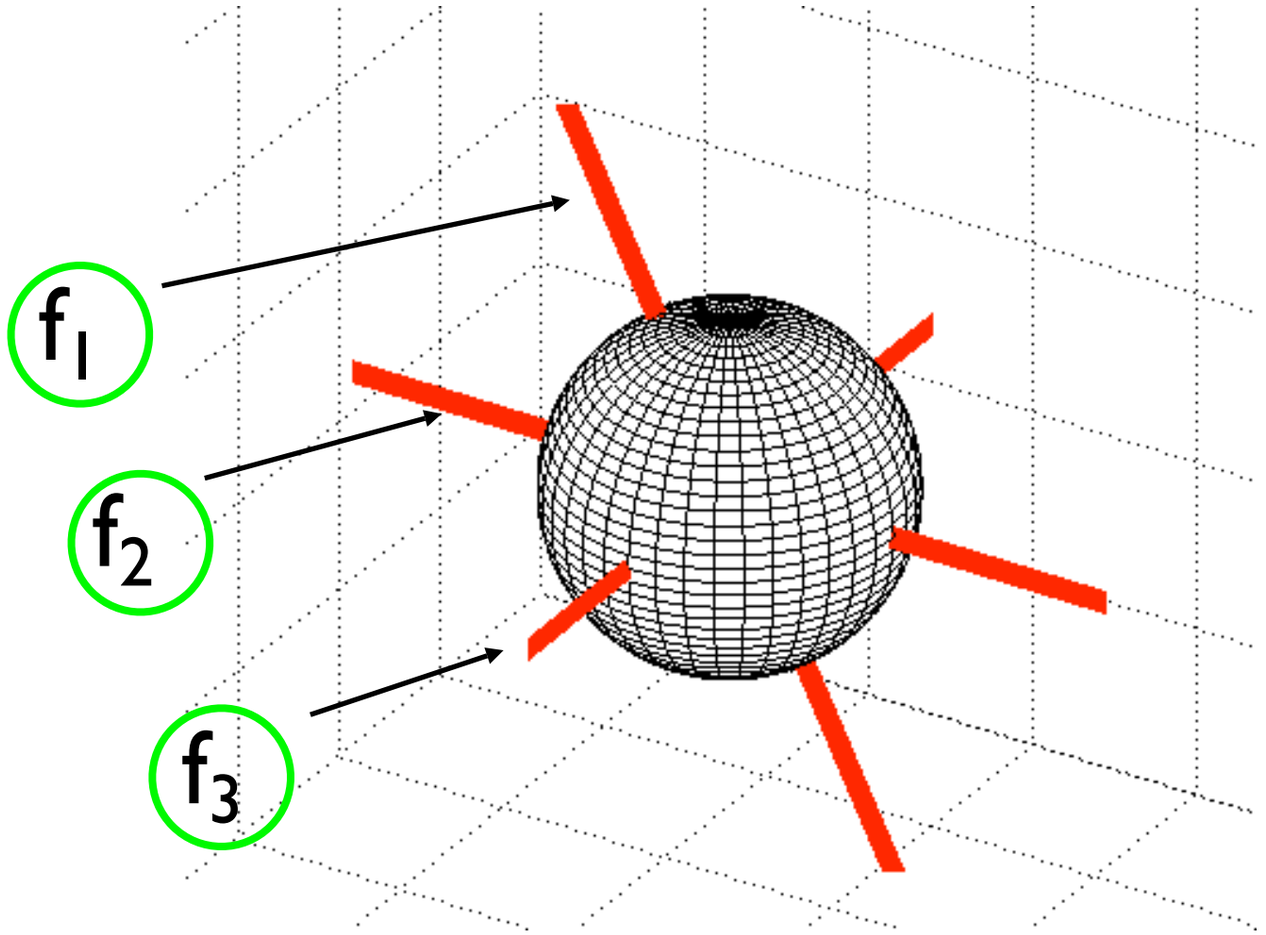
Diffusion Model in FDT tractography



* FDT tractography uses a simple model of local diffusion
  - o A single anisotropic direction with isotropic background diffusion

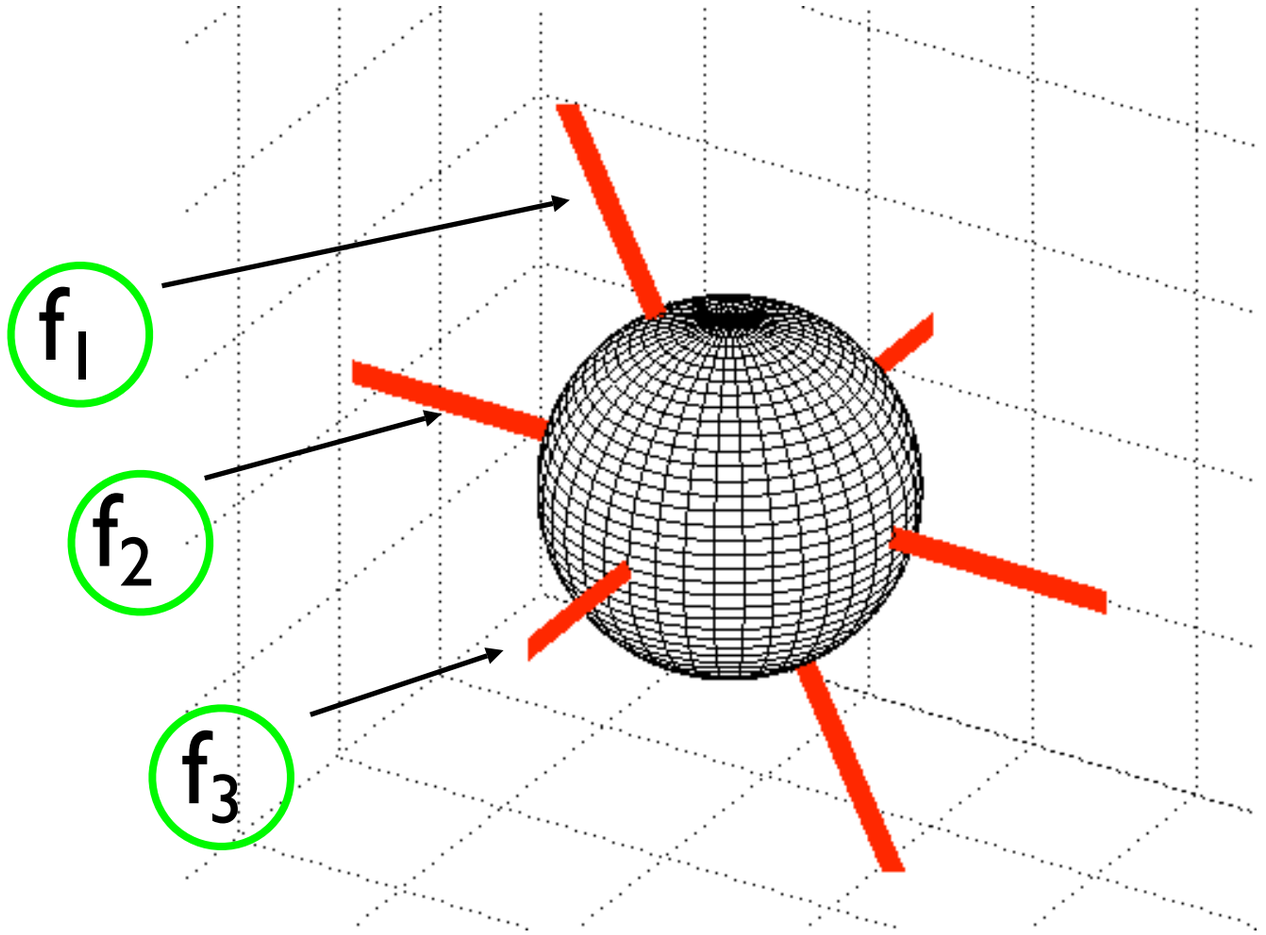
* Reasons:
  - o No ambiguity between ADC profile and uncertainty
  - o Avoid errors due to sorting eigenvectors in DTI
  - o Simplifies extensions to multiple fibre orientations

Modelling complex architecture



Modelling complex architecture

- Form testable hypotheses.
- Ask questions about parameters of interest



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- Form testable hypotheses.
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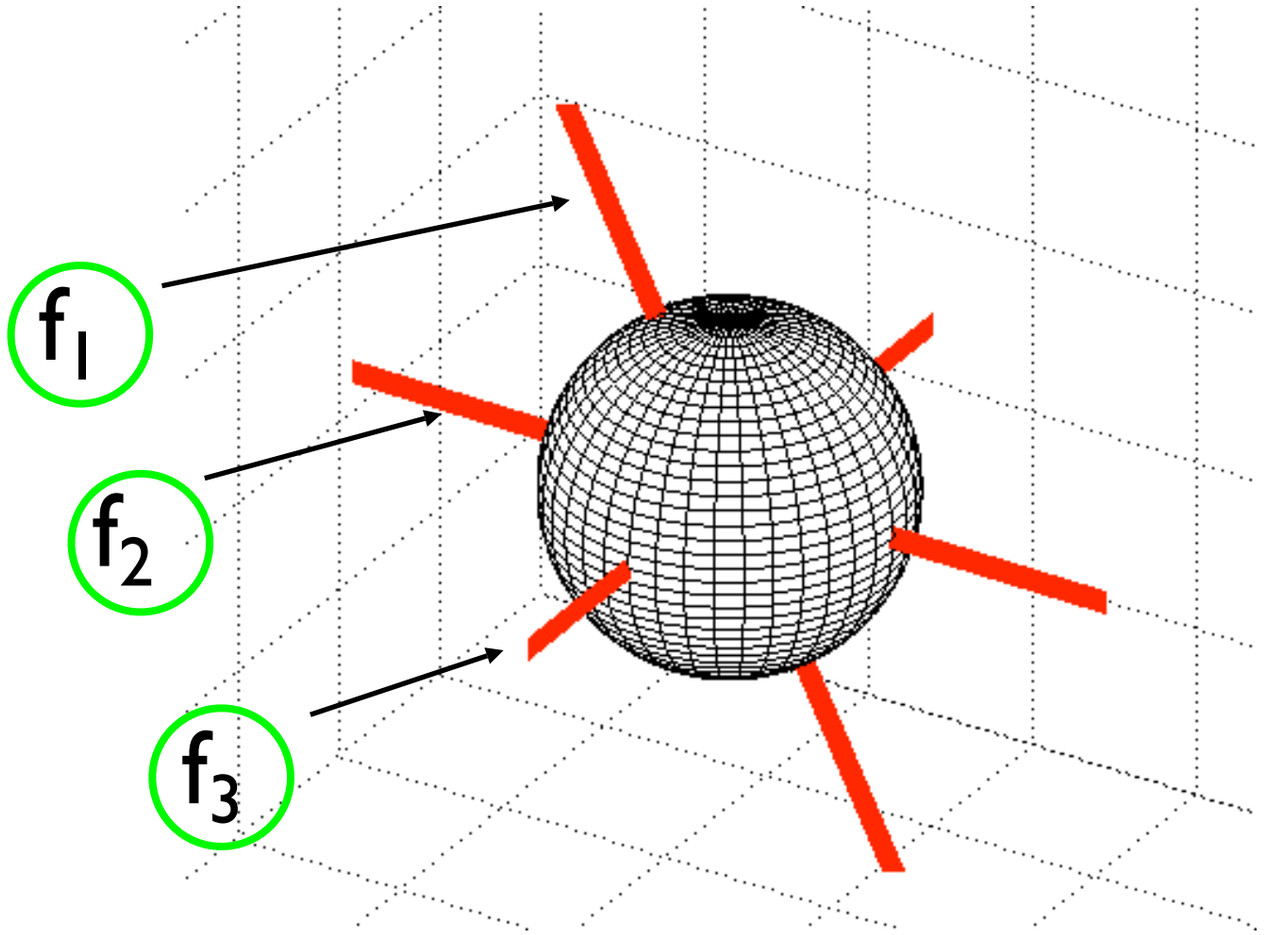
- Extra sensitivity gained from assumptions

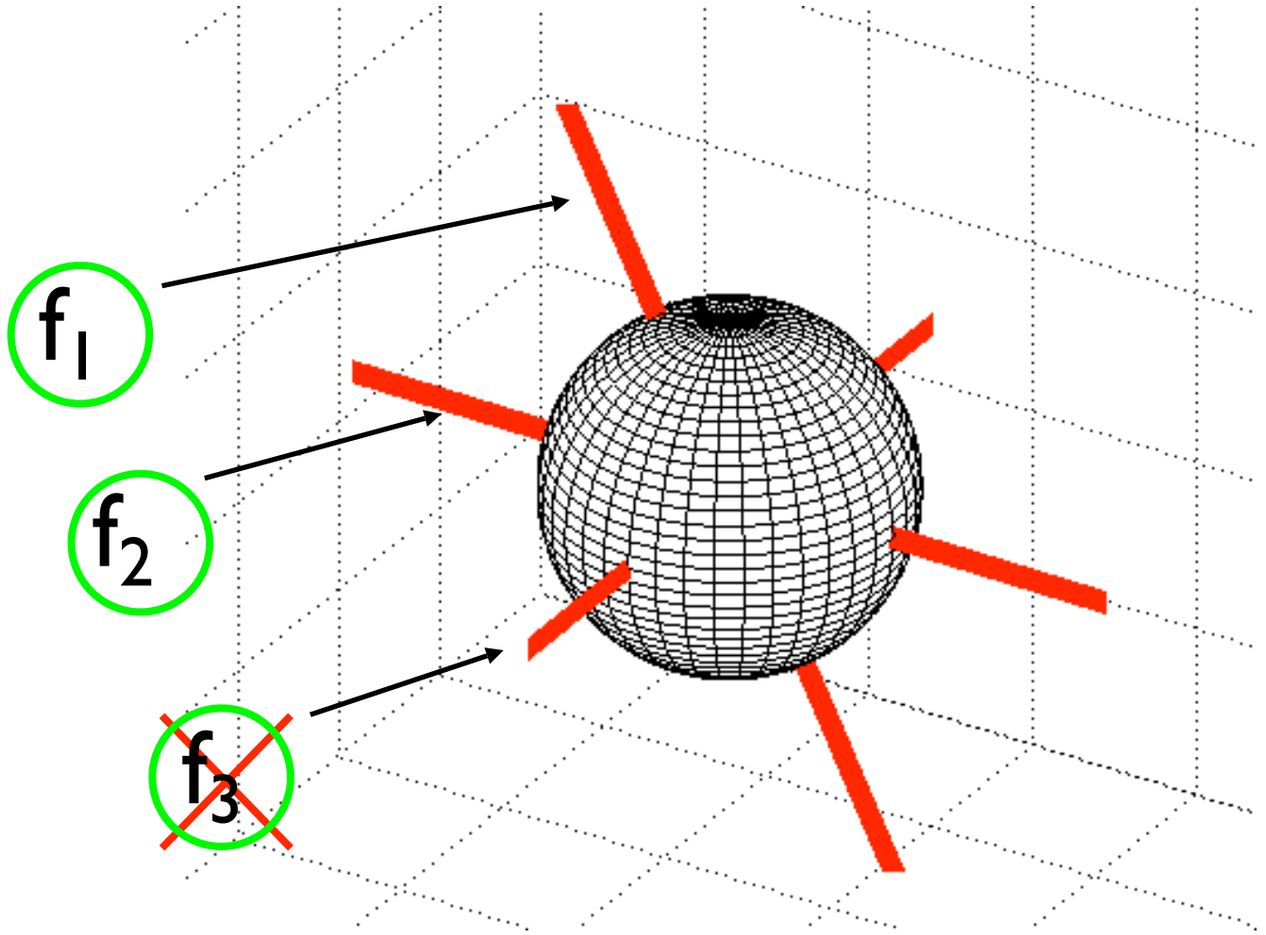


Modelling complex architecture

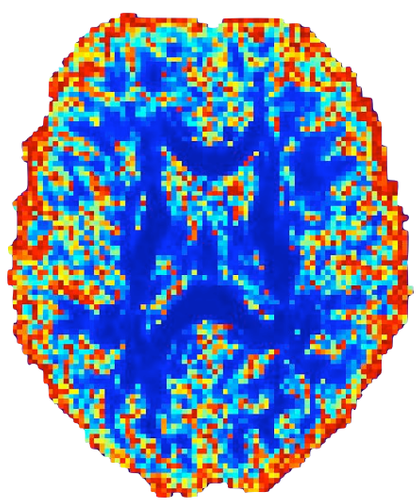
- Form testable hypotheses.
- Ask questions about parameters of interest

- Extra sensitivity gained from assumptions

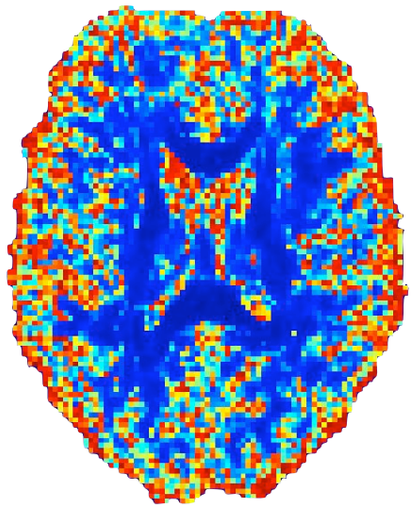
- Only estimate complexity that is supported by the data



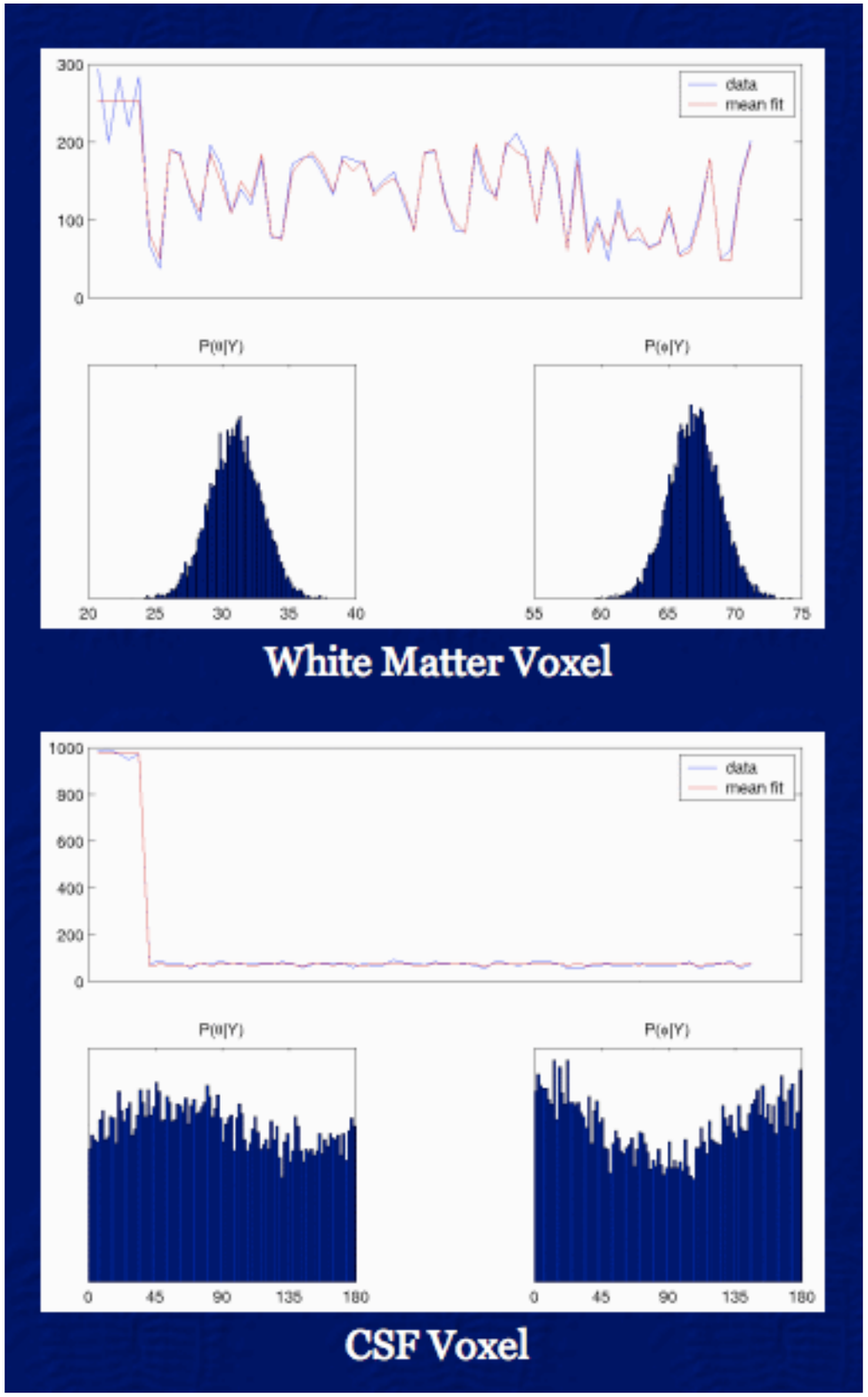
Uncertainty from a single dataset



Empirical



Bayesian

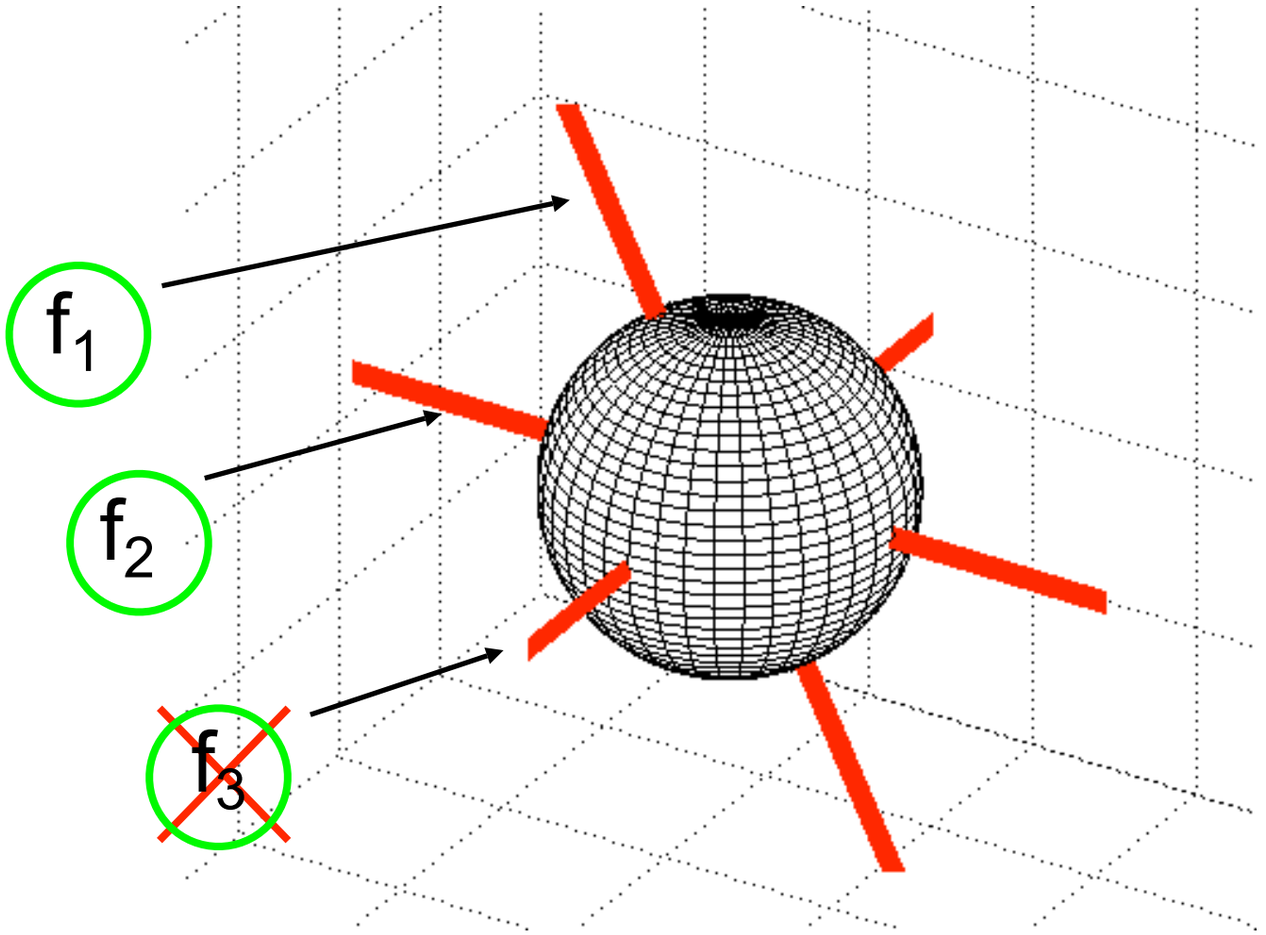


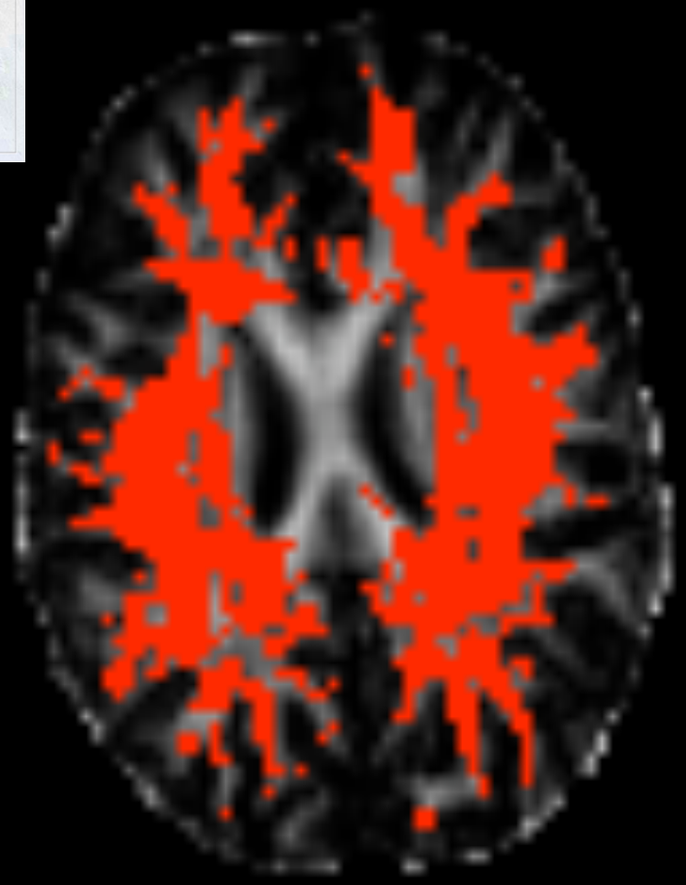
Modelling complex architecture

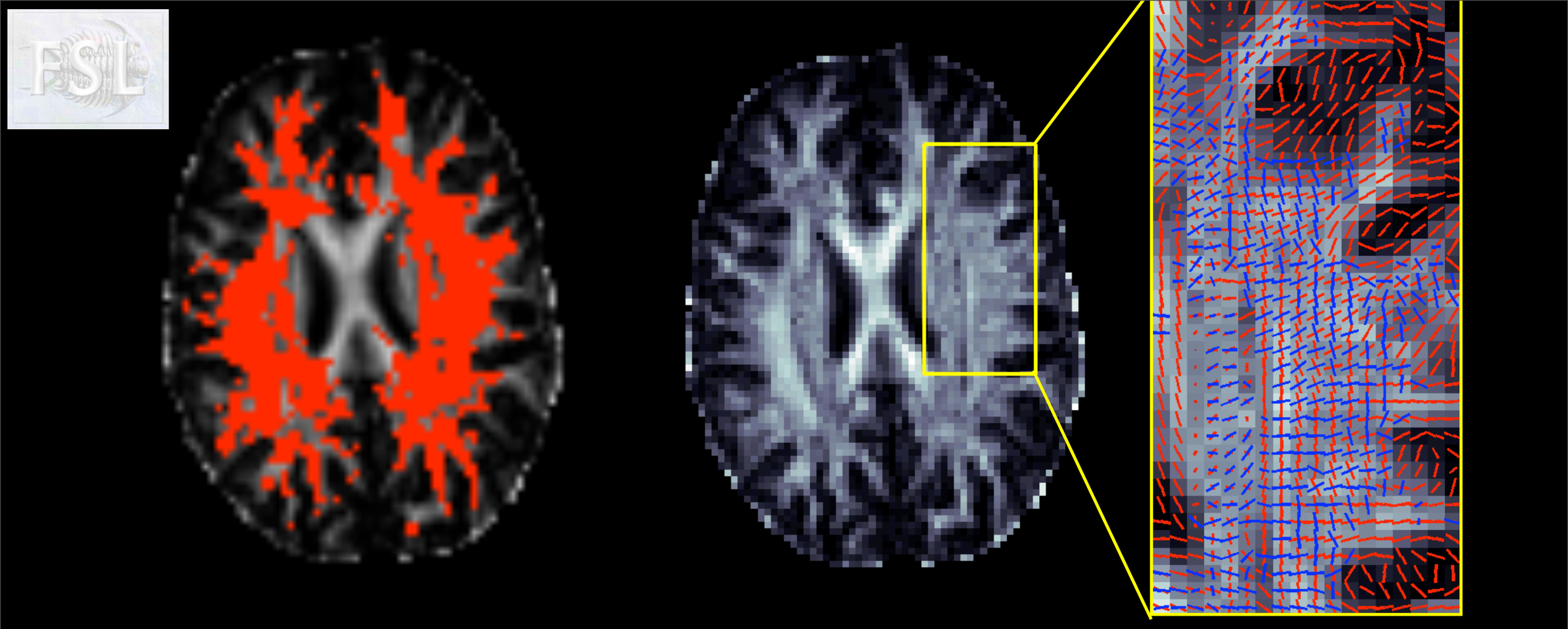
- Form testable hypotheses.
  - Ask questions about parameters of interest

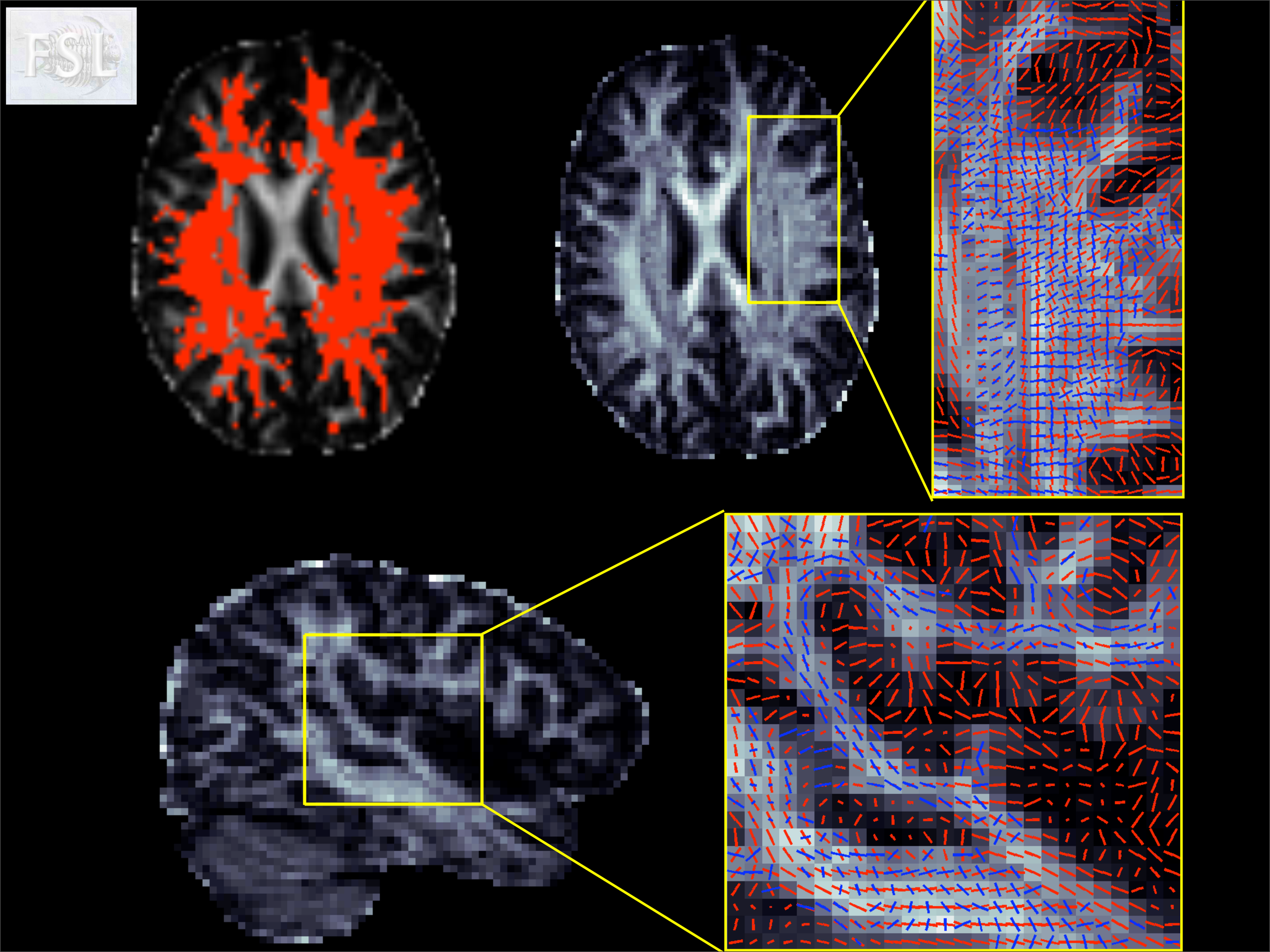
- Extra sensitivity gained from assumptions

- Only estimate complexity that is supported by the data



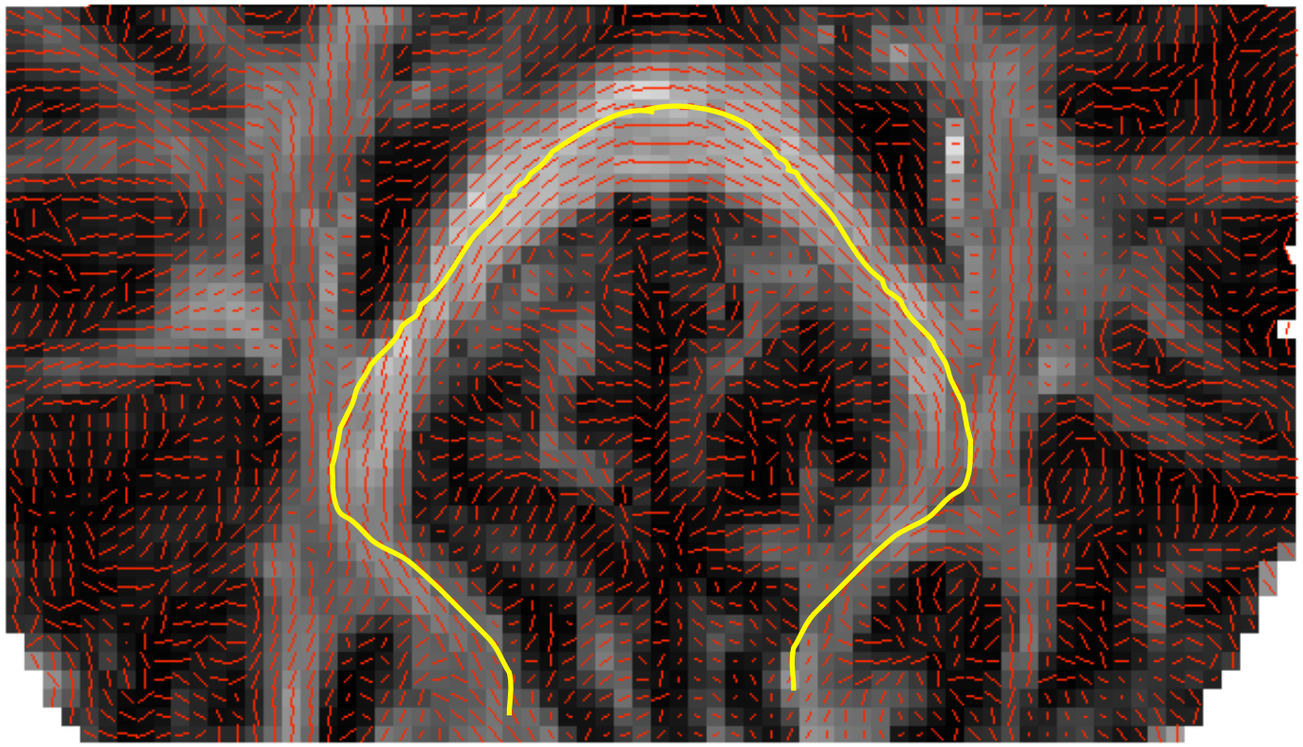




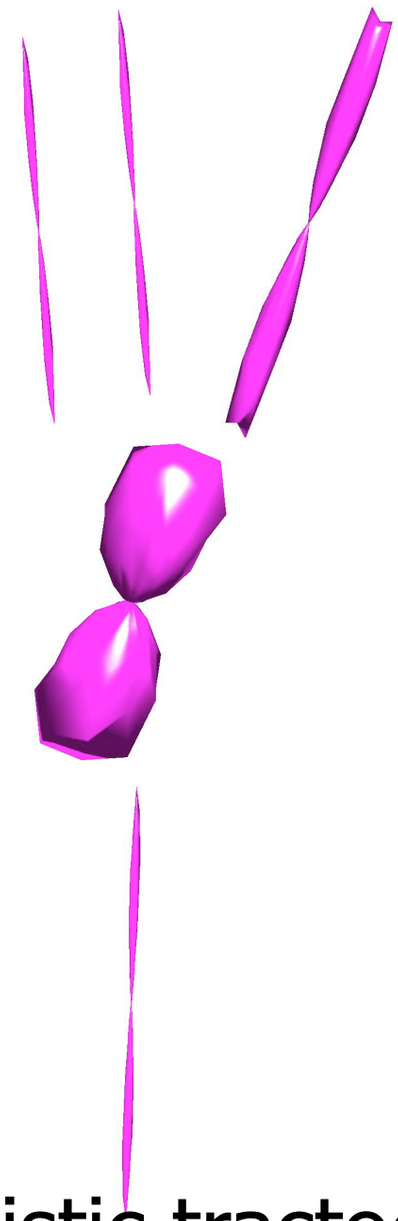


Probabilistic tractography

- But now, we no longer have a single direction at each voxel. How can we do tractography?



'Streamlining'



Probabilistic tractography

Behrens et al, 2003, Parker et al. 2003, Hagmann et al 2003, Jones et al. 2004

Probabilistic tractography

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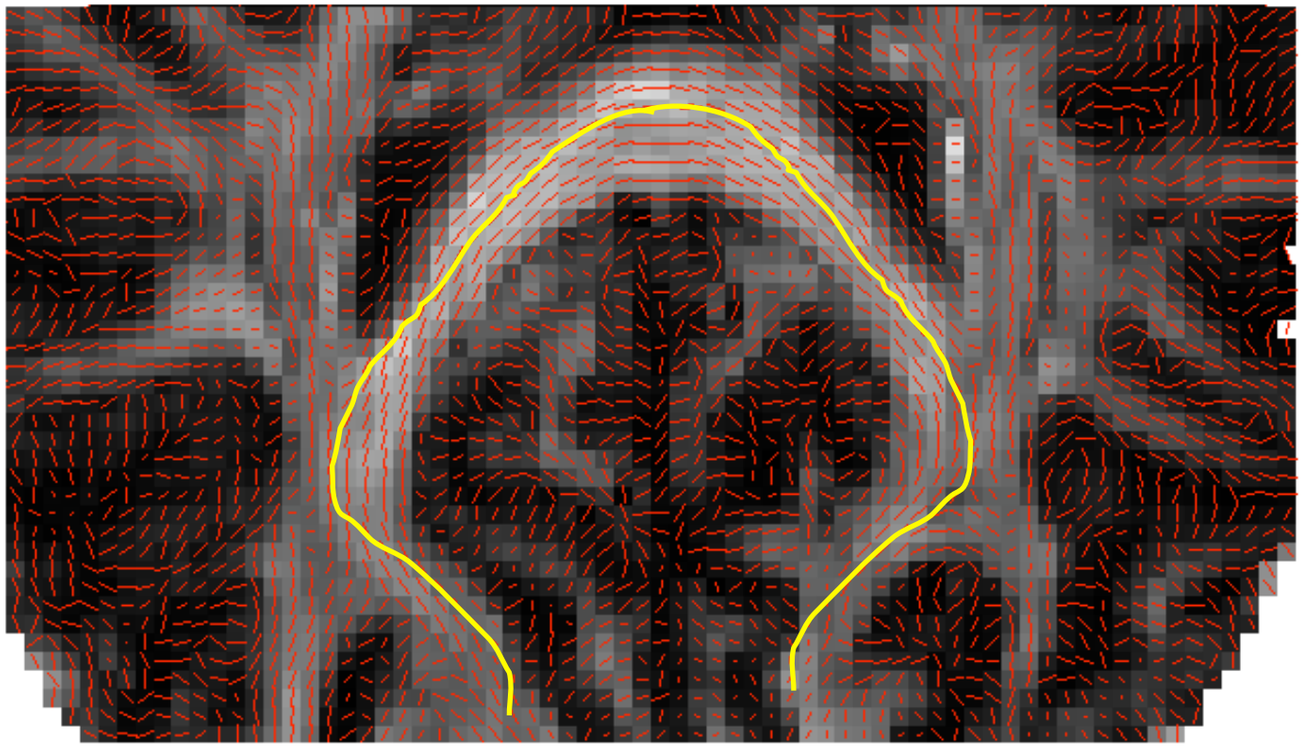

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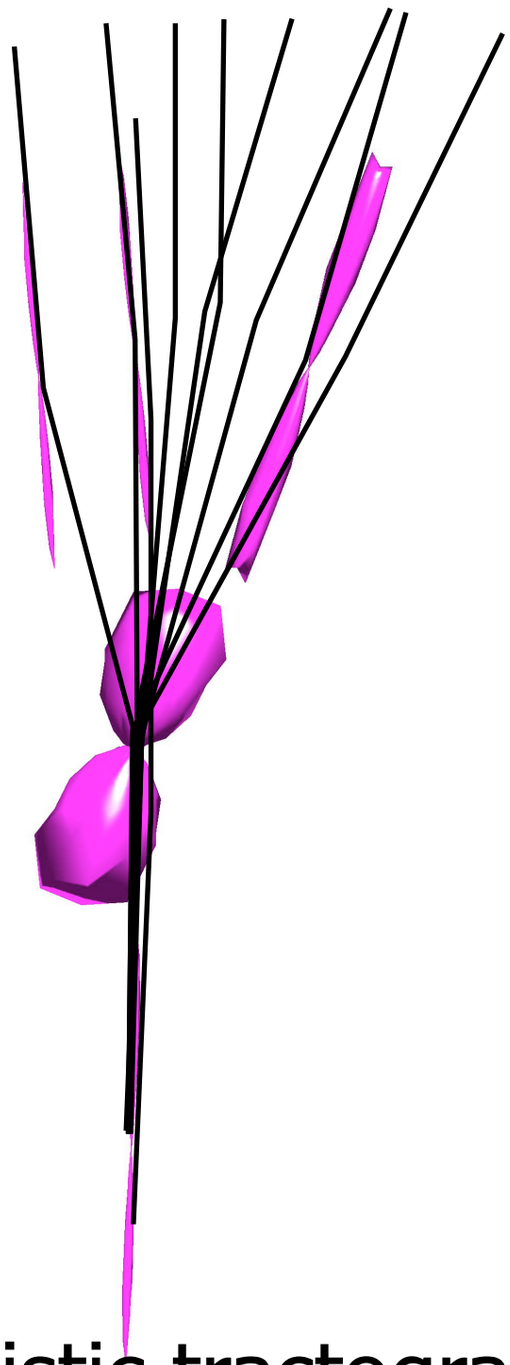

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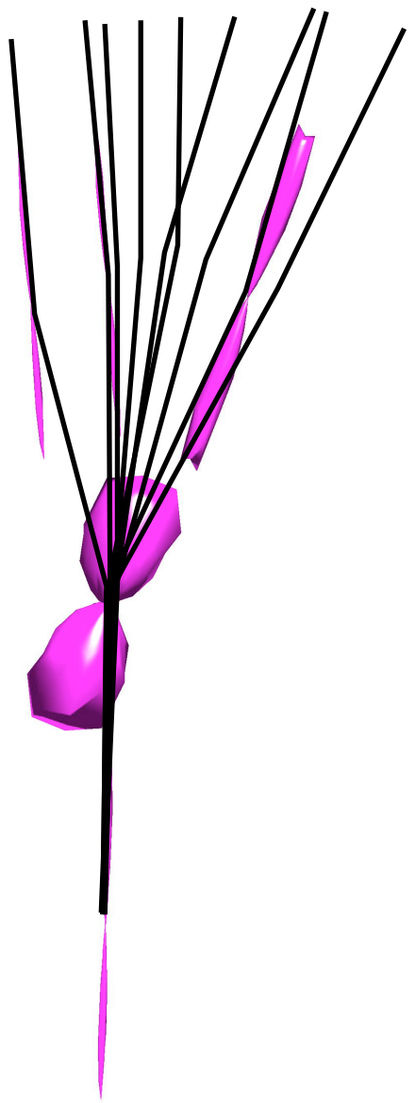
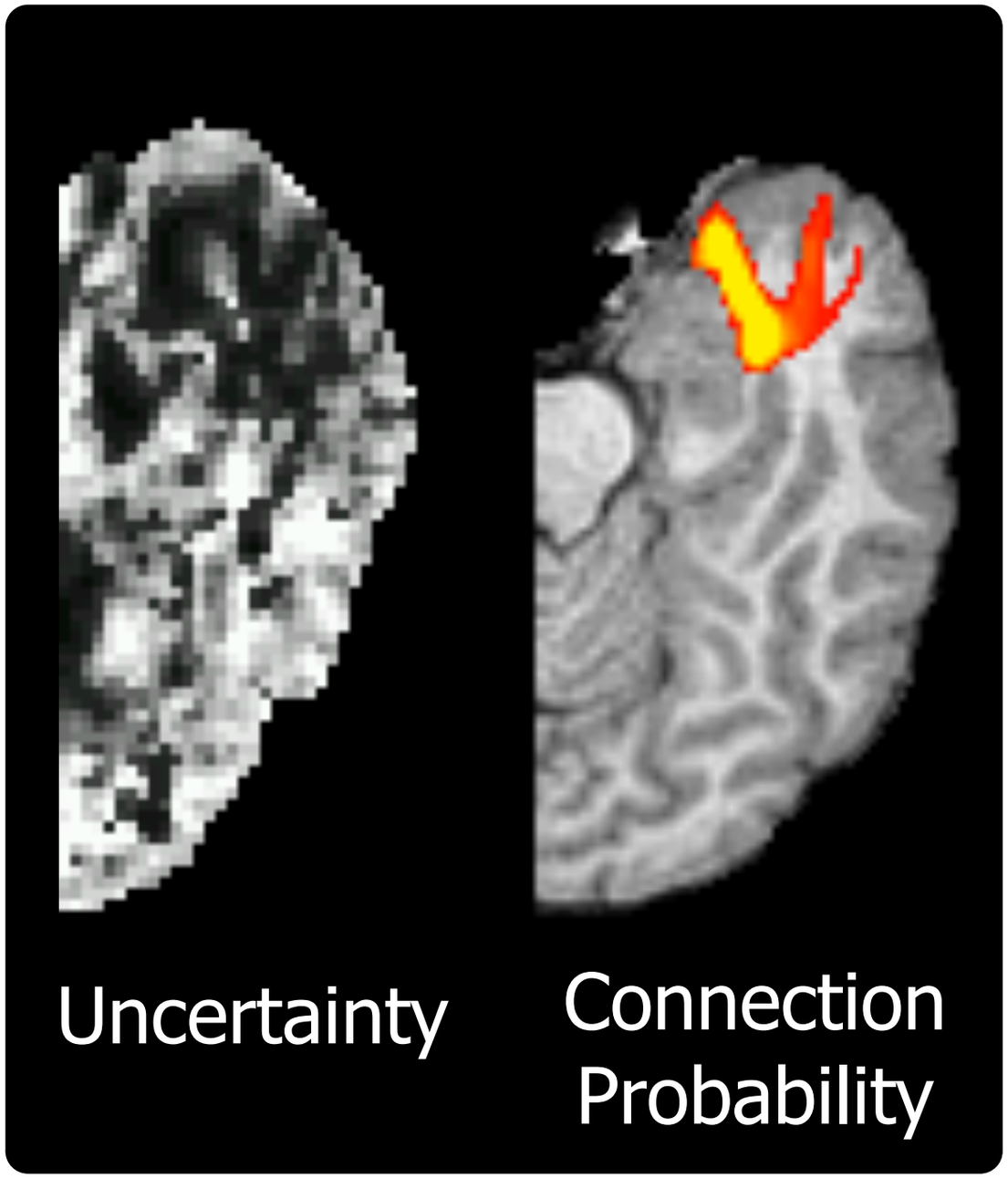
Probabilistic Tractography

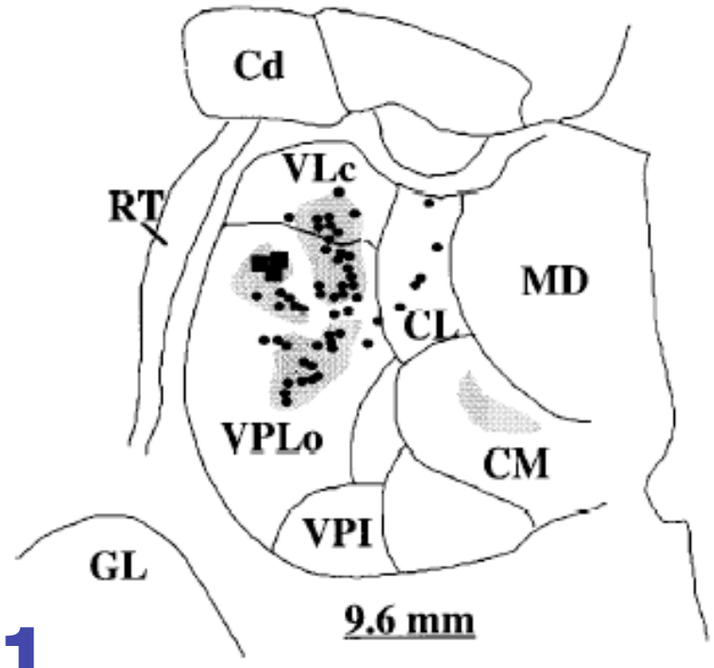




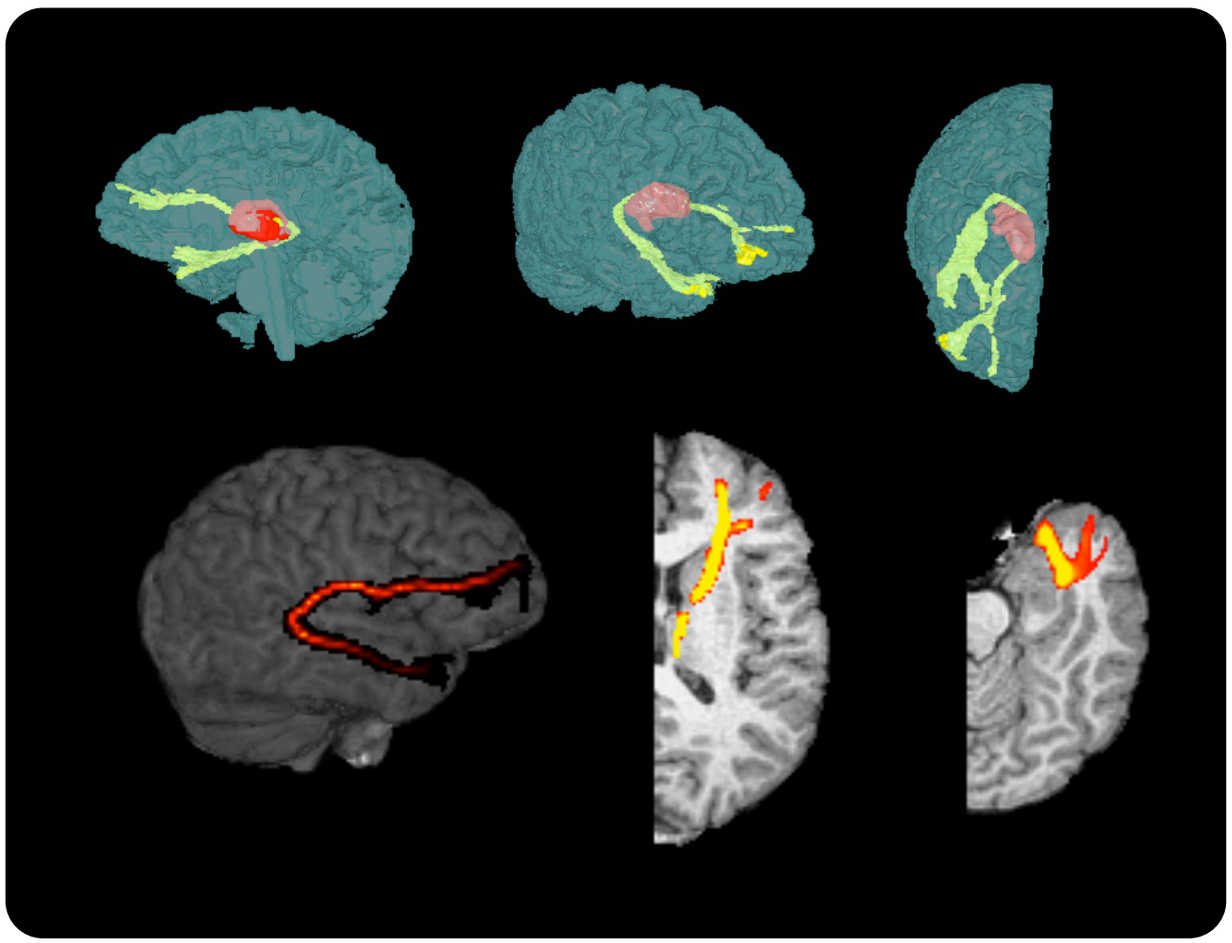
- Allows you to track into regions of low anisotropy, eg grey matter
- Provides quantitative (see later) probability of connection from A to B

Behrens et al, MRM, 2003

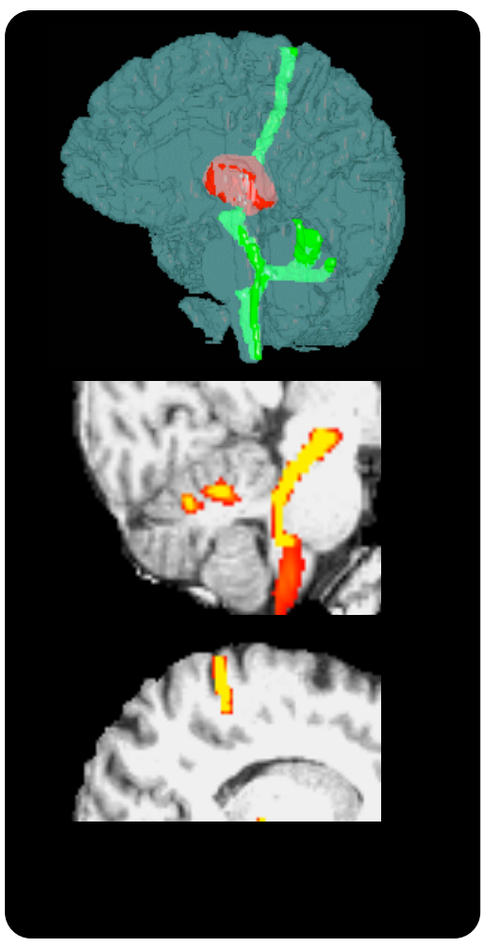
Thalamic connections with cortex



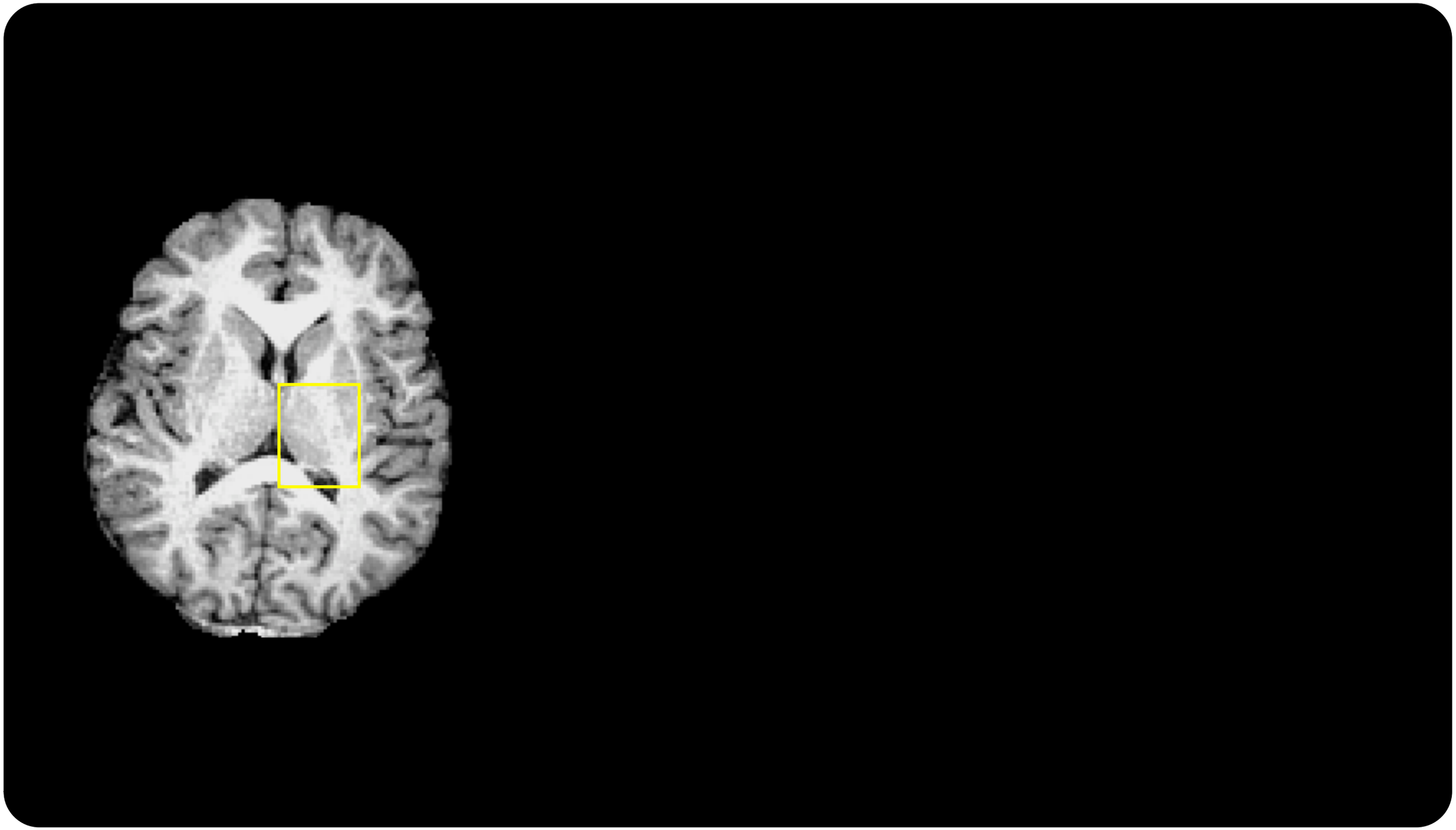
MD -> PFC



VL –> M1



Connectivity-based classification of thalamic voxels produces clusters



Behrens, Johansen-Berg et al, Nature Neuroscience, 2003

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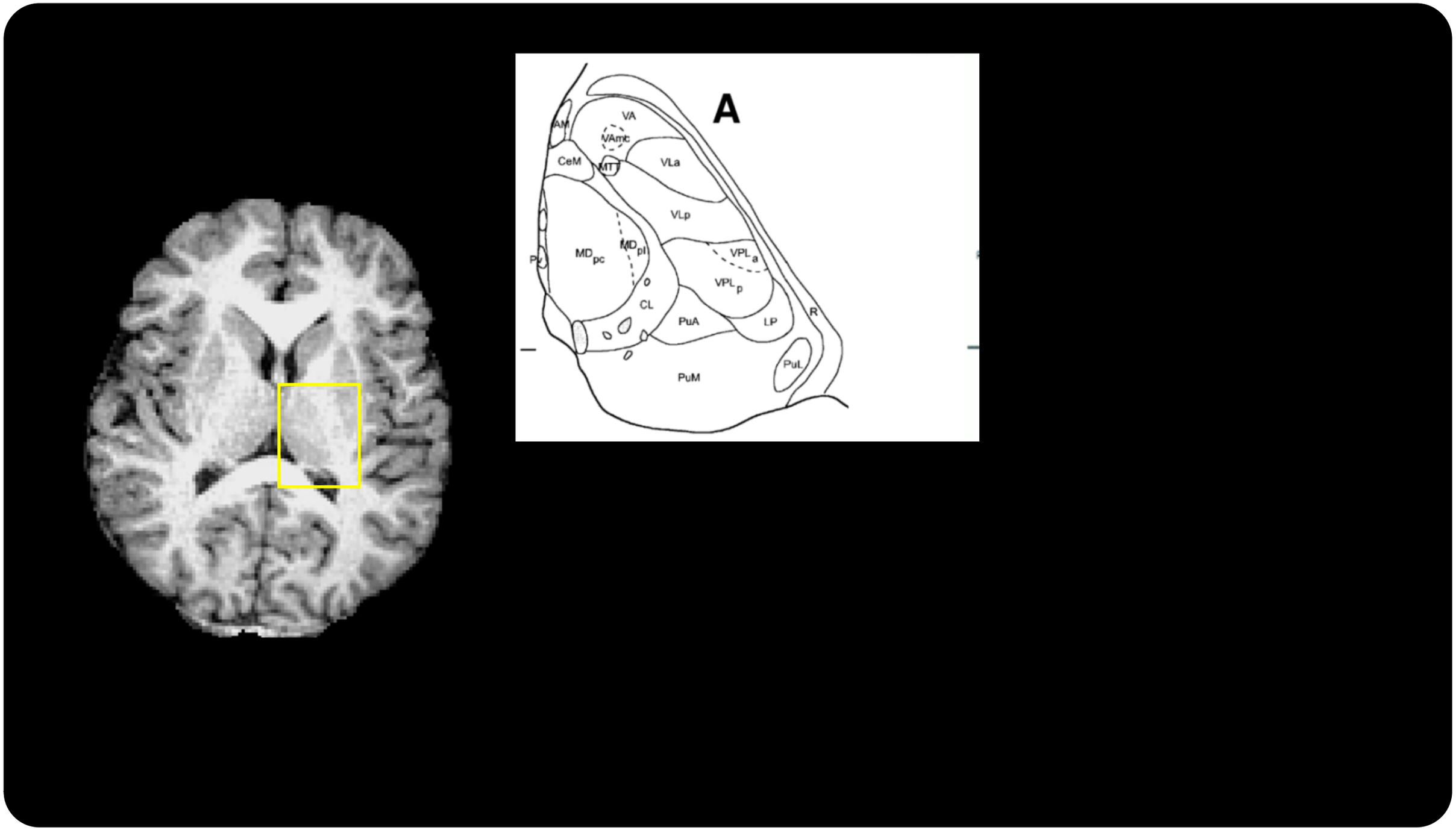

Behrens, Johansen-Berg et al, Nature Neuroscience, 2003

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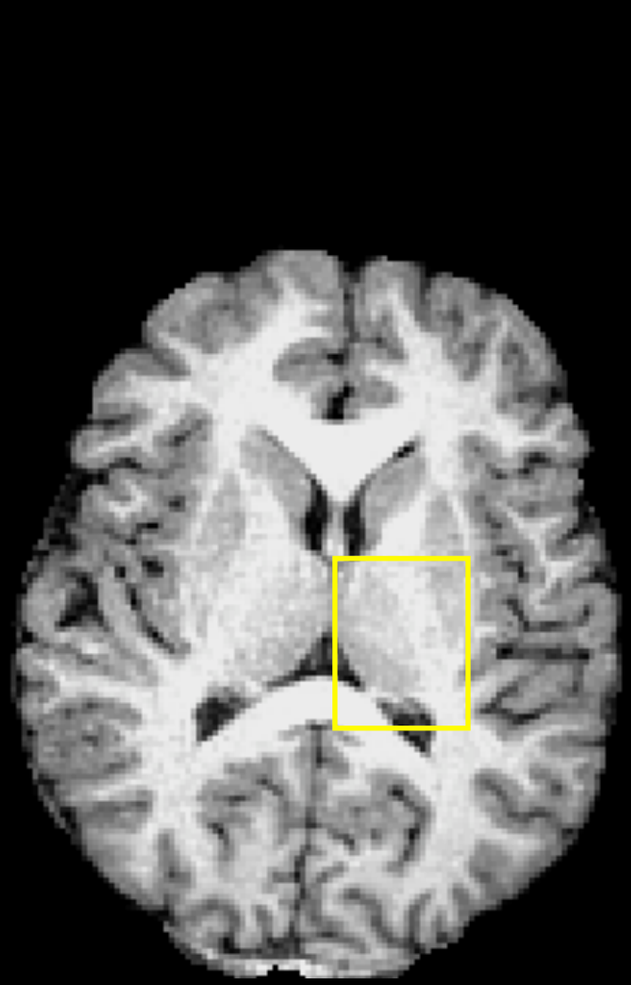

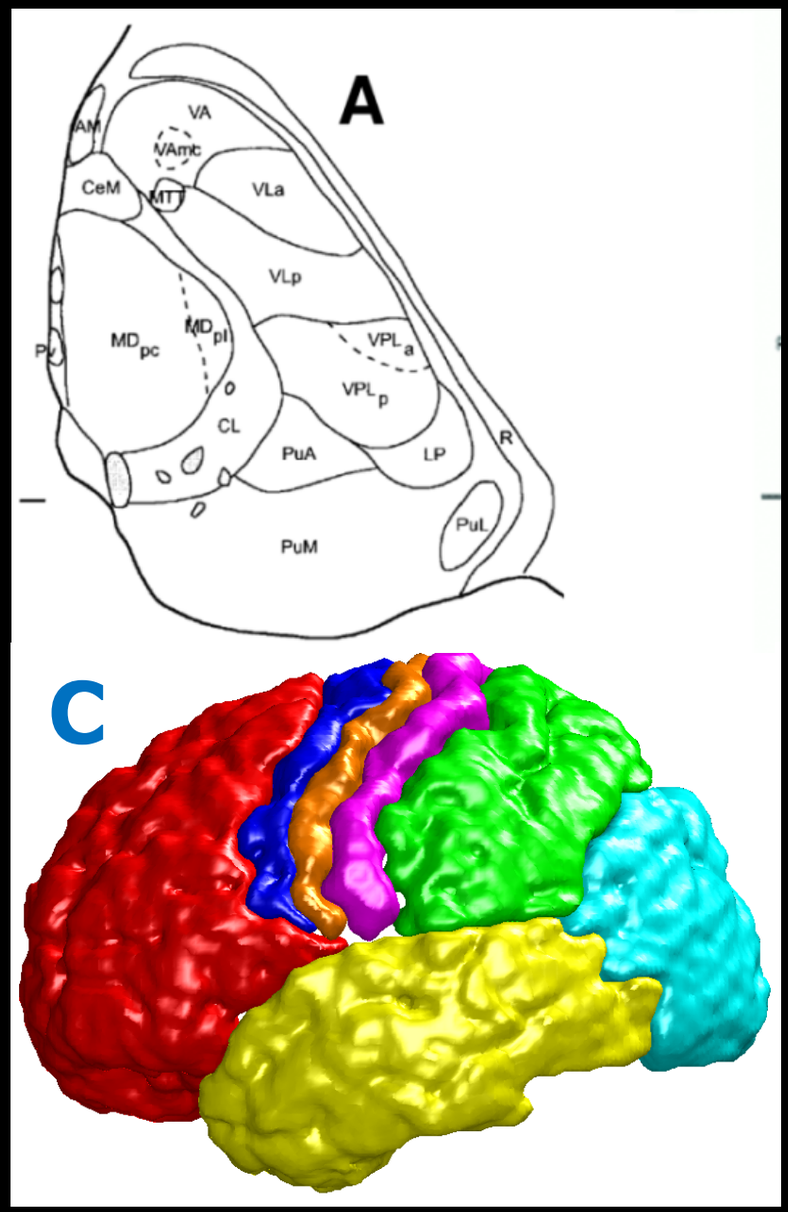

Behrens, Johansen-Berg et al, Nature Neuroscience, 2003

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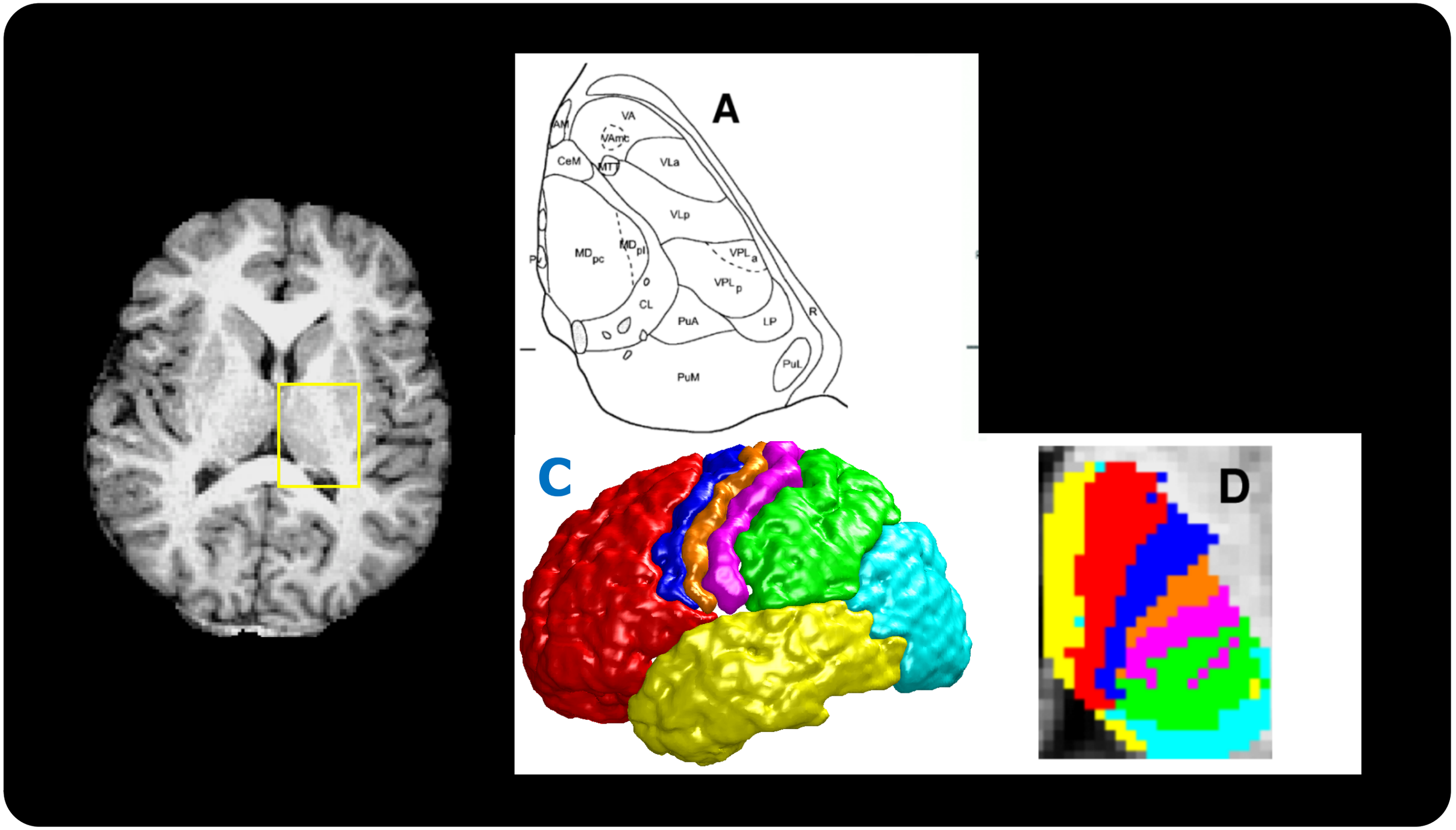

Behrens, Johansen-Berg et al, Nature Neuroscience, 2003

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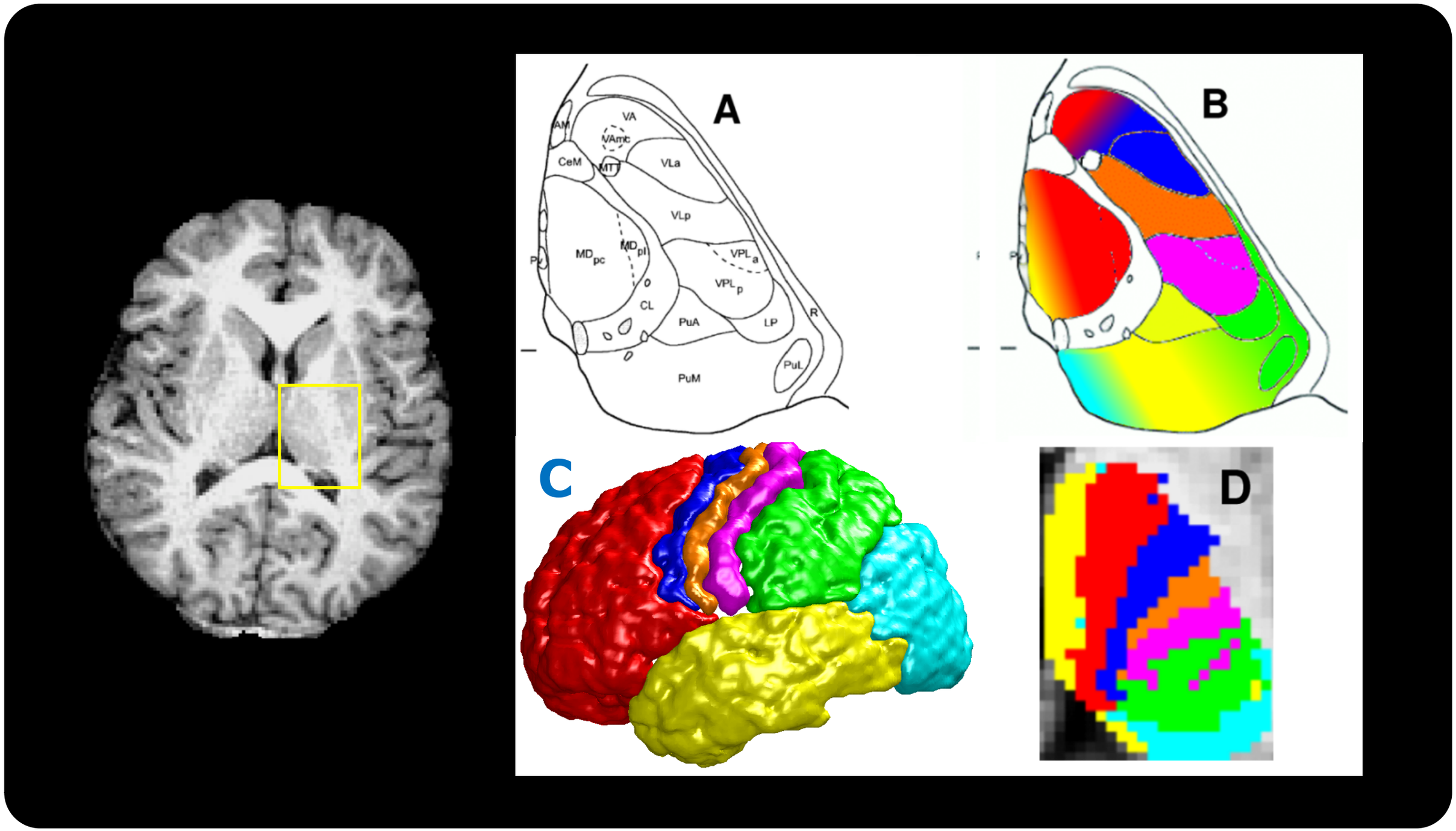
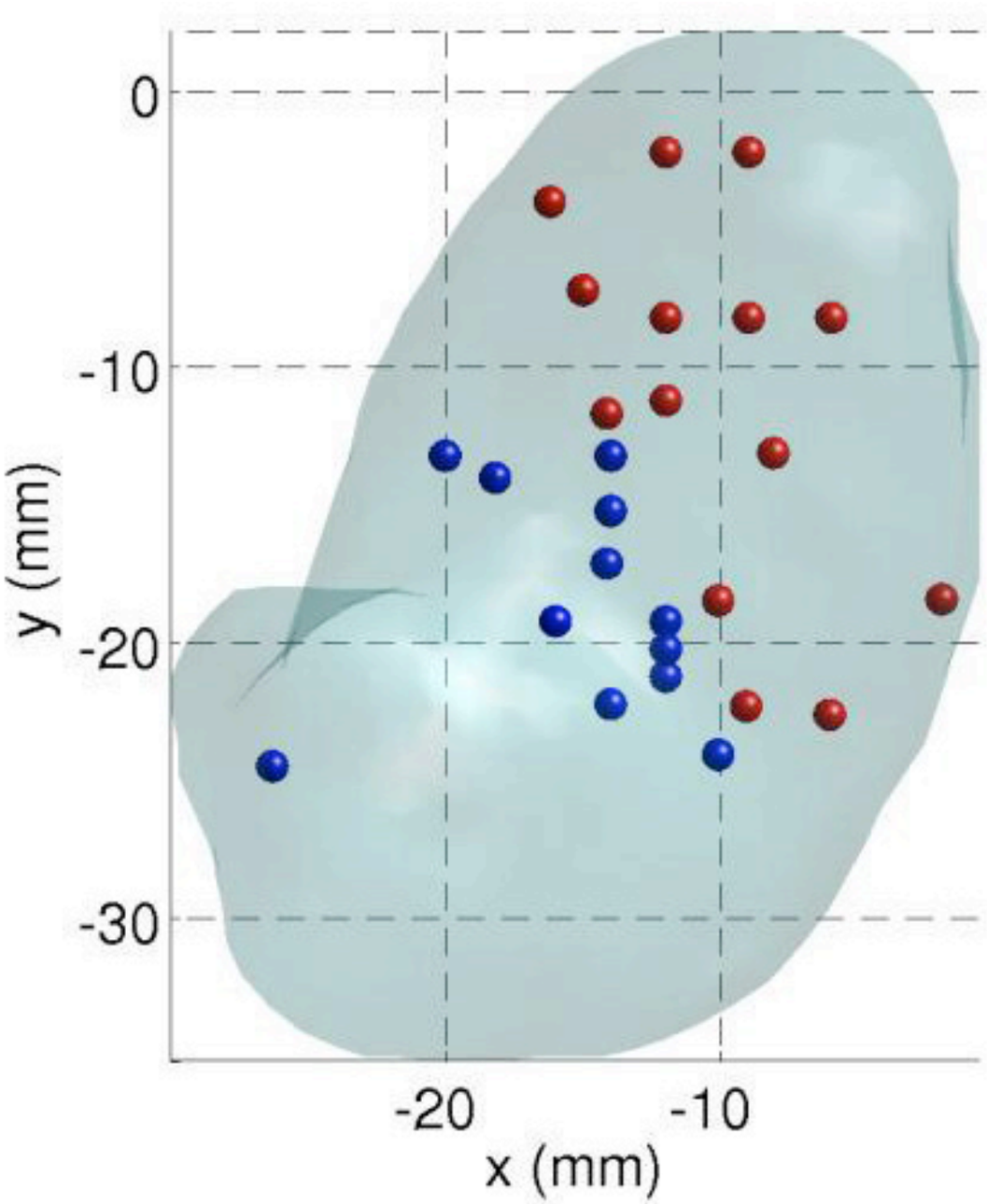
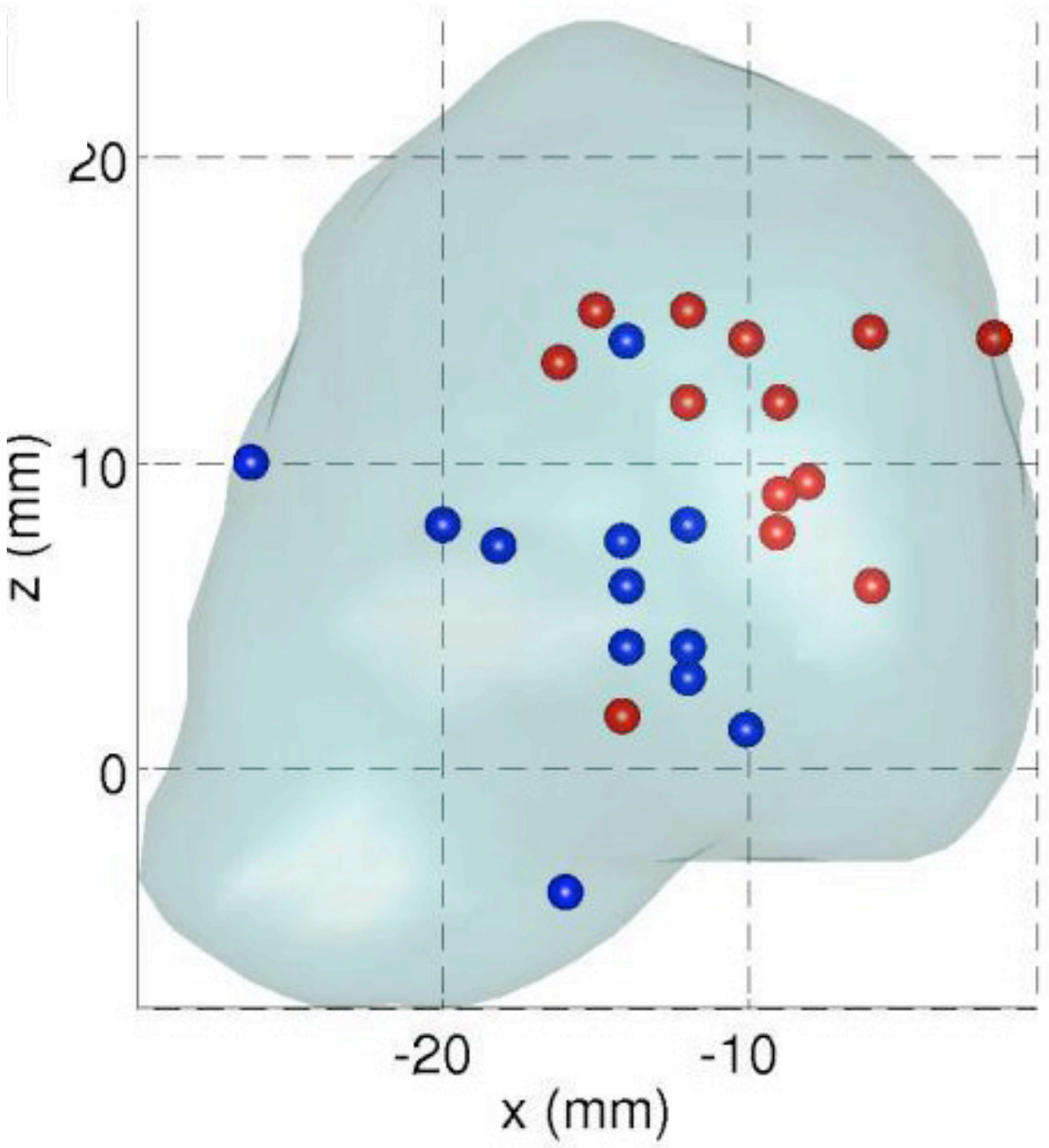


Behrens, Johansen-Berg et al, Nature Neuroscience, 2003

Functional validation: meta-analysis of FMRI activations within thalamus



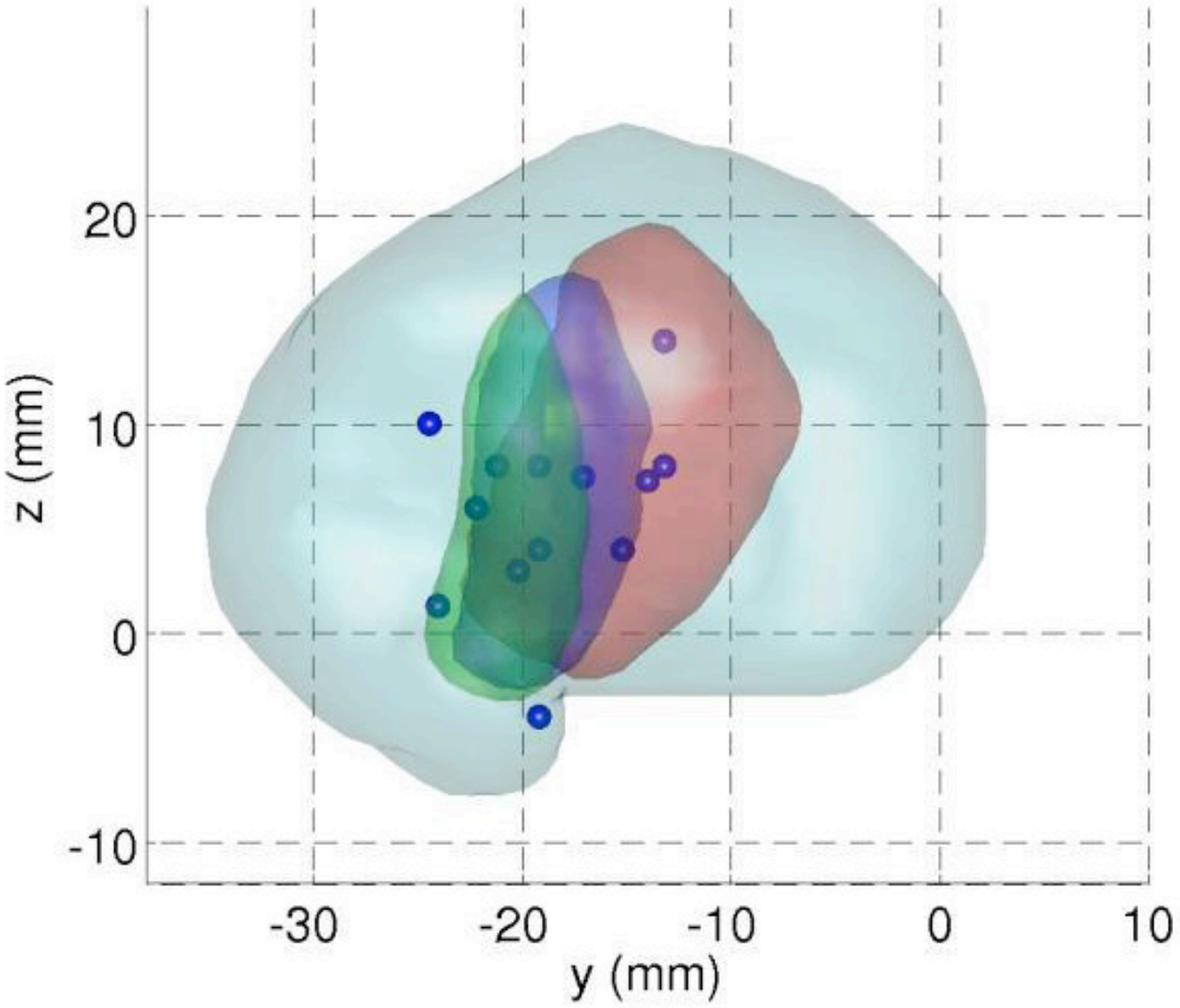


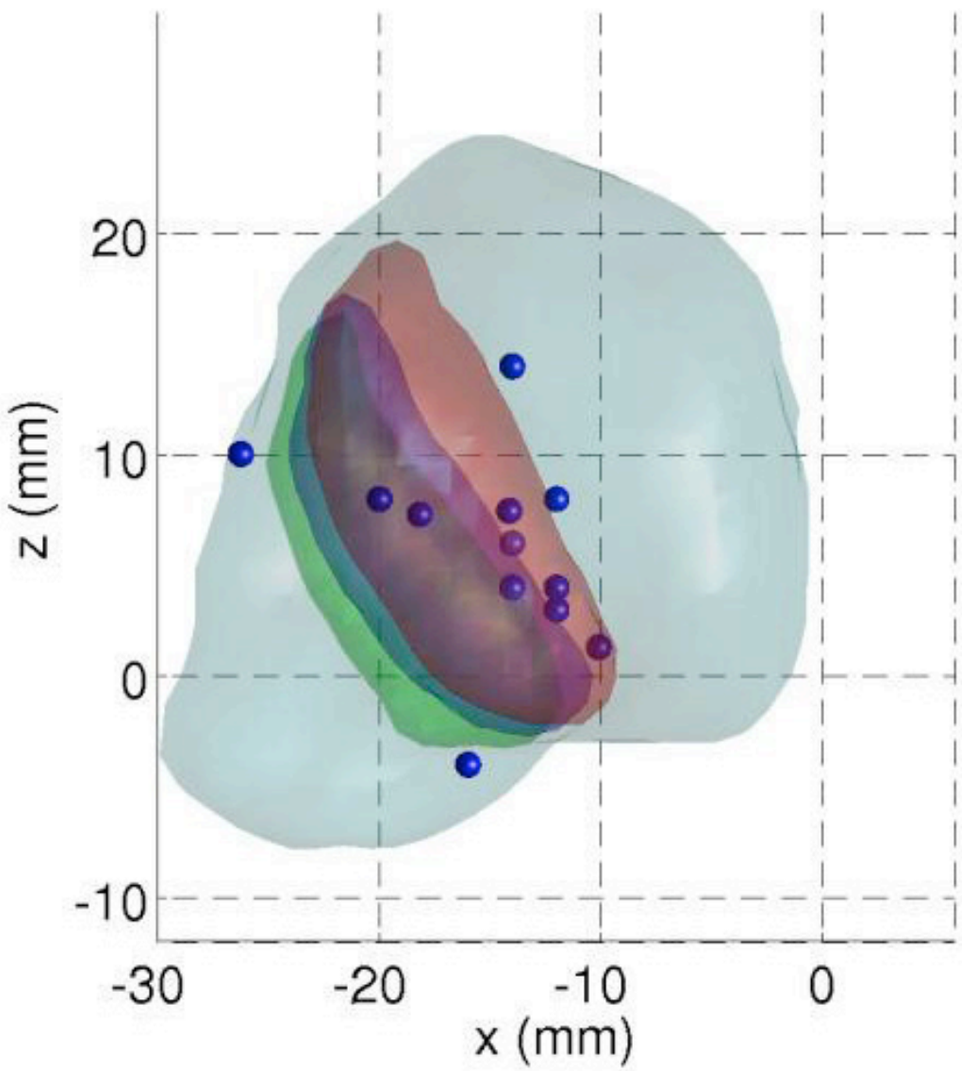
Executive tasks

Motor tasks

Johansen-Berg et al, Cerebral Cortex, 2005

Correspondence between functional activations and connectivity-defined volumes: motor tasks





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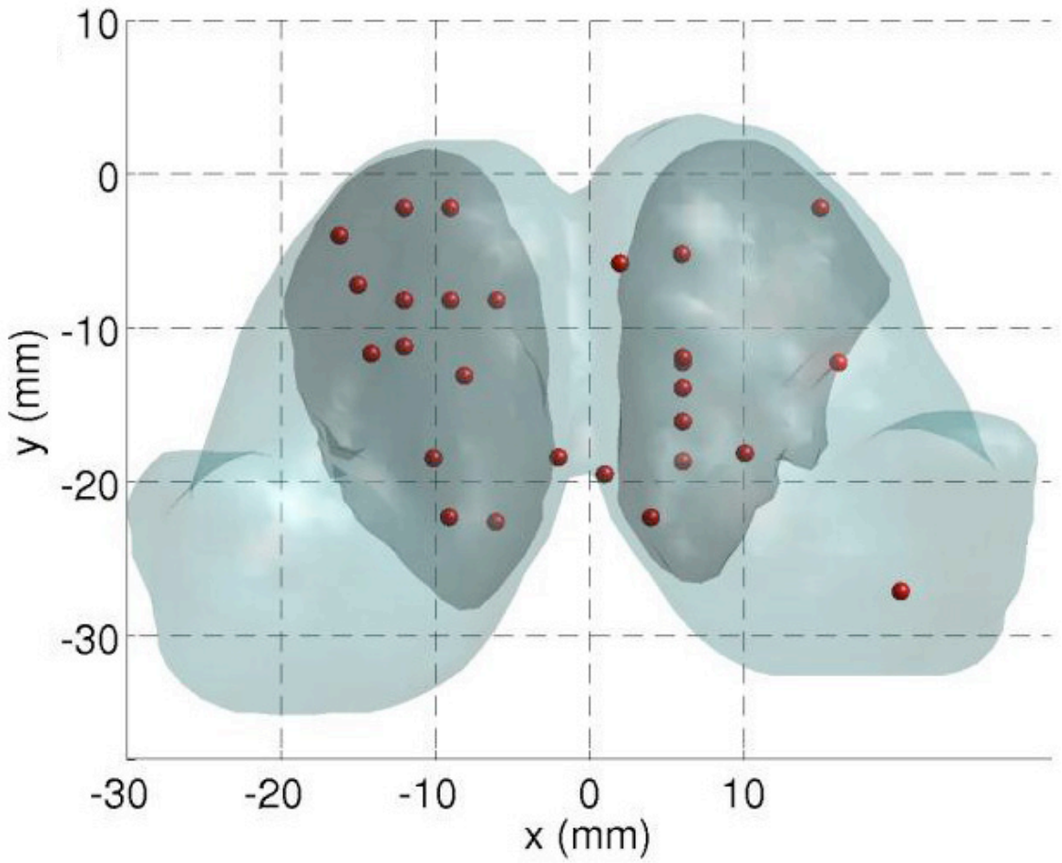
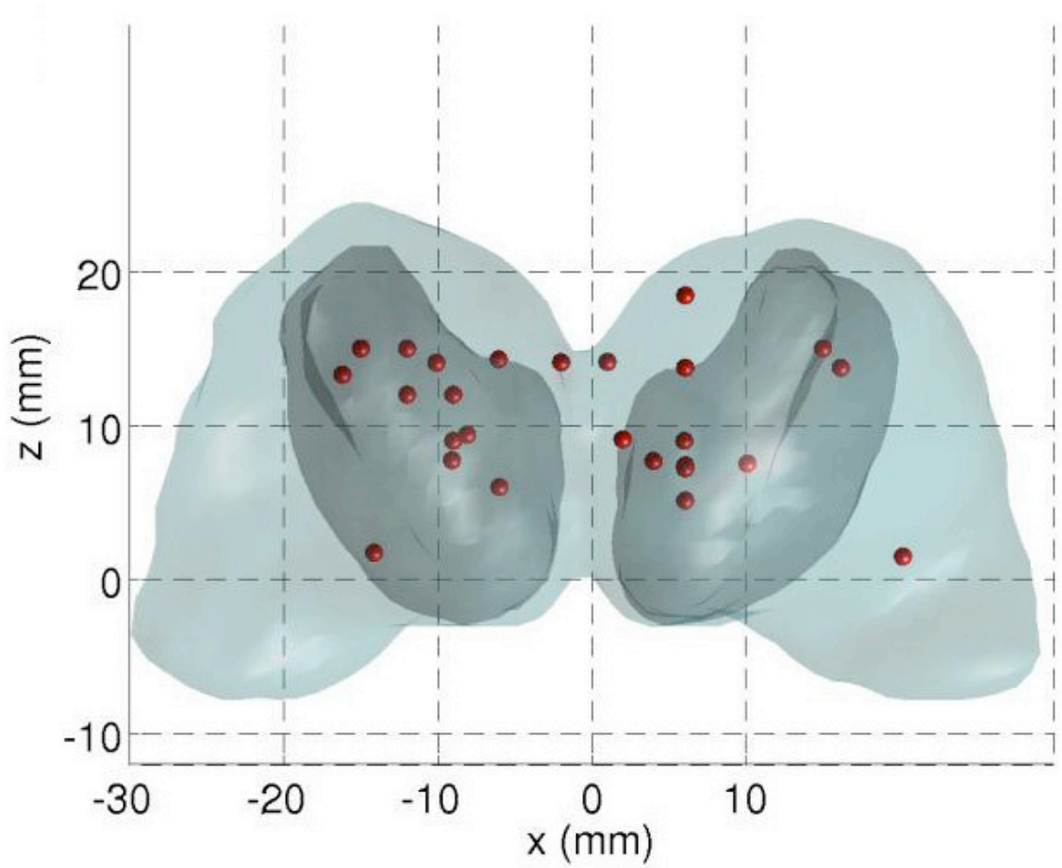
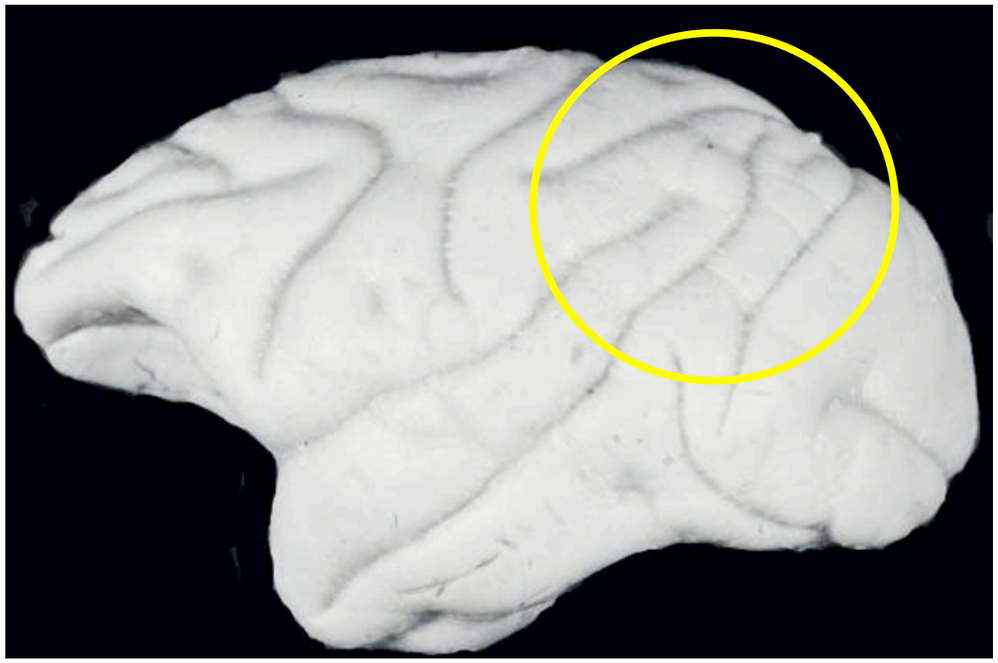
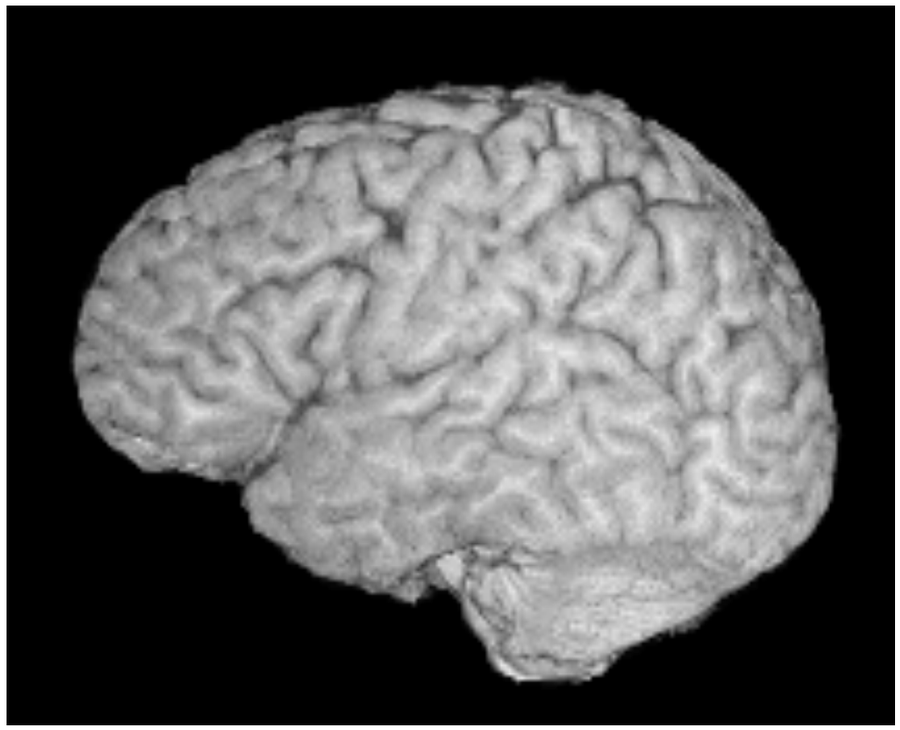




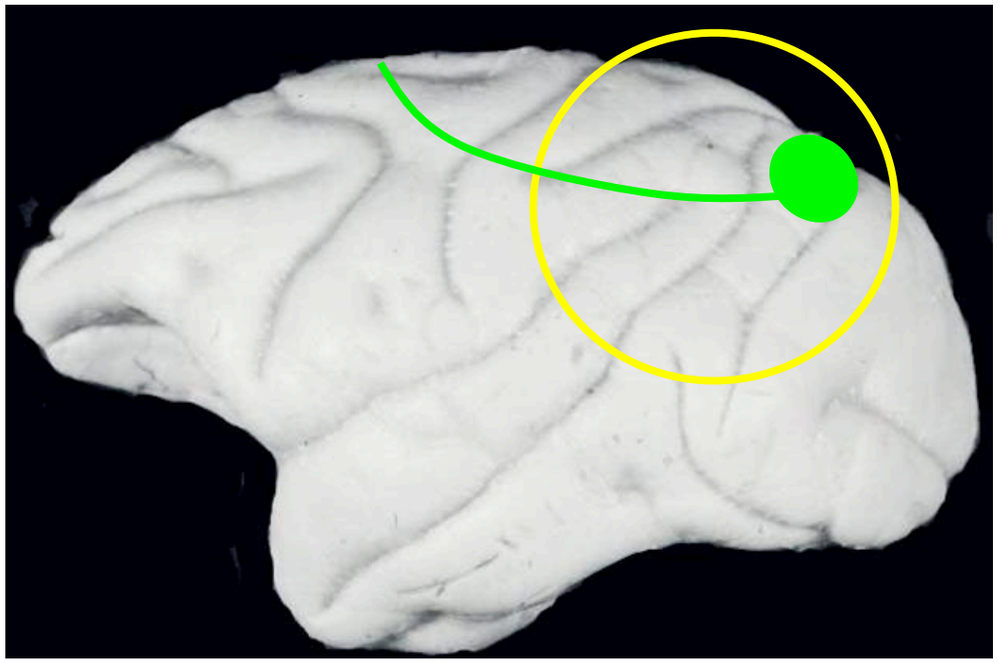
Parieto-premotor connections

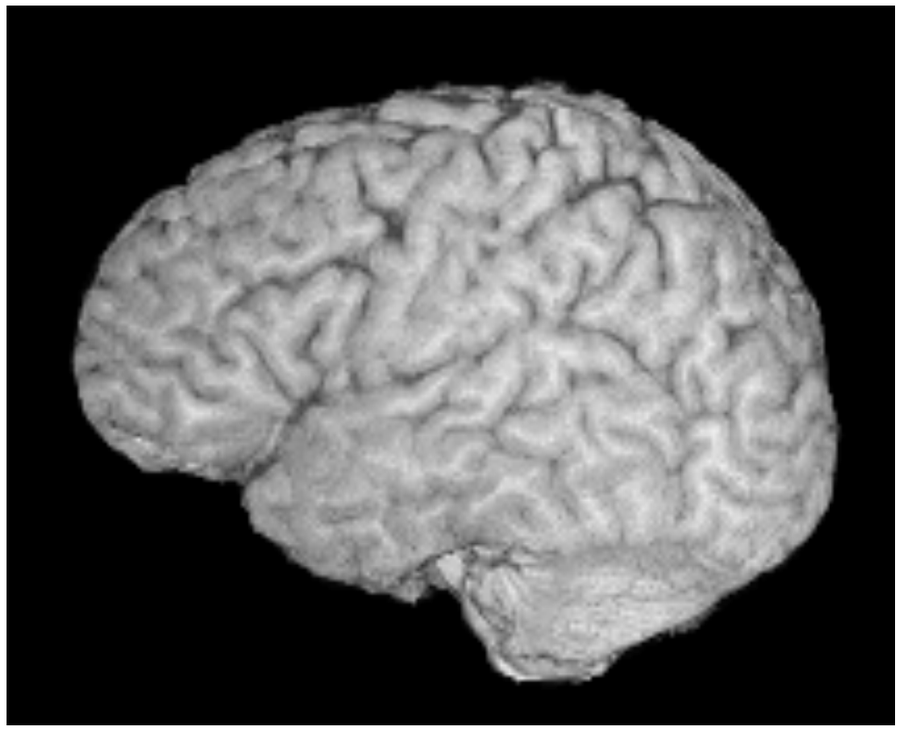




Behrens and Rushworth

Parieto-premotor connections





Posterior PL <->Anterior PMC

Behrens and Rushworth

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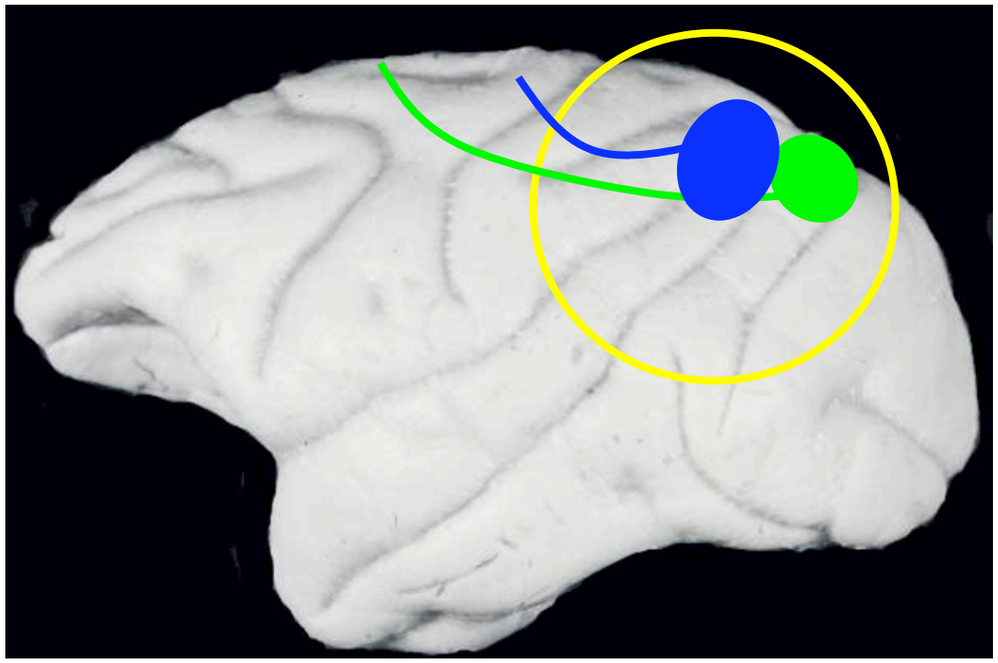

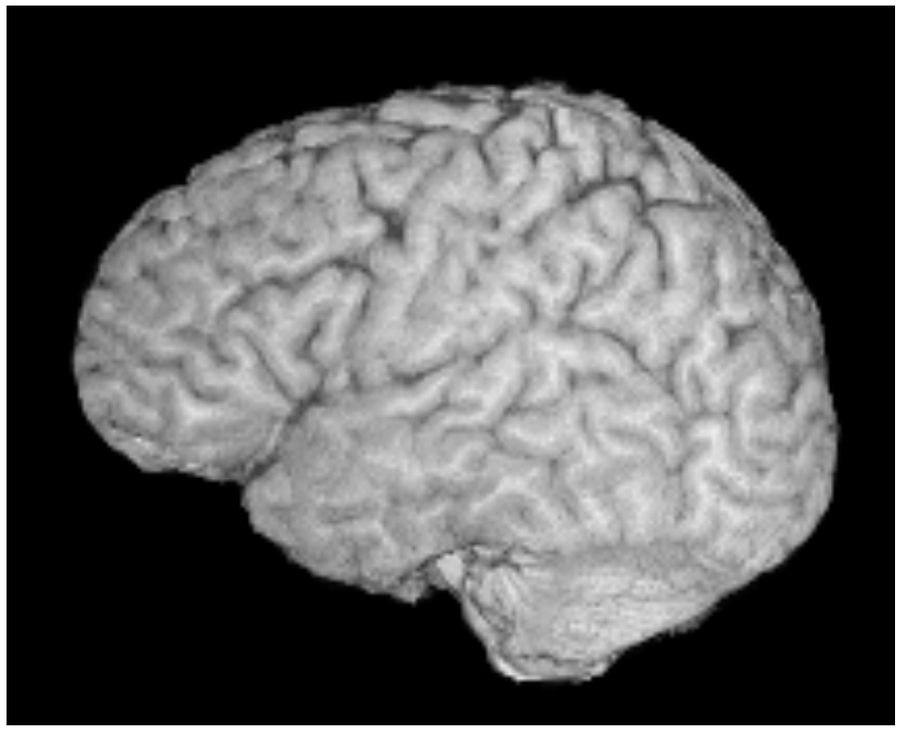

Posterior PL <->Anterior PMC

Anterior PL <-> Posterior PMC

Behrens and Rushworth

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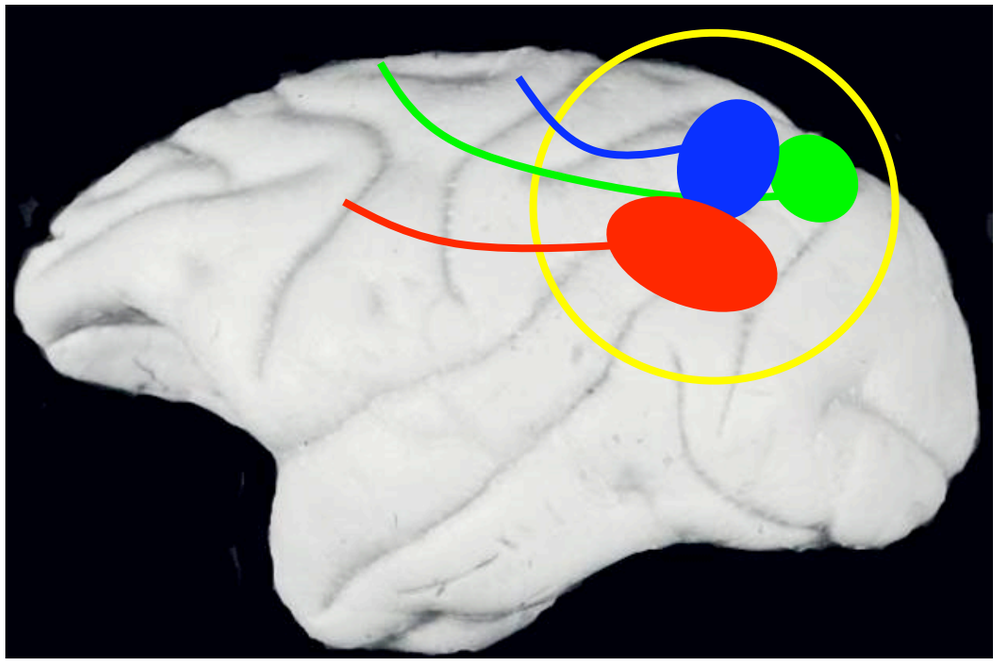
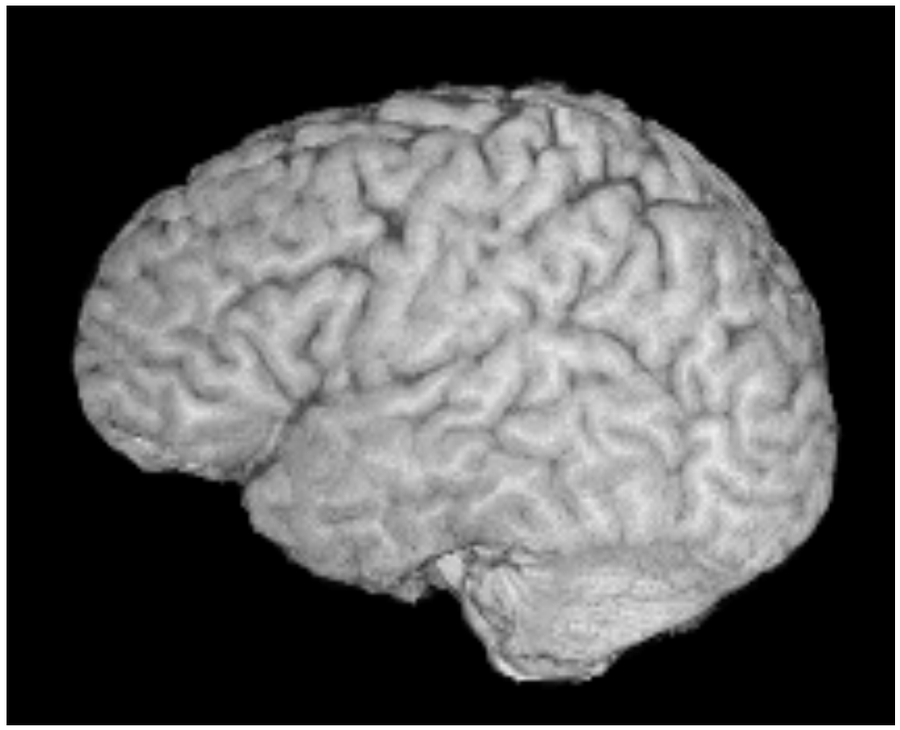




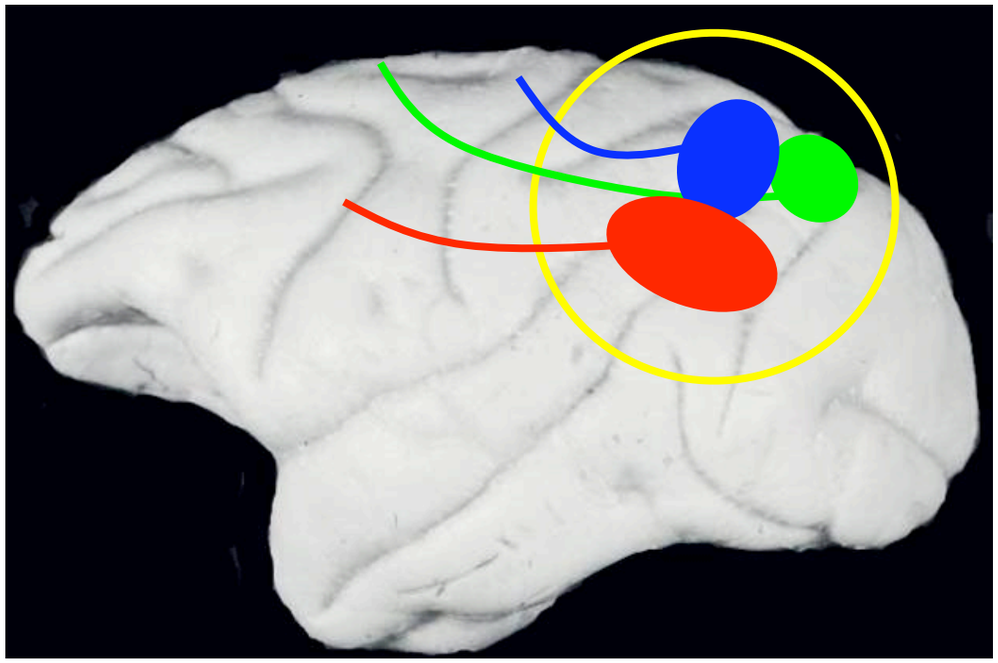
Posterior PL <->Anterior PMC

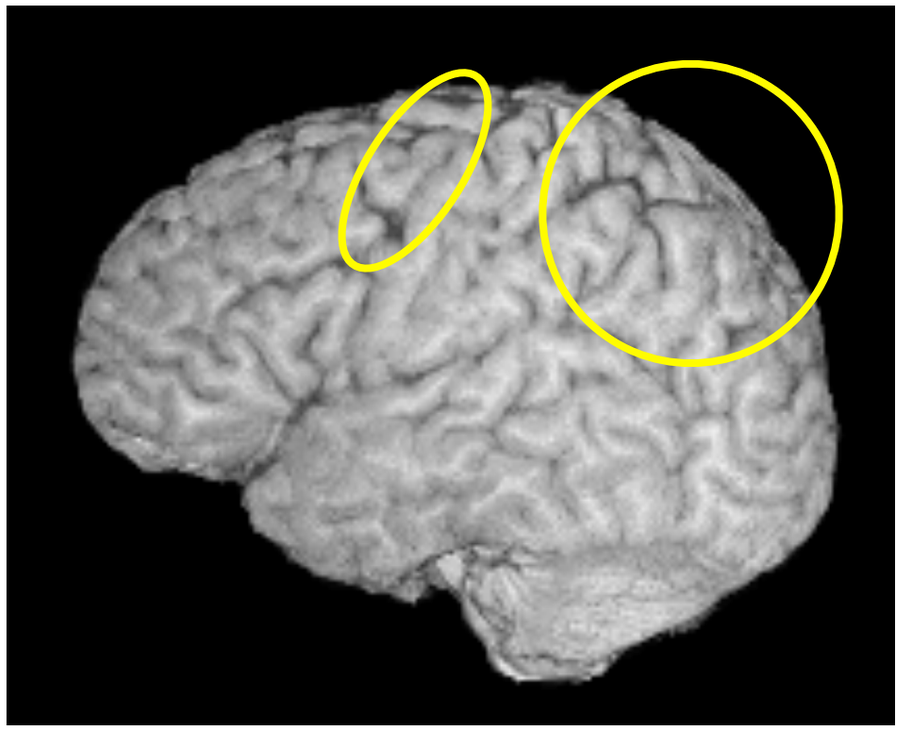
Anterior PL <-> Posterior PMC

Lateral PL <-> Frontal Eye Fields

Behrens and Rushworth

Parieto-premotor connections





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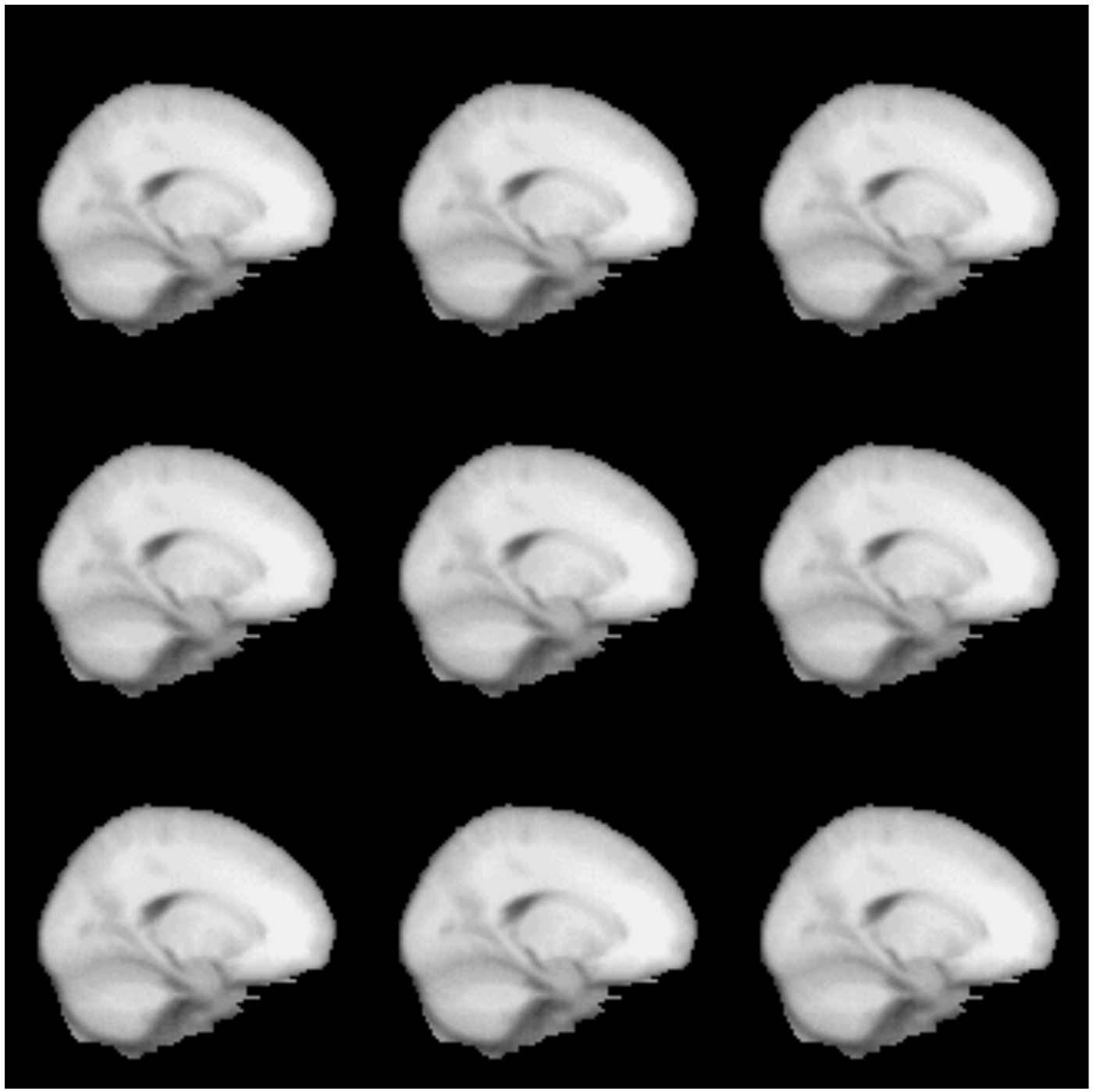
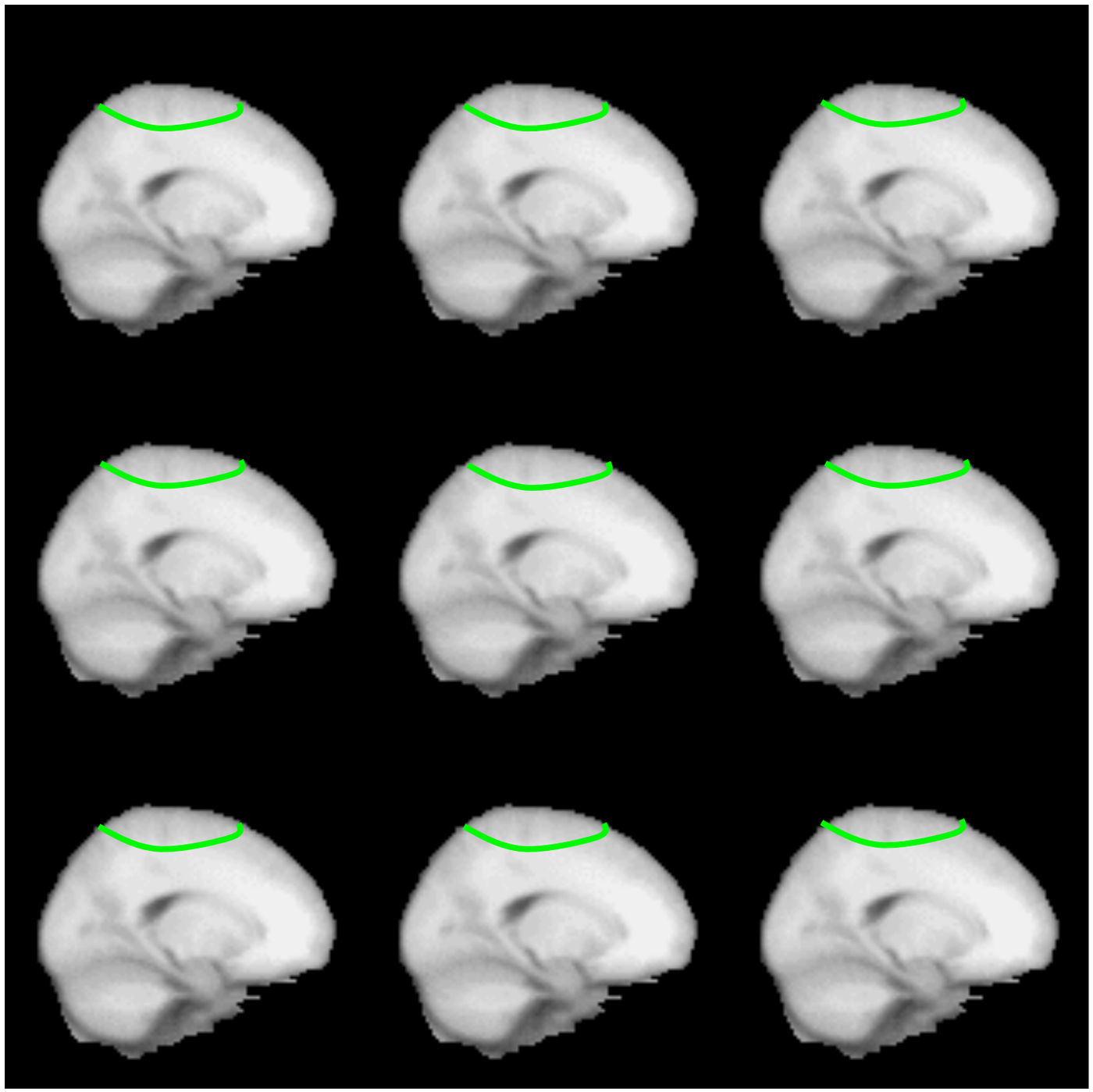
Behrens and Rushworth

But….



Tracking Parietal -> Medial premotor regions in 9 subjects

But….



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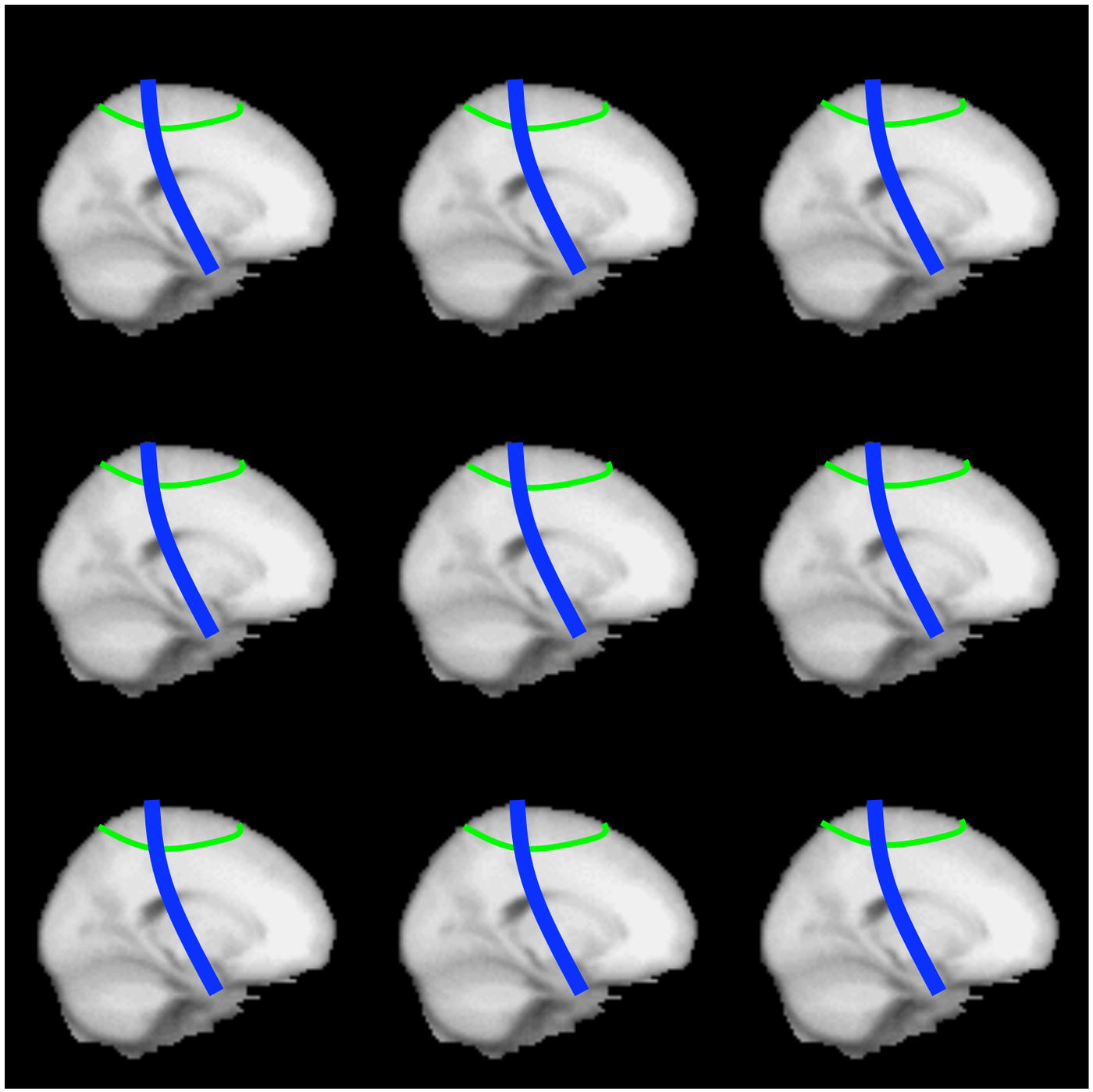
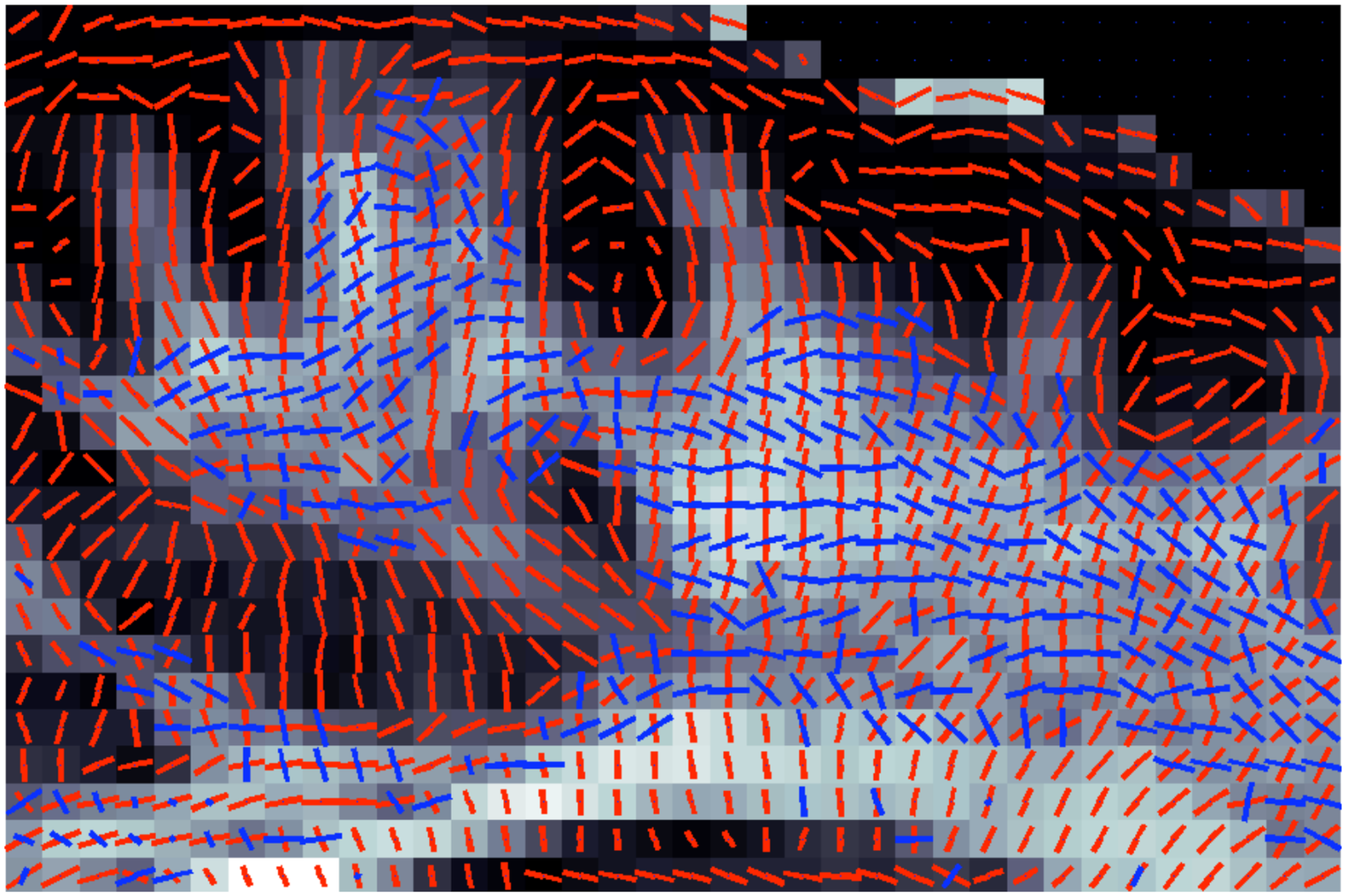


Tracking Parietal -> Medial premotor regions in 9 subjects

Using multi-fibre modelling.



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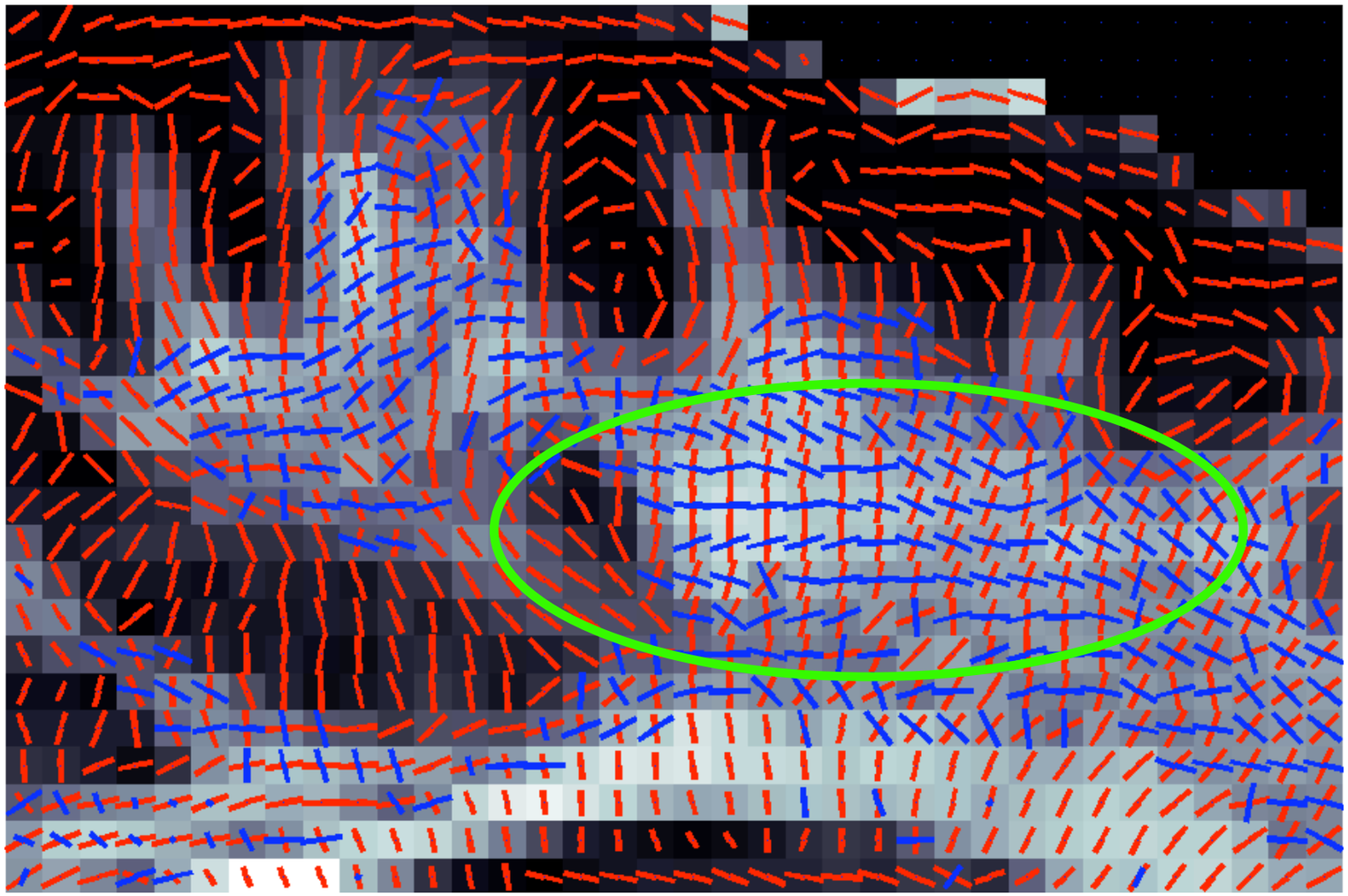

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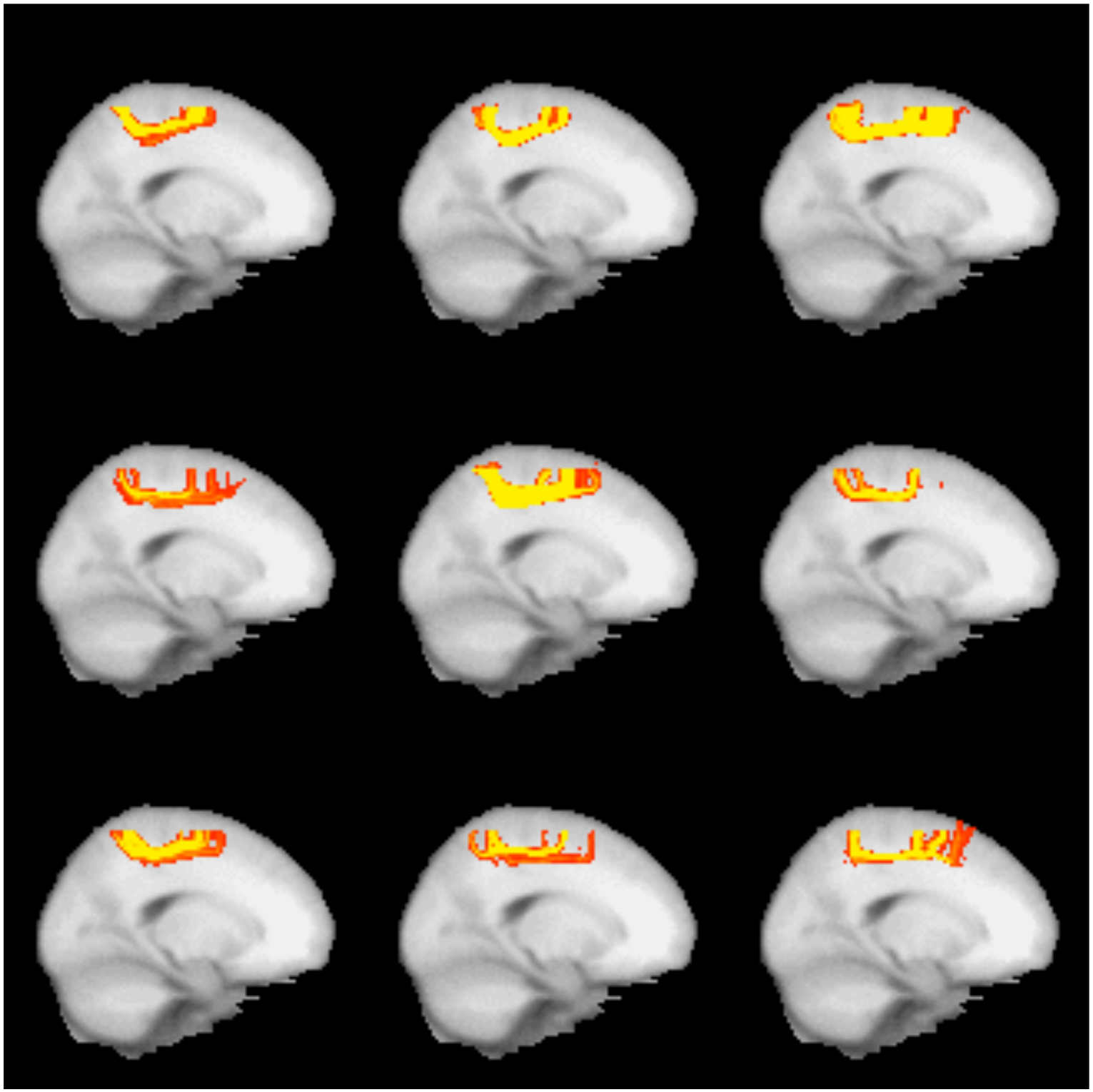
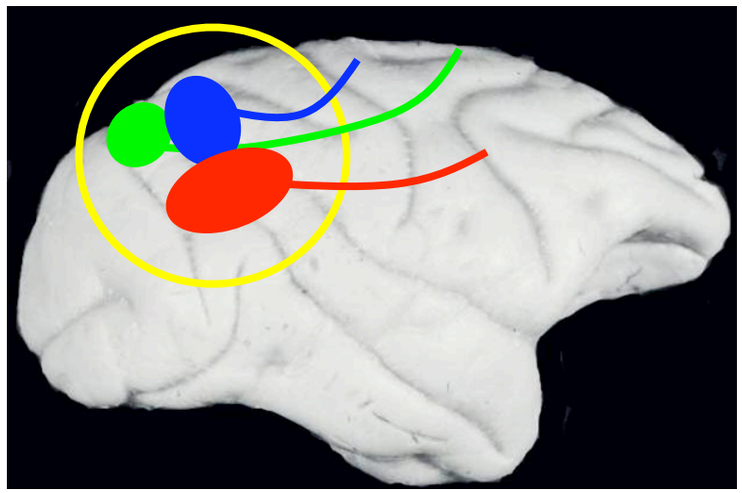


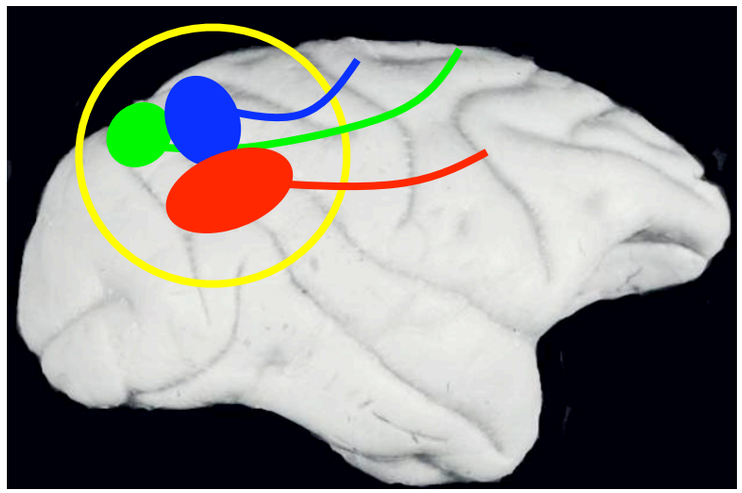
Topography of premotor connections in parietal lobe.



Average of 9 subjects.
Tracking from parietal
To:
Anterior Premotor
Posterior Premotor
Frontal Eye Fields

Behrens and Rushworth

Topography of premotor connections in parietal lobe.



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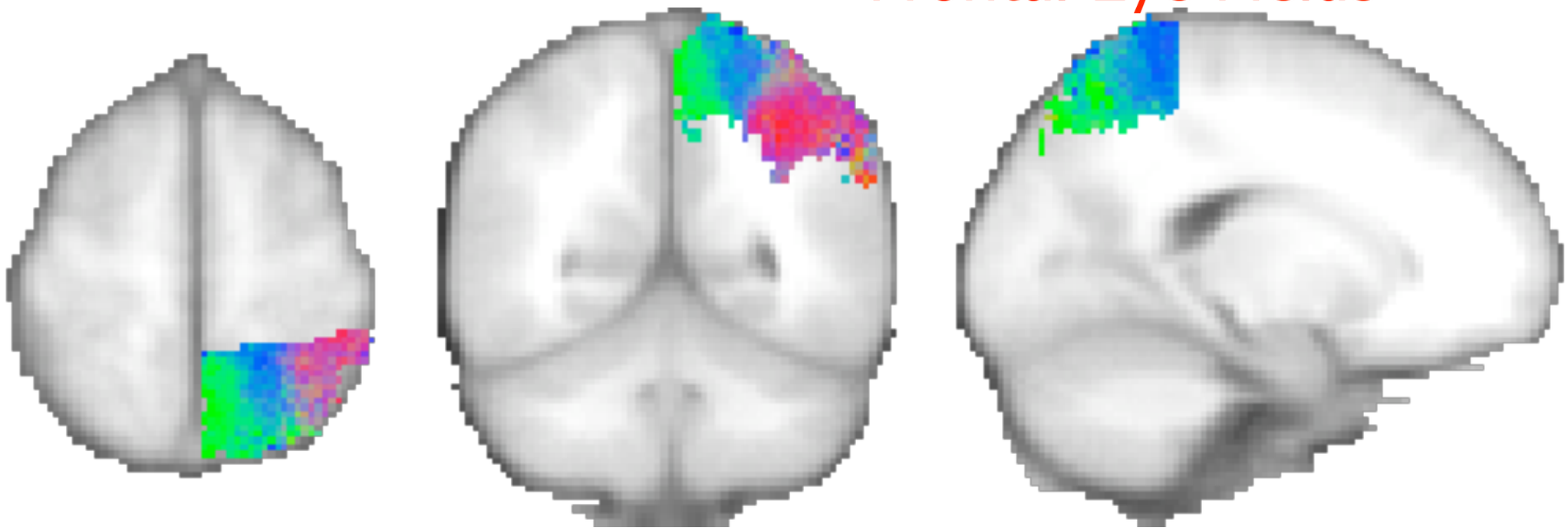
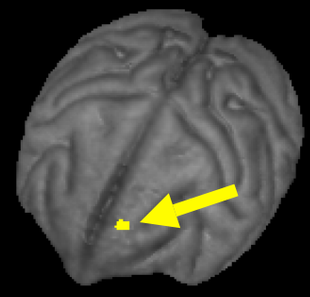


Behrens and Rushworth

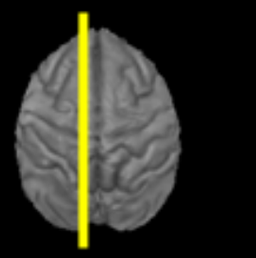
Connectivity of prefrontal cortex

DWI **Mn**

24h 48h 72h 96h 168h

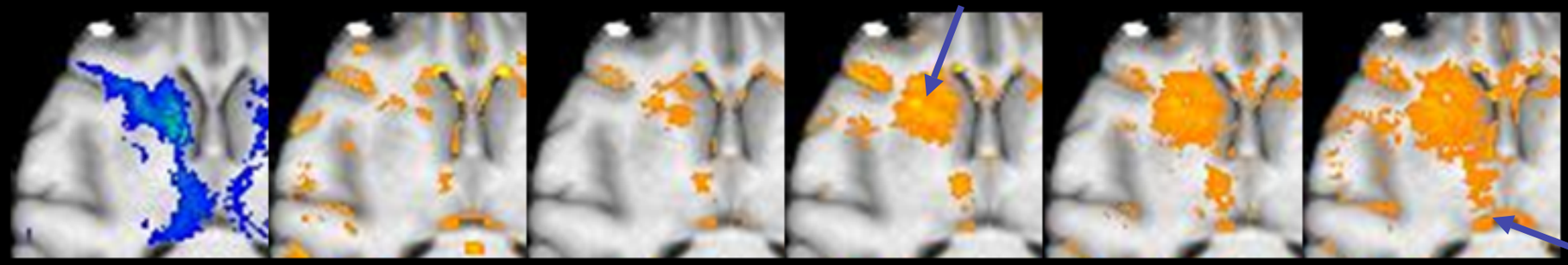


BA9 BA9

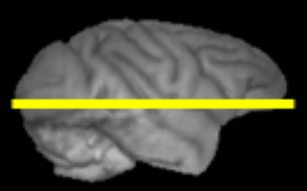


X= -4.0mm

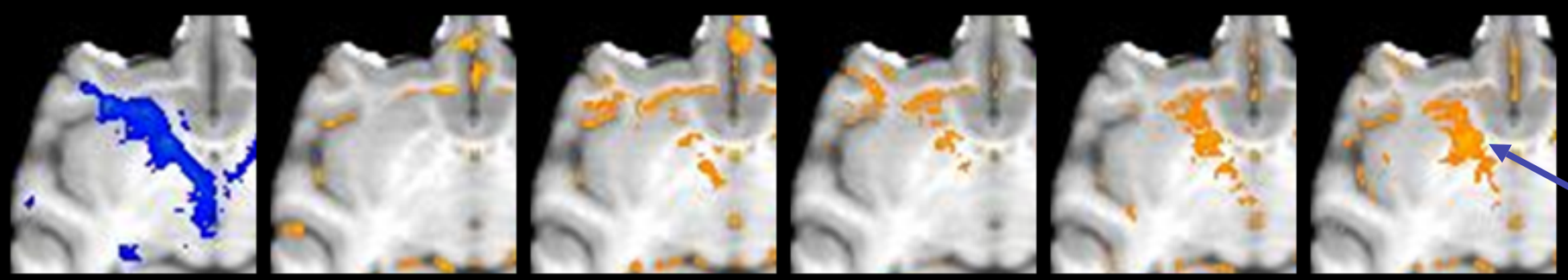
Caudate



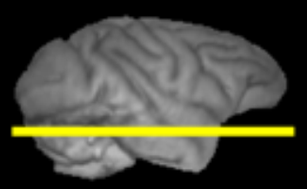
Thalamus



Z=1.0mm



Pallidum



Z=-6.5mm

Midbrain peduncle

3 100

Probability (%)

40 120

t

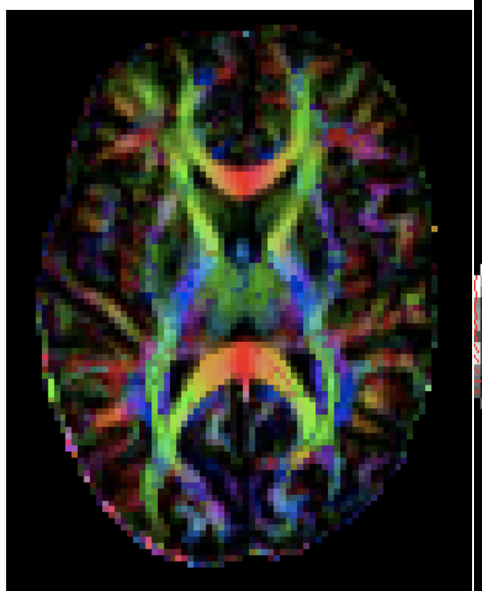
Hayashi T et al. Society for Neuroscience, Atlanta 2006

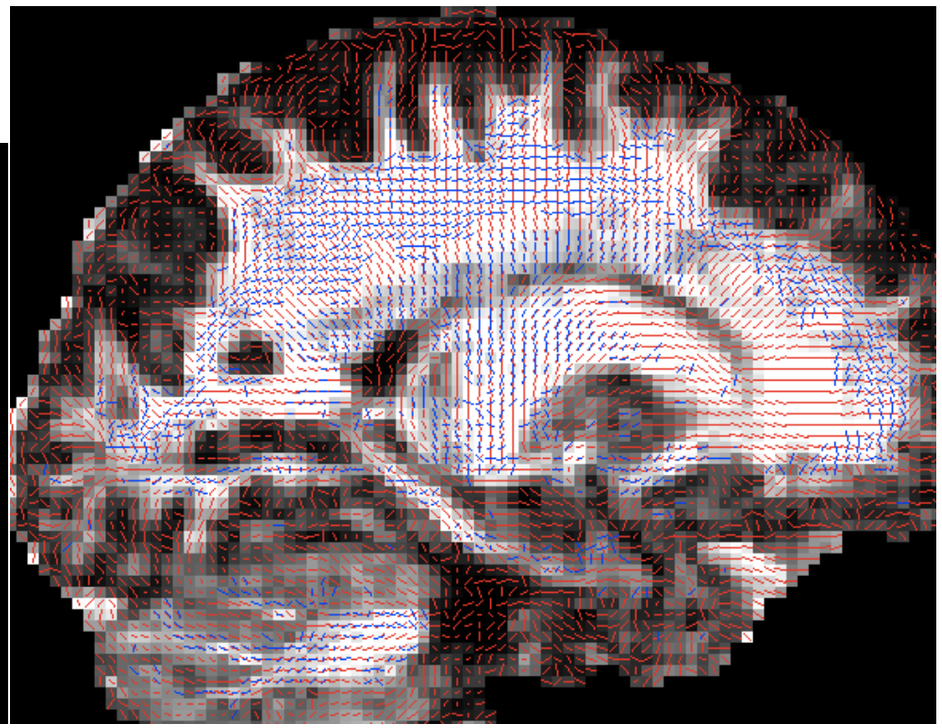
What is a quantitative measure of connectivity?

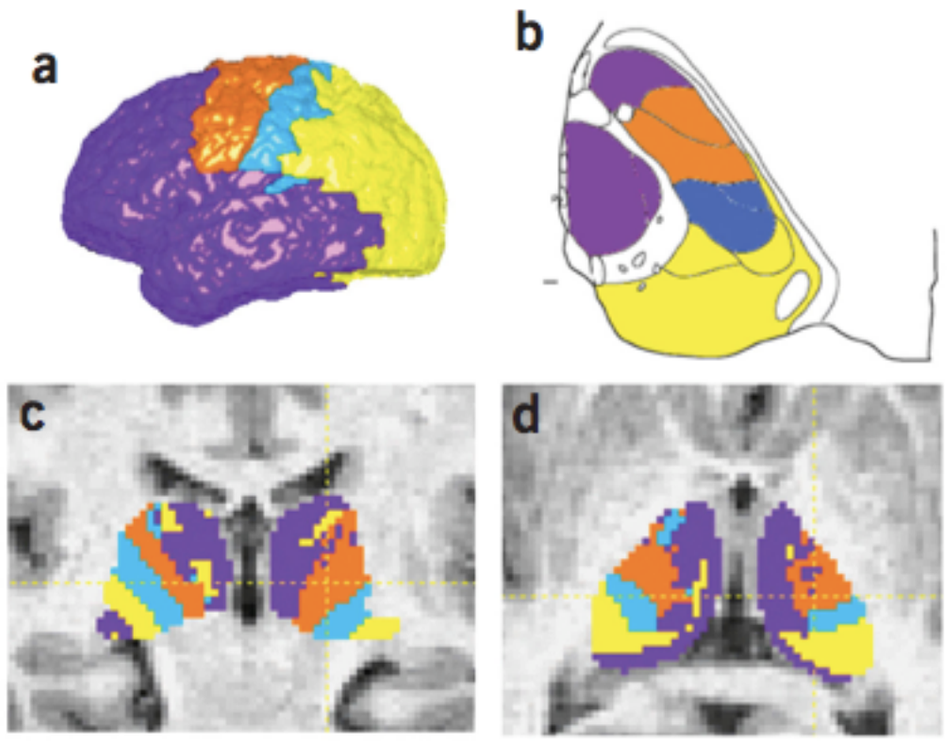
- Number of axons connecting 2 areas?
- Proportion of axons from a seed that reach a target?
- "Integrity" of the connecting white matter …
  - Effective conductivity?
  - Degree of myelination?
  - Packing density?
- What are we measuring?
  - The probability that the **dominant** path through the diffusion field passes through this region.

FMRIB Diffusion Toolbox

- DTI model fit
- Eddy current correction
- Voxel-Based diffusion analysis (TBSS)
- BEDPOSTX modelling crossing fibres
- PROBTRACKX propagating uncertainty in tractography



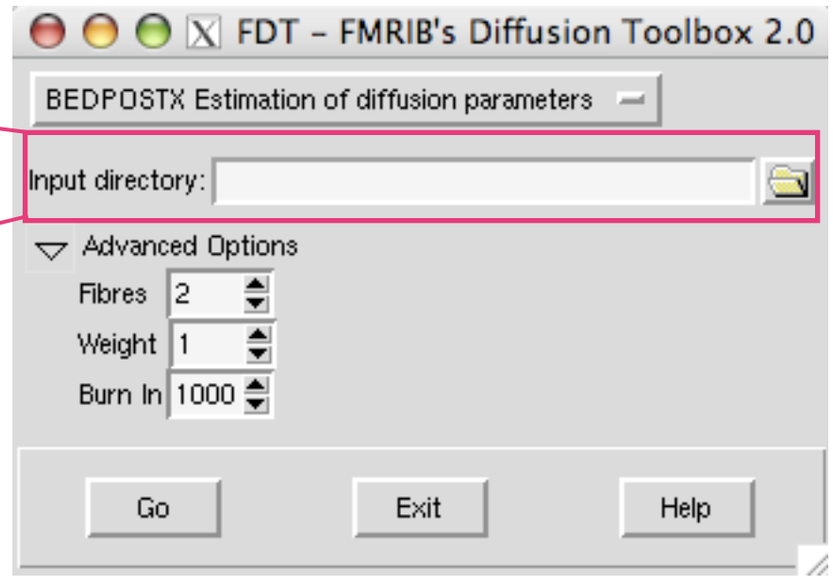


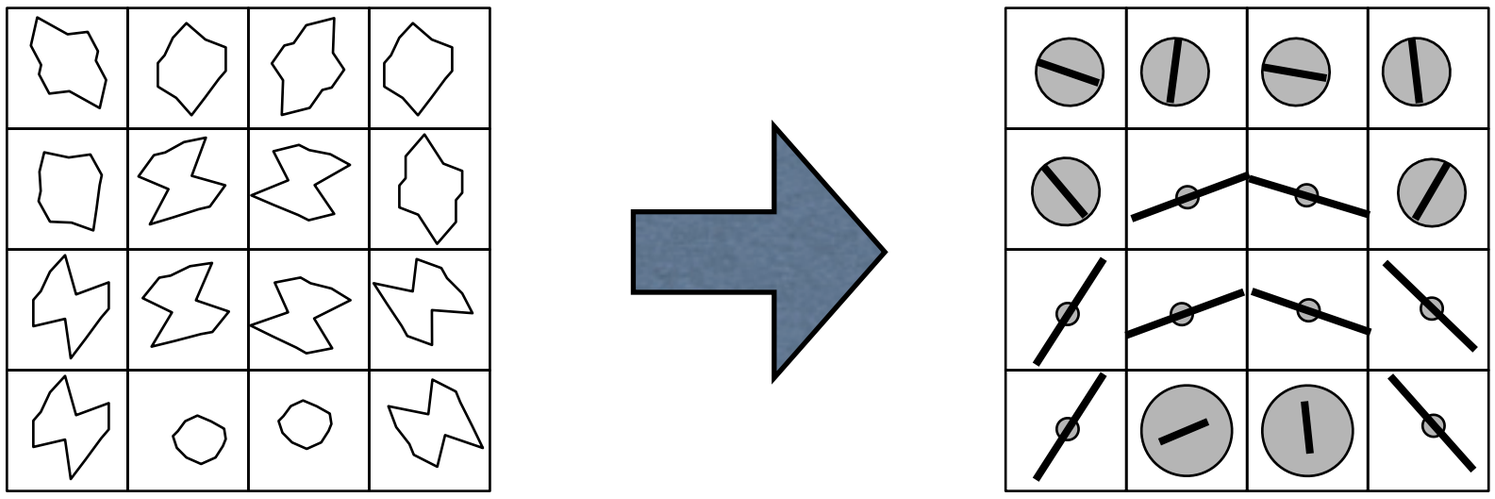


BEDPOSTX

GUI options

data.nii.gz
nodif_brain_mask.nii.gz
bvecs
bvals



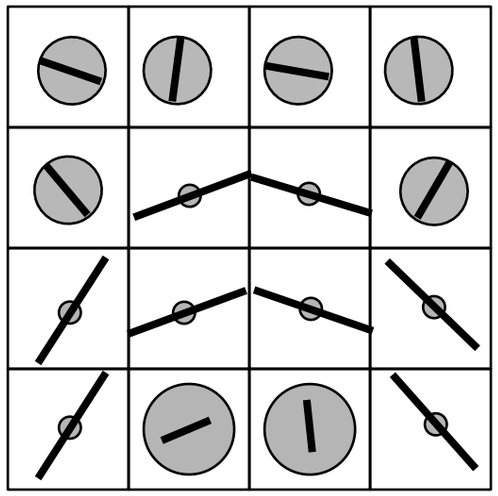


Data

Model parameters

BEDPOSTX

Results

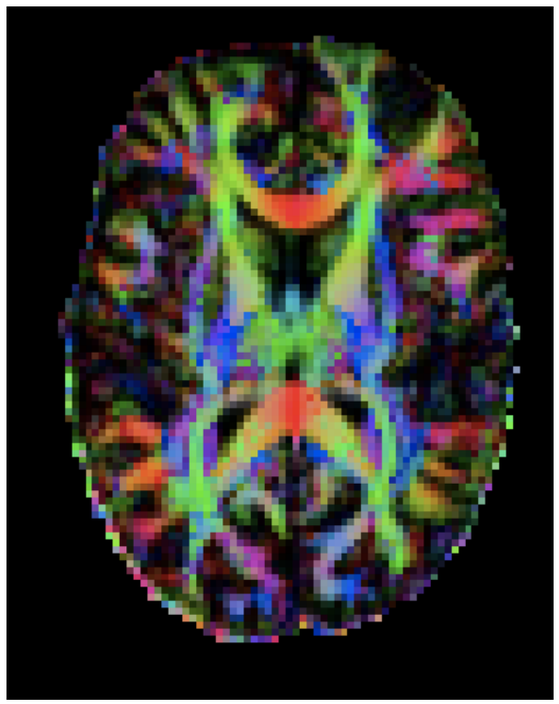


- Sample orientations → merged_th1samples.nii.gz, merged_ph1samples.nii.gz, merged_th2samples.nii.gz, merged_ph2samples.nii.gz
- Sample fractional volumes → merged_f1samples.nii.gz, merged_f2samples.nii.gz
- Mean orientation → dyads1.nii.gz, dyads2.nii.gz
- Mean fractional volumes → mean_f1samples.nii.gz, mean_f2samples.nii.gz

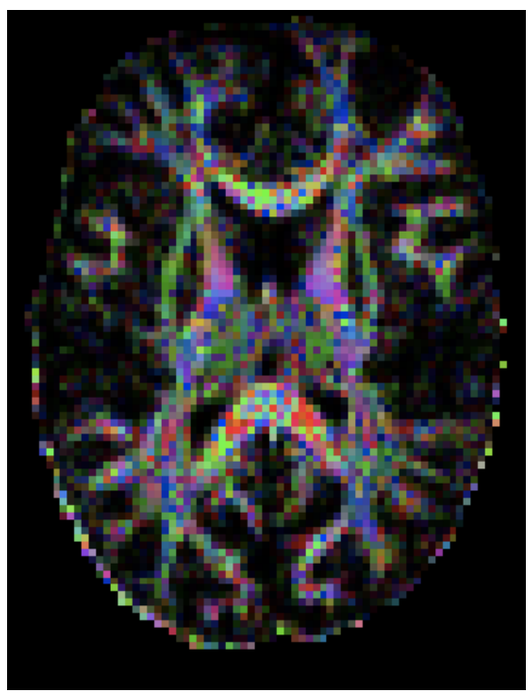
BEDPOSTX

Results

- Mean orientation



dyads1.nii.gz

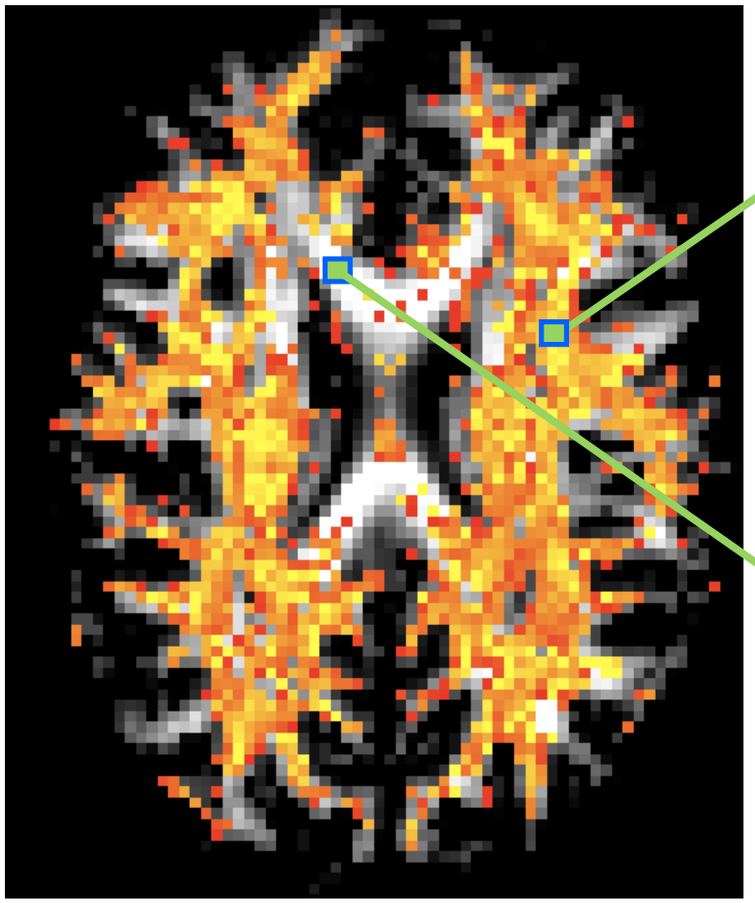


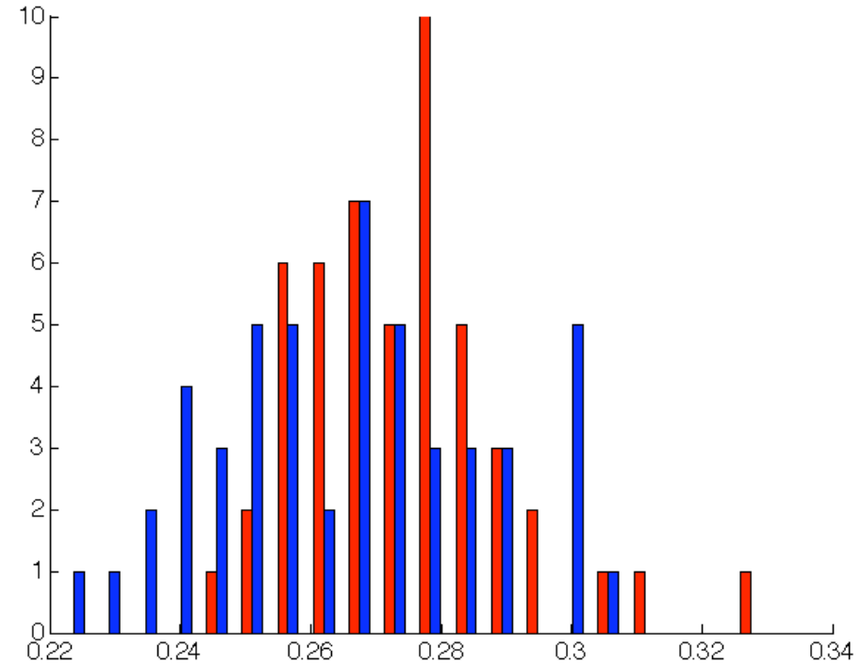
dyads2.nii.gz

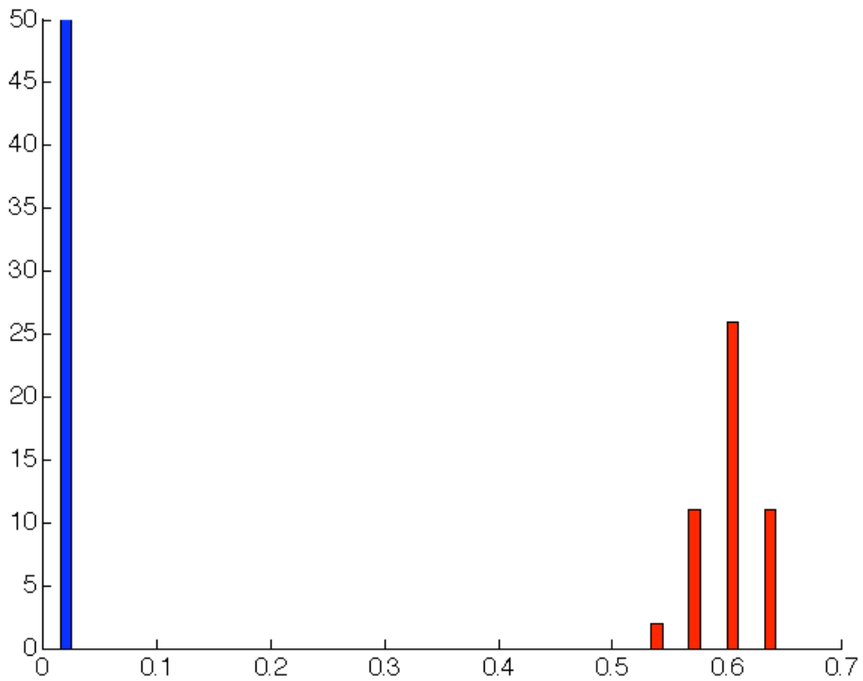
BEDPOSTX

Results

- Mean fractional volumes



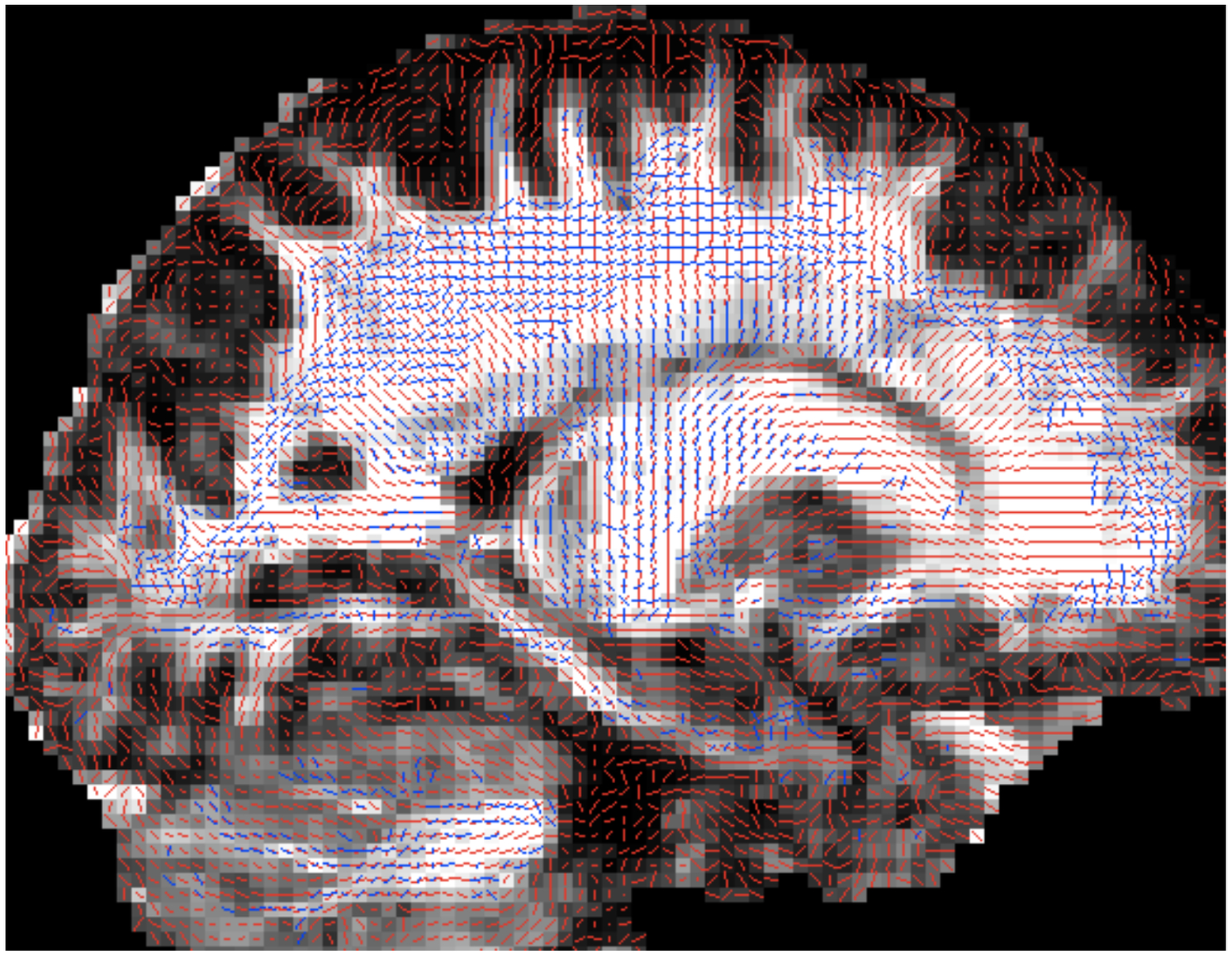




BEDPOSTX

Results

- Mean orientation



dyads1.nii.gz

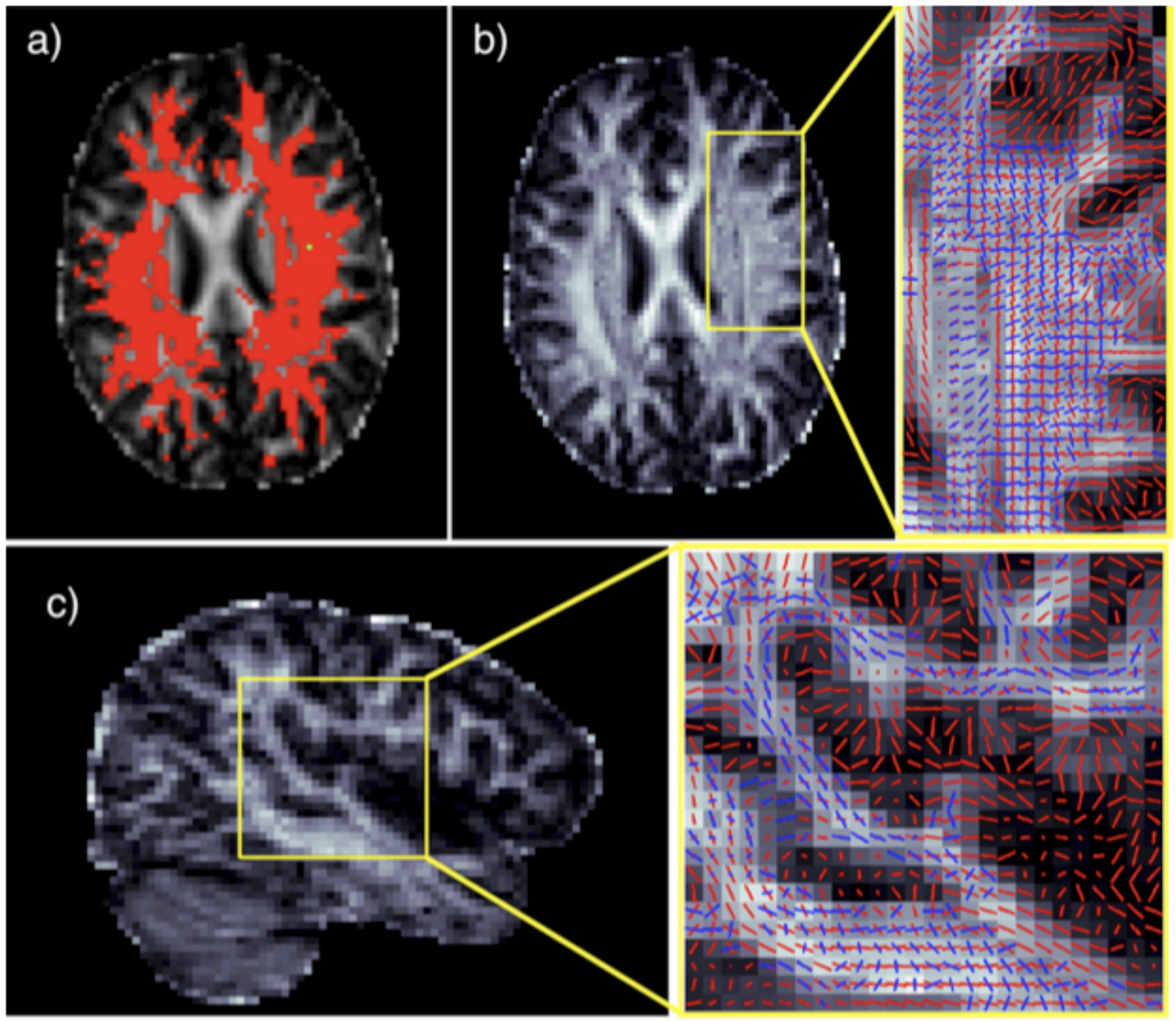
dyads2.nii.gz

maskdyads dyads2 mean_f2samples

BEDPOSTX

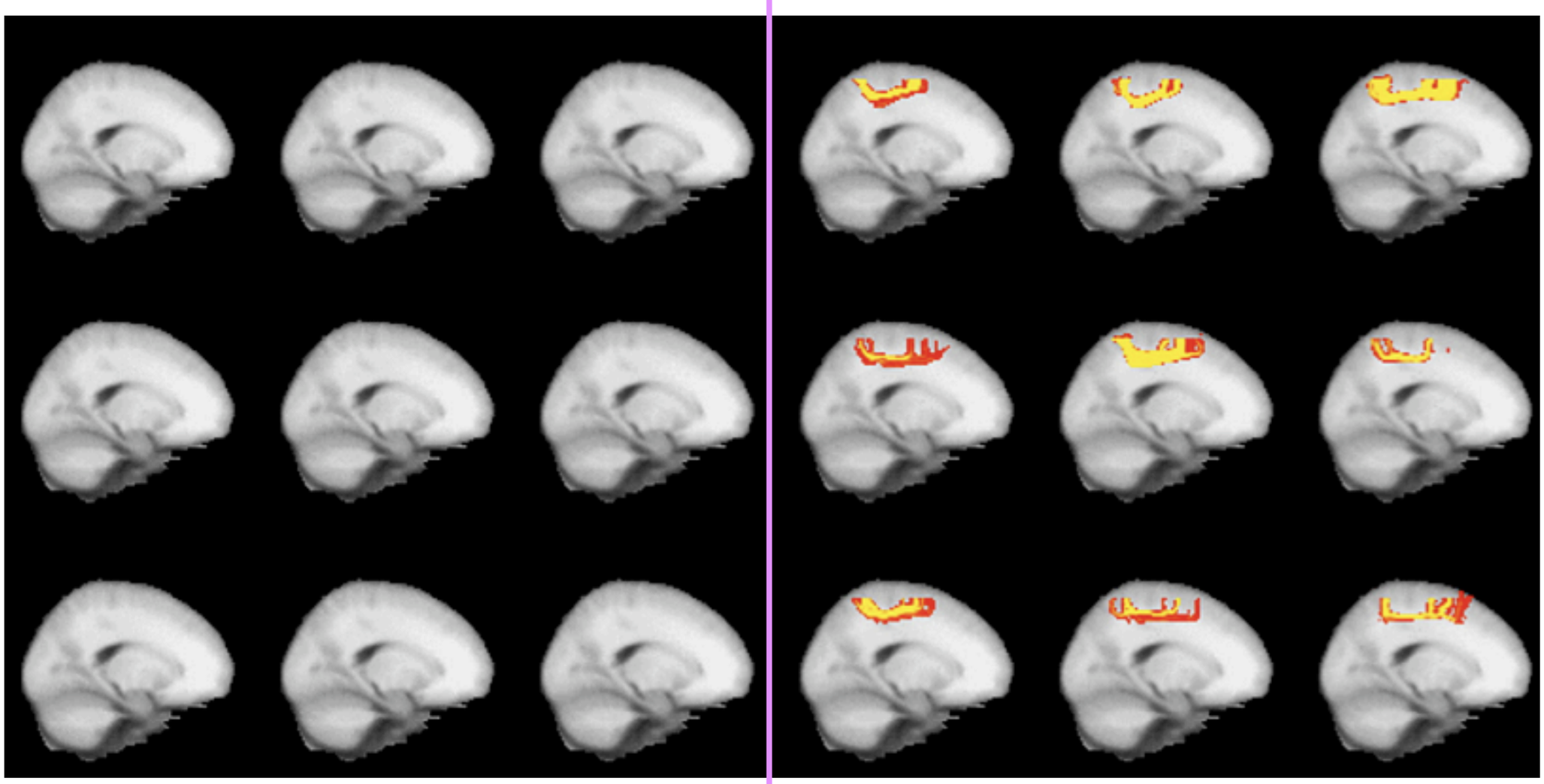
Modelling crossing fibres

- large portion of the white matter voxels has two fibres
- Crossing fibres form form coherent bundles



BEDPOSTX

Modelling crossing fibres



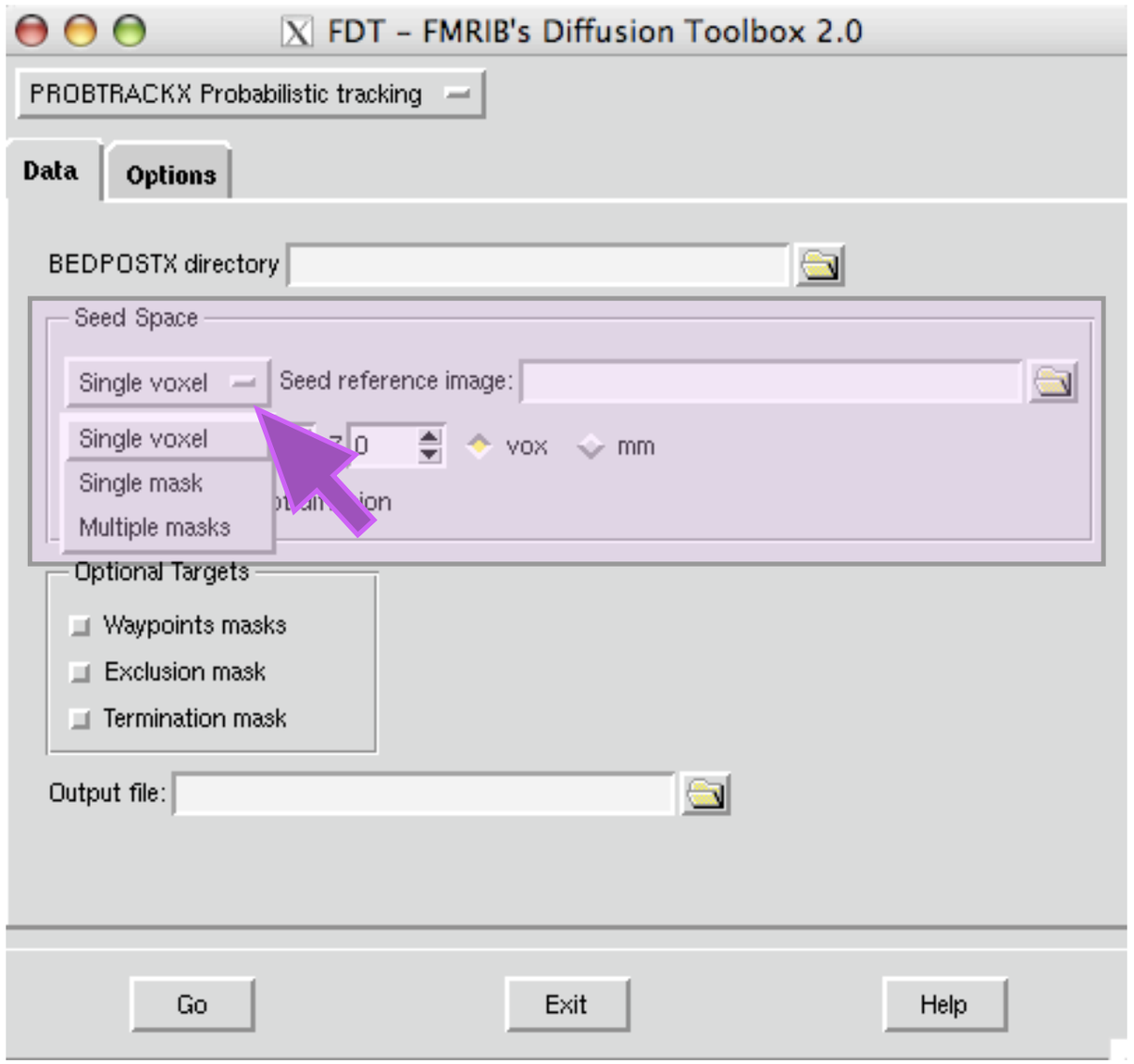
1 fibre

2 fibres

PROBTRACKX

Seed specification

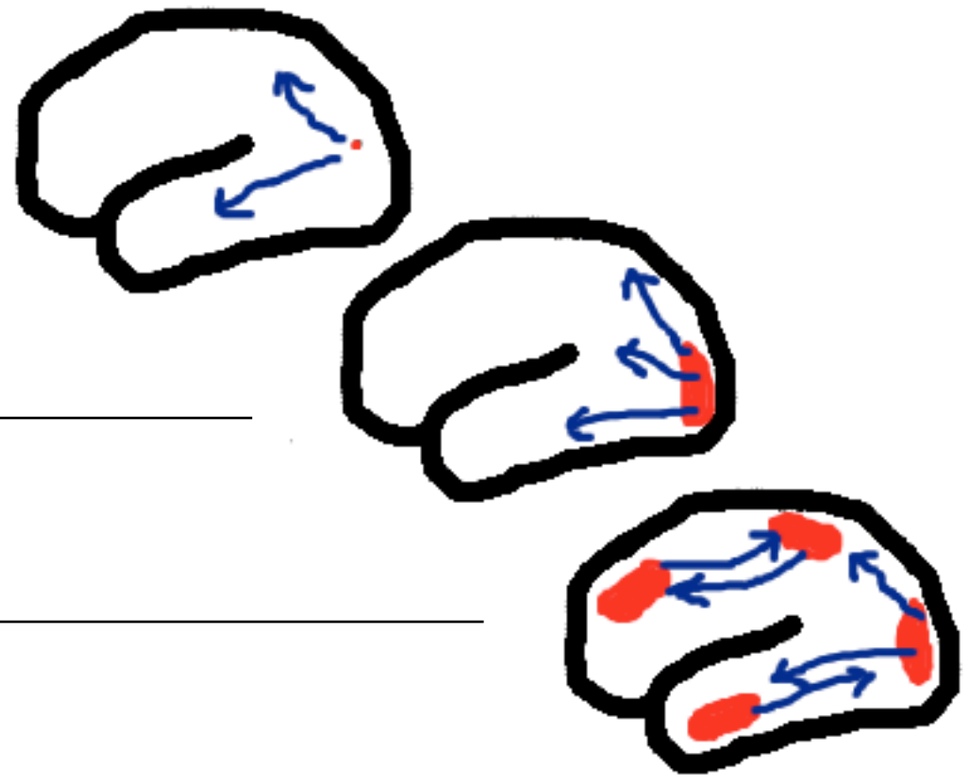
- Different ways of specifying seeds
- Allow seed specification in a different space



PROBTRACKX

Seed specification

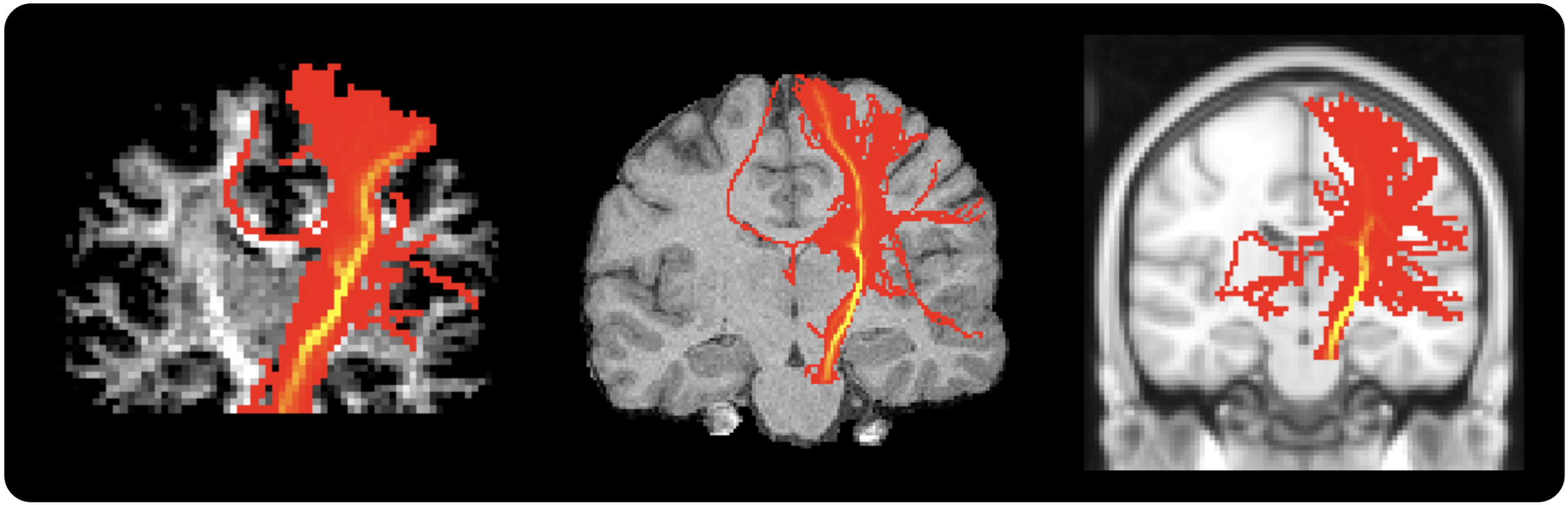
- single voxel
- single mask
- multiple masks



PROBTRACKX

Seed specification

- Different seed spaces



Diffusion space Structural space Standard space

PROBTRACKX

(optional) Targets specification

- Waypoints
- Exclusion
- Termination

Dissecting specific tracts

- Classification

Quantification of connectivity

PROBTRACKX

(optional) Targets specification

- Waypoints
- Exclusion
- Termination

Dissecting specific tracts

- Classification

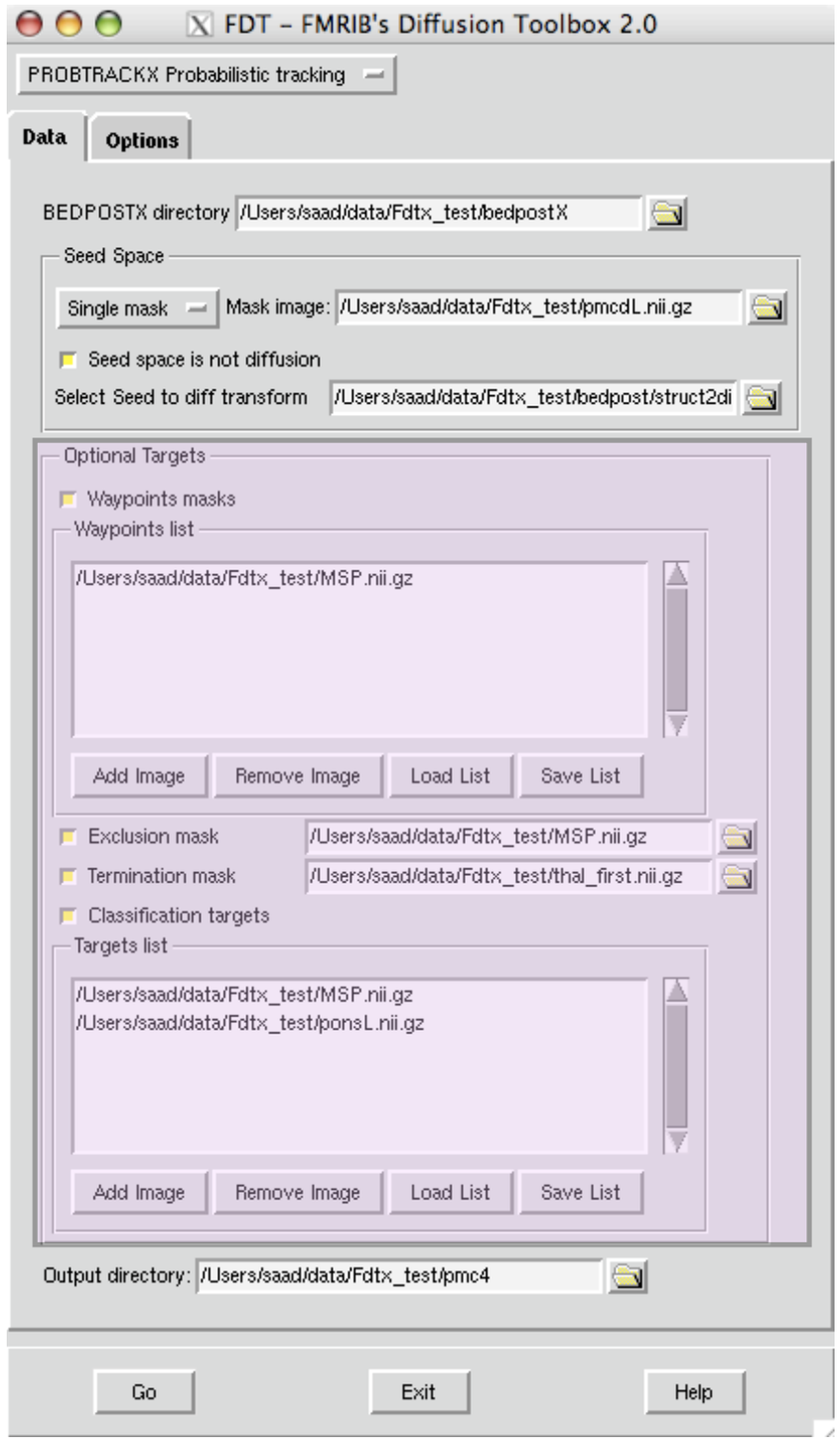
Quantification of connectivity

ALL THE TARGETS IN THE SAME SPACE AS THE SEEDS

PROBTRACKX

(optional) Targets specification

- Waypoints
- Exclusion
- Termination
- Classification

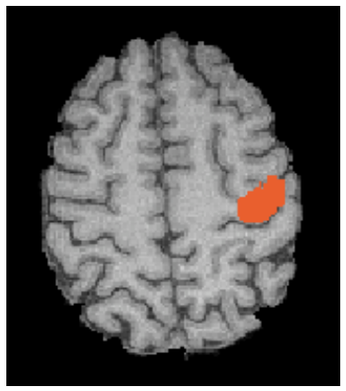


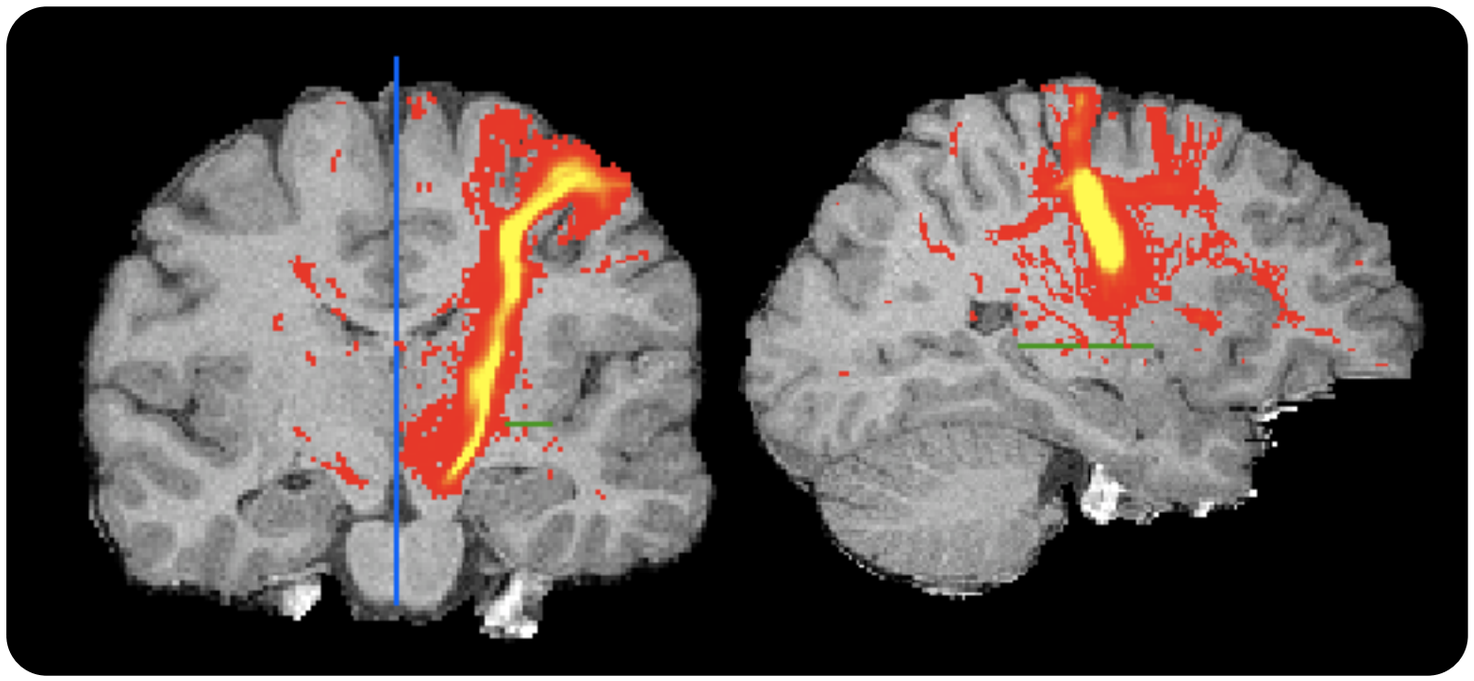
PROBTRACKX

Dissecting a specific tract

Cortico-spinal tract

Seed: M1, hand area





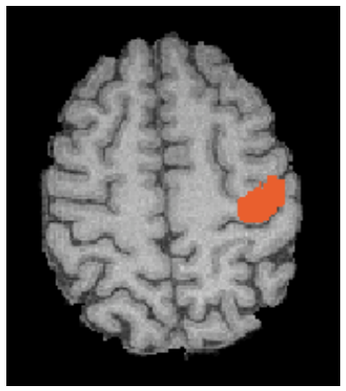
No targets

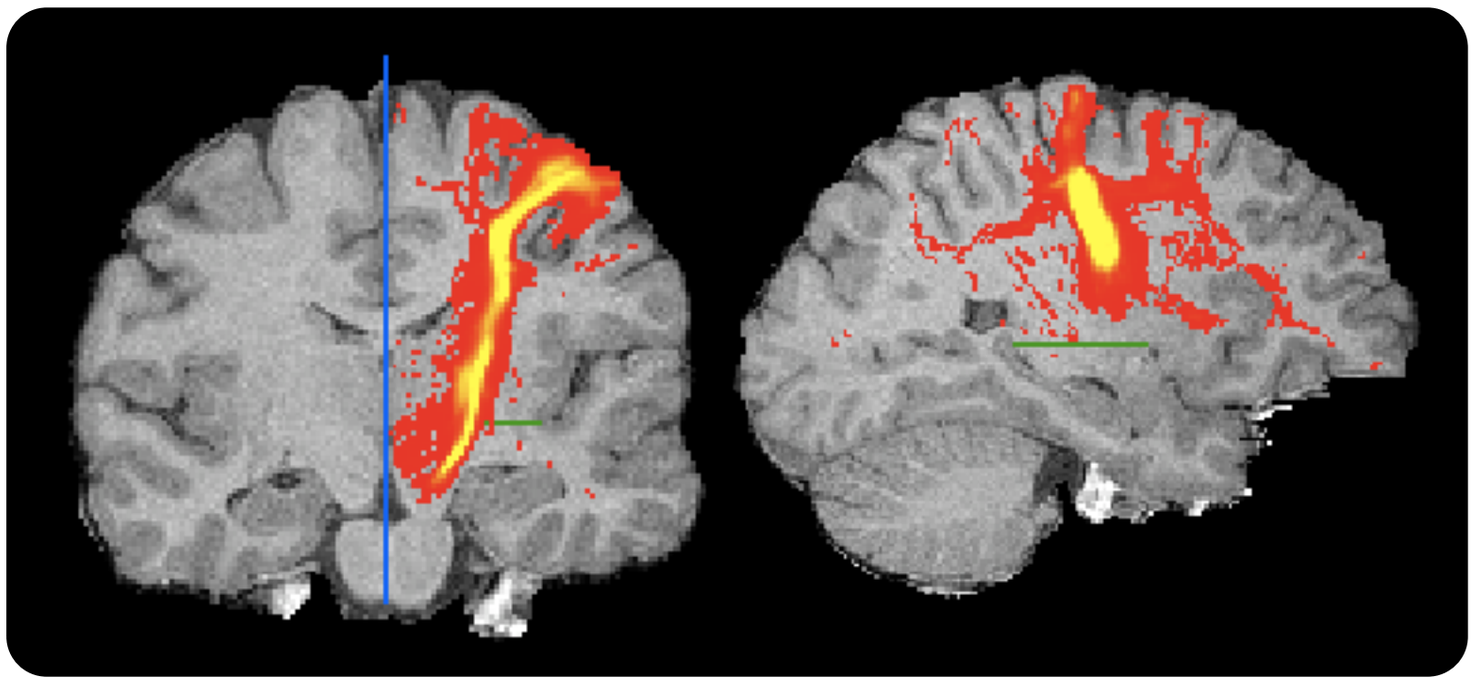
PROBTRACKX

Dissecting a specific tract

Cortico-spinal tract

Seed: M1, hand area





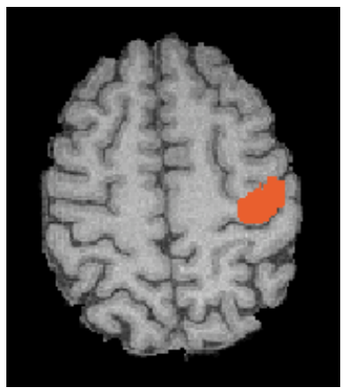
Exclusion: Mid-Sagittal plane

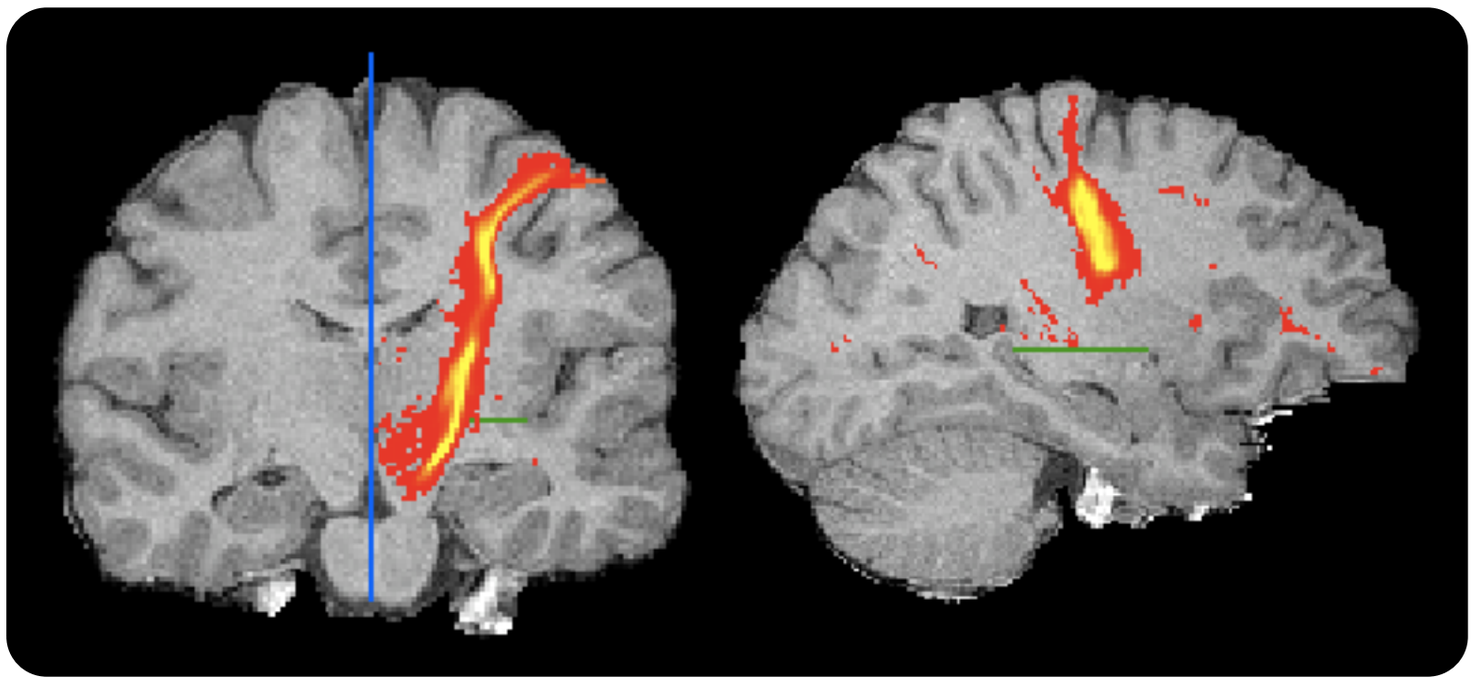
PROBTRACKX

Dissecting a specific tract

Cortico-spinal tract

Seed: M1, hand area





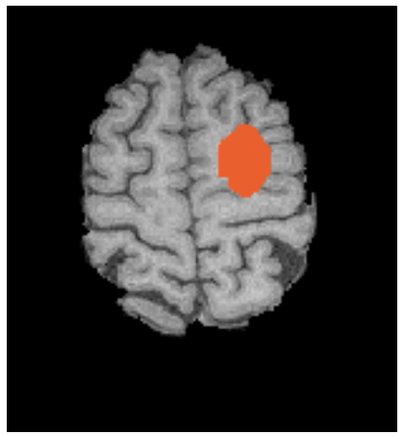
Waypoint: Internal Capsule

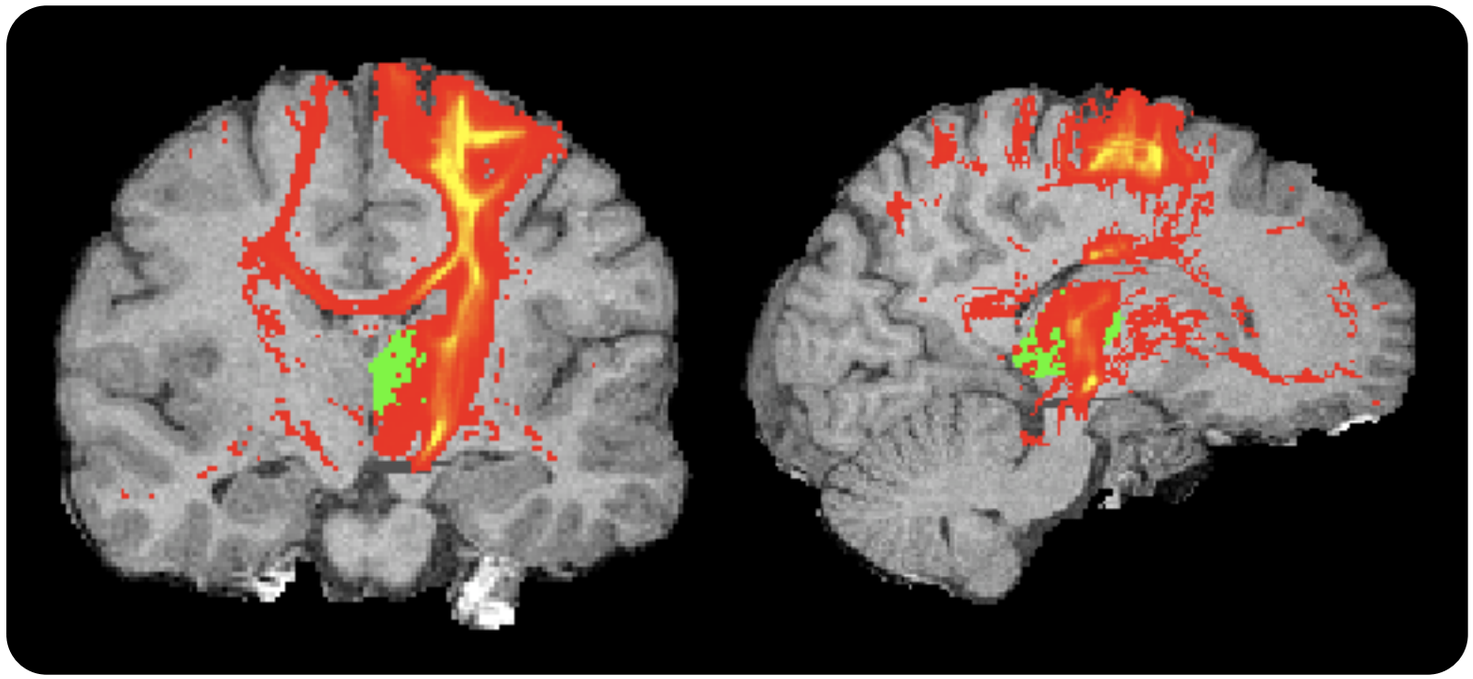
PROBTRACKX

Dissecting a specific tract

Cortico-spinal tract

Seed: dorsal PMC





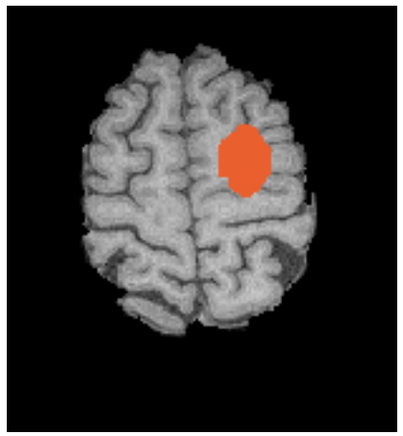
No targets

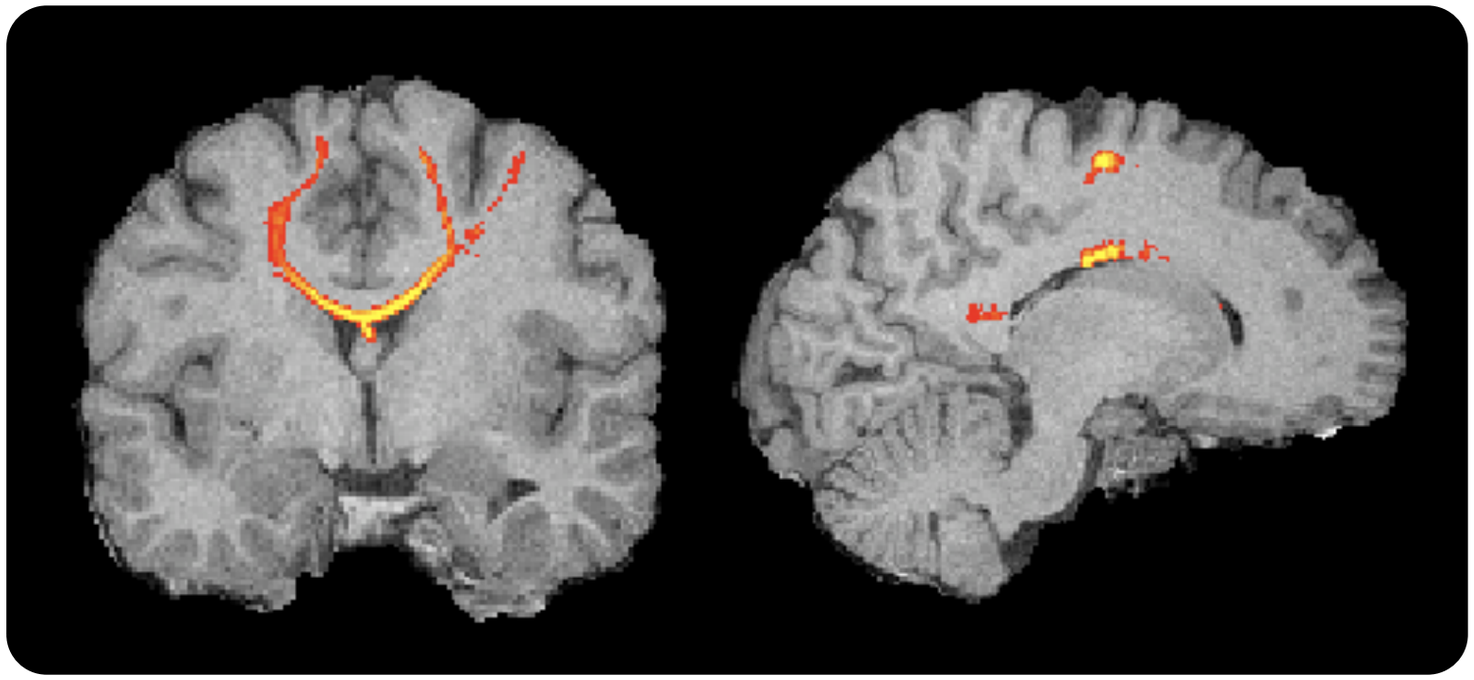
PROBTRACKX

Dissecting a specific tract

Cortico-spinal tract

Seed: dorsal PMC



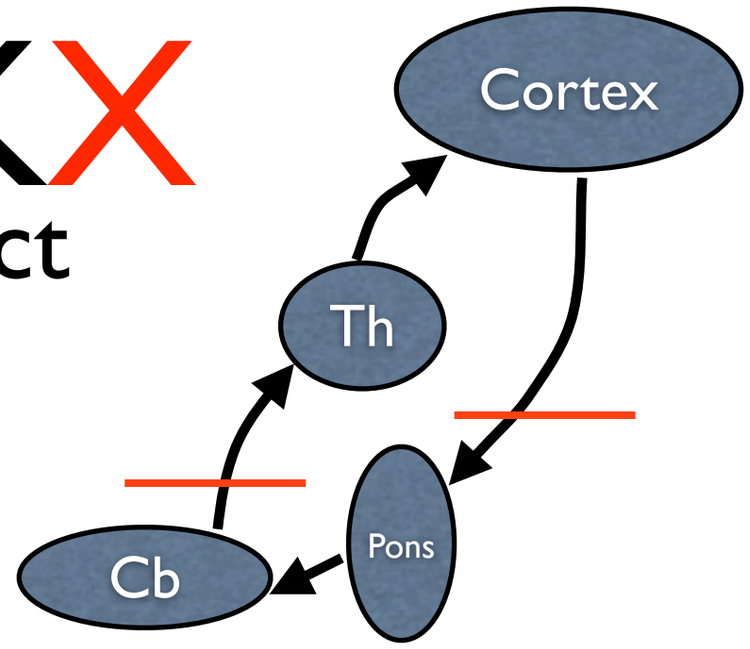


Waypoint: Corpus Callosum

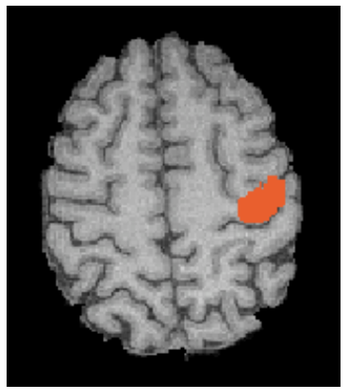
PROBTRACKX

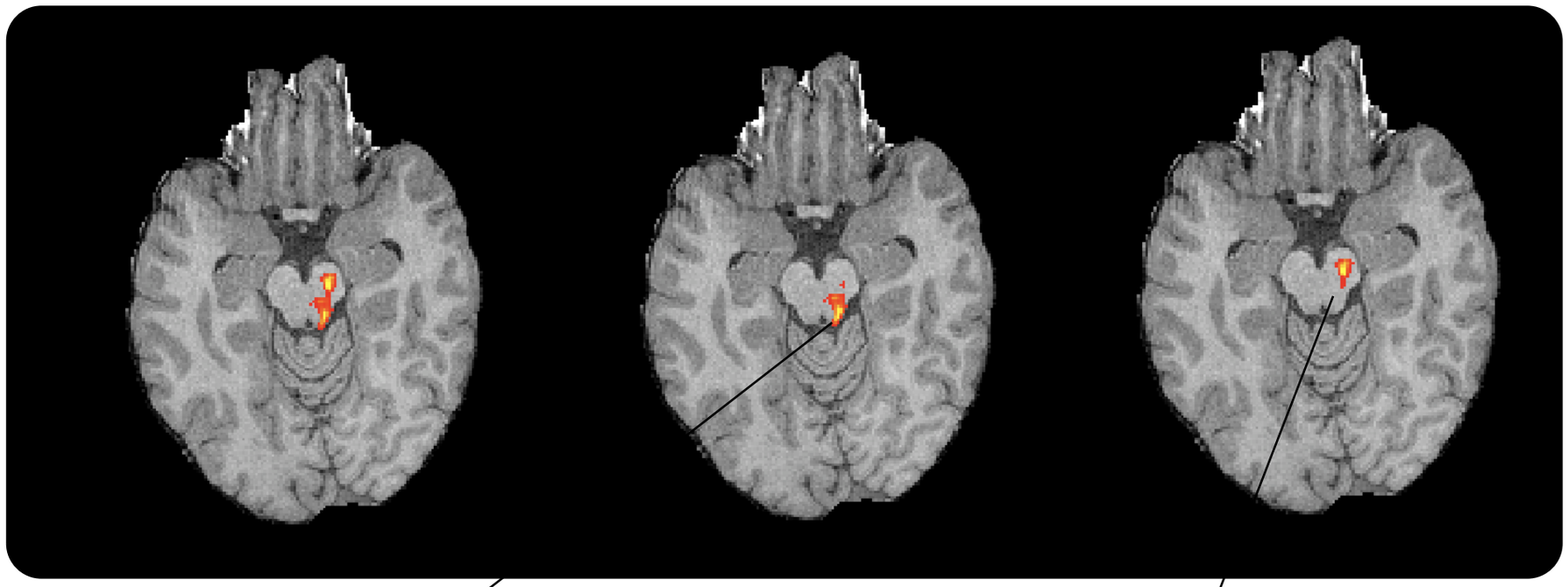
Dissecting a specific tract

Cortico-cerebellar projections



Seed: M1 hand





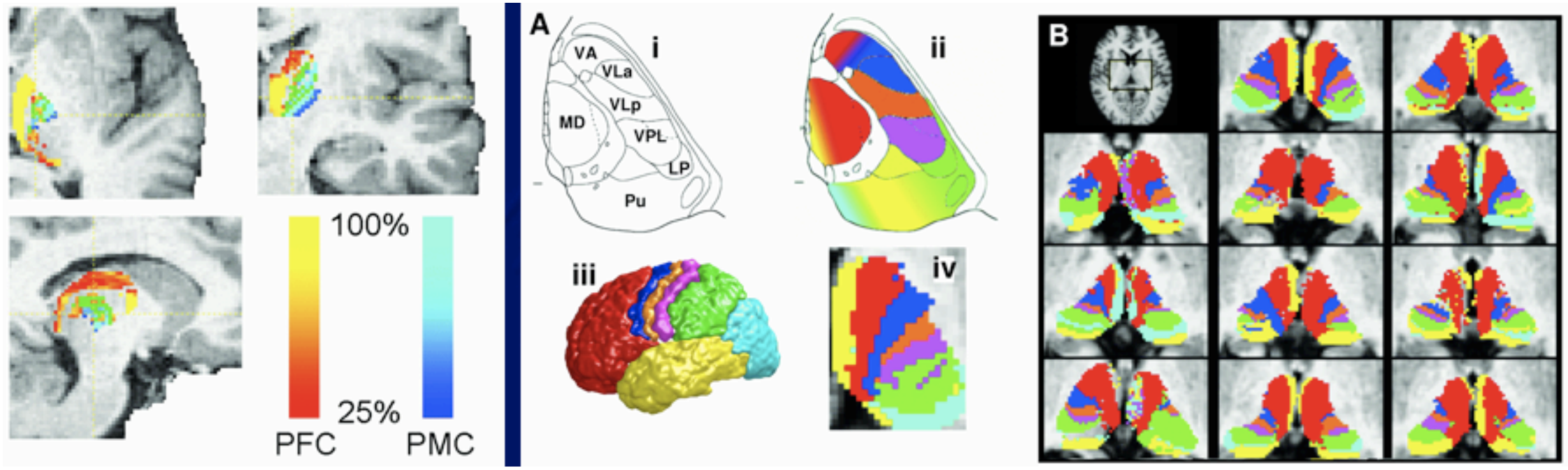
Waypoint: Thalamus

Termination: Thalamus

PROBTRACKX

Connectivity-based seed classification

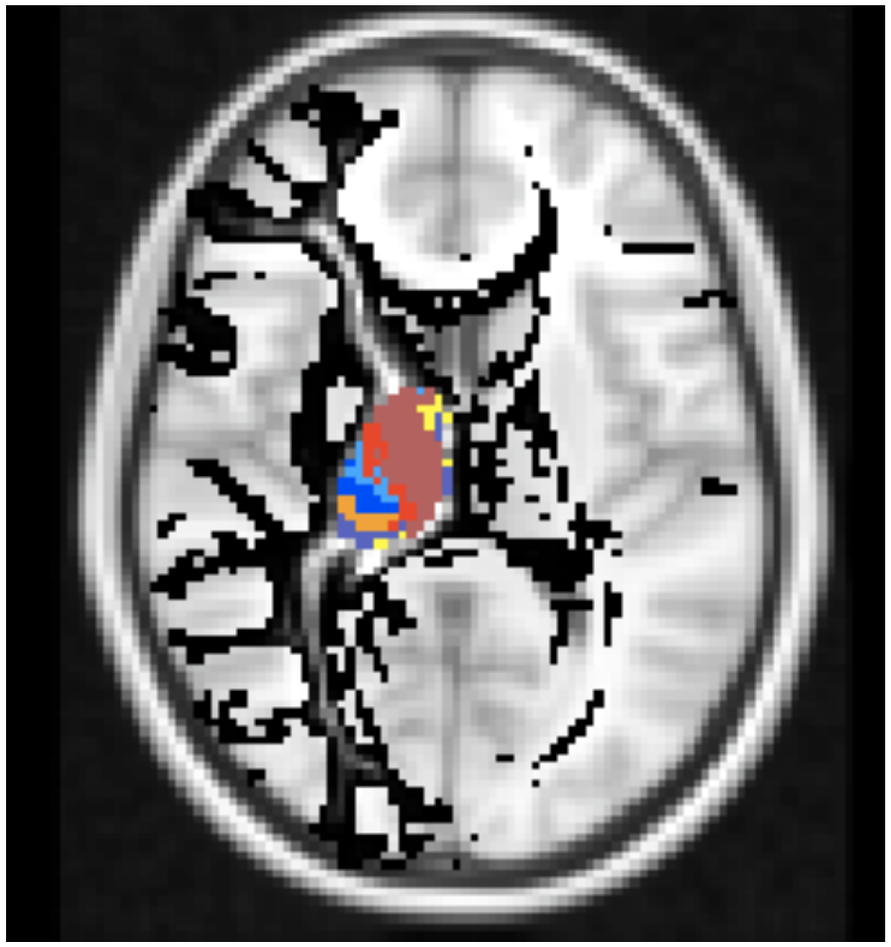
- Quantify the connectivity of seed regions to target regions
- e.g. thalamic voxels can be classified according to their probability of connection to specific cortical targets

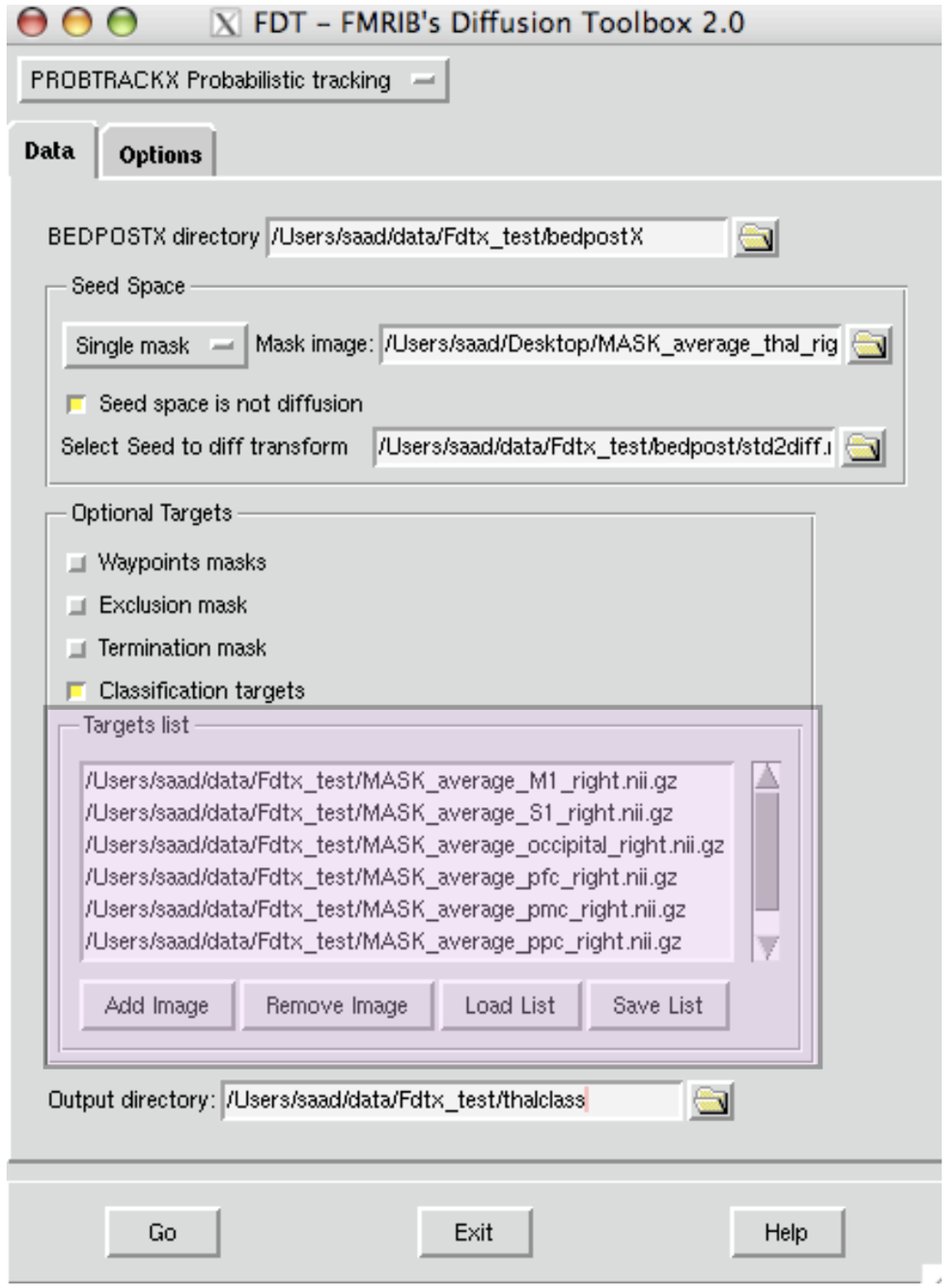


PROBTRACKX

Connectivity-based seed classification

Thalamic segmentation





Discussion

What are we (not) measuring?

- Distribution of a fibre orientation rather than distribution of fibre orientations
- Thresholding tract distribution is tricky
- Bins (voxels) are arbitrary
- Favour seed classification for quantitative analysis (masks are meaningful)

FMRIB Diffusion Toolbox

- DTI model fit
- Eddy current correction
- Voxel-Based diffusion analysis (TBSS)
- BEDPOSTX modelling crossing fibres
- PROBTRACKX propagating uncertainty in tractography