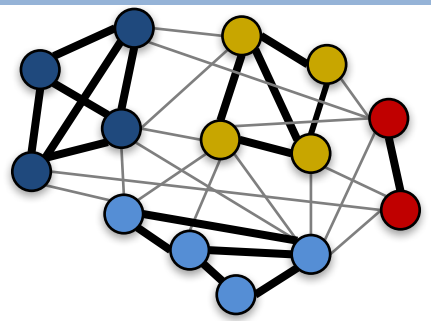
Carolina NRG

Group Organizers:
Jessica Cohen, Psychology, UNC
Simon Davis, Neurology, Duke
Felipe De Brigard, Philosophy, Duke



THE POINT: Our general observation is that most new connectome papers espouses *a new measure (e.g., between-module degree)*, *a new interpretation of an existing measure (e.g., segregation / integration)*, or *a novel application of a measure designed for something completely different (e.g., control theory).*

In other words, we're all writing code that tries new things, and we don't necessarily know what we're doing.

Organizational Notes

Format of Meetings

- *NRG meetings are styled as workshops, with 1-3 individuals leading a discussion centered on one issue within connectomics research.*
- *These discussions will be led by individuals with new data/tools/ideas they wish to present to the group*
- *This is not a talk series. Researchers are encouraged to bring laptops to test new toolboxes, and be critical about how connectomics should be done.*

- Computer stuff
  - *Useful software, w/ install location:*
    - FSL
    - MRtrix
      - a C++11 compliant compiler (e.g. clang in Xcode)
      - Python version >= 2.7 (already included in macOS)
      - The zlib compression library (already included in macOS)
      - Eigen version >= 3.2
      - Qt version >= 5.1 *[GUI components only]*
    - Slicer

  - *NRG Code resources*
    - https://github.com/ElectricDinoLab/CarolinaNRG
    - Individual lab websites, as needed.

Future Meetings/Topics

Second Wednesday of every month 4:00pm-5:30pm

Date & Location
10/11 – UNC
11/8 – Duke
12/13 – UNC
1/10 – Duke
…etc

Planned Topics Fall 2017:

- Modularity
- Visualization of Graph Data
- Functions of a Network
- Dynamic Functional Connectivity

Possible Topics for Spring 2018:

- Informational Connectivity
- Integrating Univariate and Multivariate Data
- Development & Ageing in Connectomics
- Defining State Transitions
- TMS & Brain Stimulation
- Suggestions for future topics welcome!

Today's Schedule: Defining Architecture with DWI

THEORY	DWI Background
APPLICATION	DWI Code & QA
THEORY	Struct Connectome Background
APPLICATION	Struct Connectome Code & QA

DWI Background

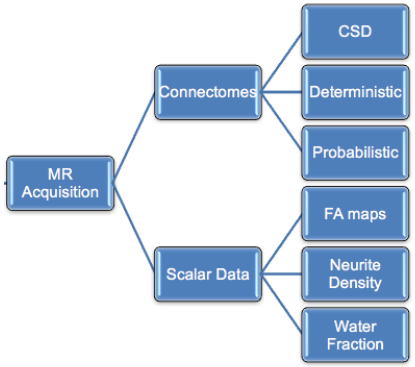
what I want to do:

"here, have this hammer, build your house!"

what today will feel like:

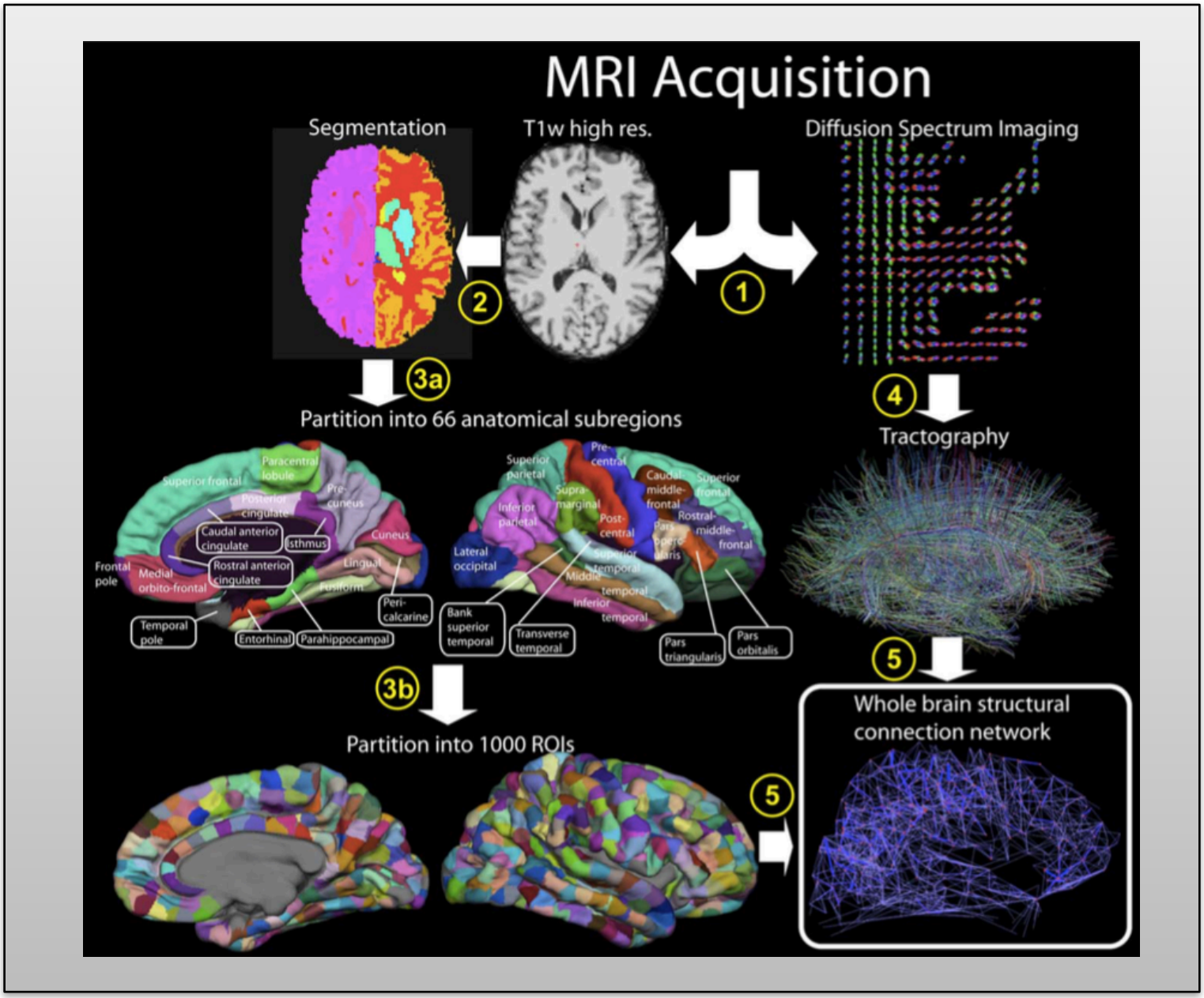
"here, have this giant user's manual for building a house-like structure, written in an ancient Mayan dialect"

the least you should get:



"here are your choices for building a house"

DWI Background



DWI Background

Decisions at the Acquisition Stage

We have a limited amount of time at the scanner, so we should be aware of the trade-offs in acquisition, and how they influence connectomes.

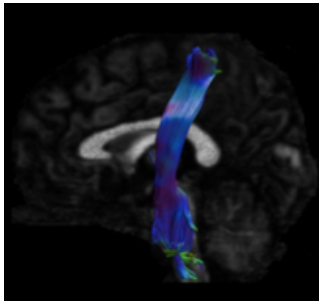
As a reseracher collecting data, you (ideally) can decide the balance between 3 factors:

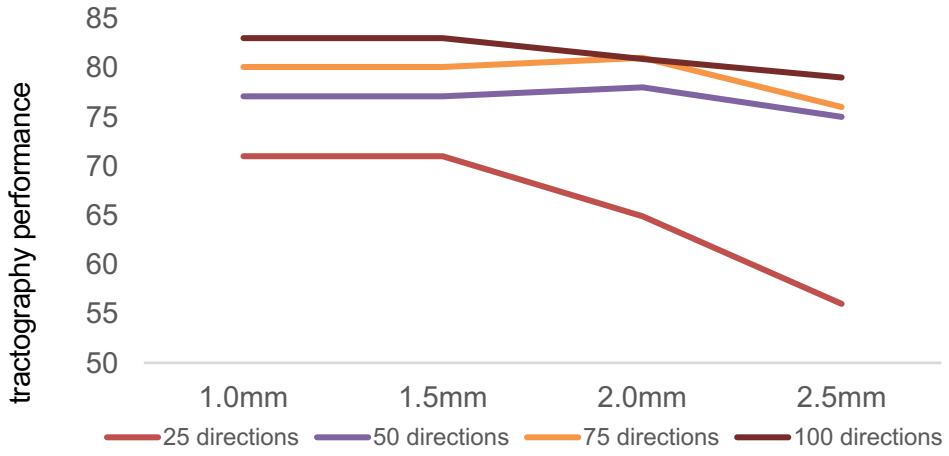
factor	what does it buy you?
voxel size (spatial resolution)	more accurate localization of anatomy
# of directions (angular resolution)	more accurate diffusion modeling per voxel
# of b-values	better FA, neurobiological metrics

Trade-off between angular and spatial resolutions in in vivo fiber tractography

Sjoerd B. Vos [a,b,*], Murat Aksoy [b], Zhaoying Han [b], Samantha J. Holdsworth [b], Julian Maclaren [b], Max A. Viergever [a], Alexander Leemans [a], Roland Bammer [b]

[a] Image Sciences Institute, University Medical Center Utrecht, Utrecht, The Netherlands
[b] Department of Radiology, Lucas Center, Stanford University, Stanford, CA, United States

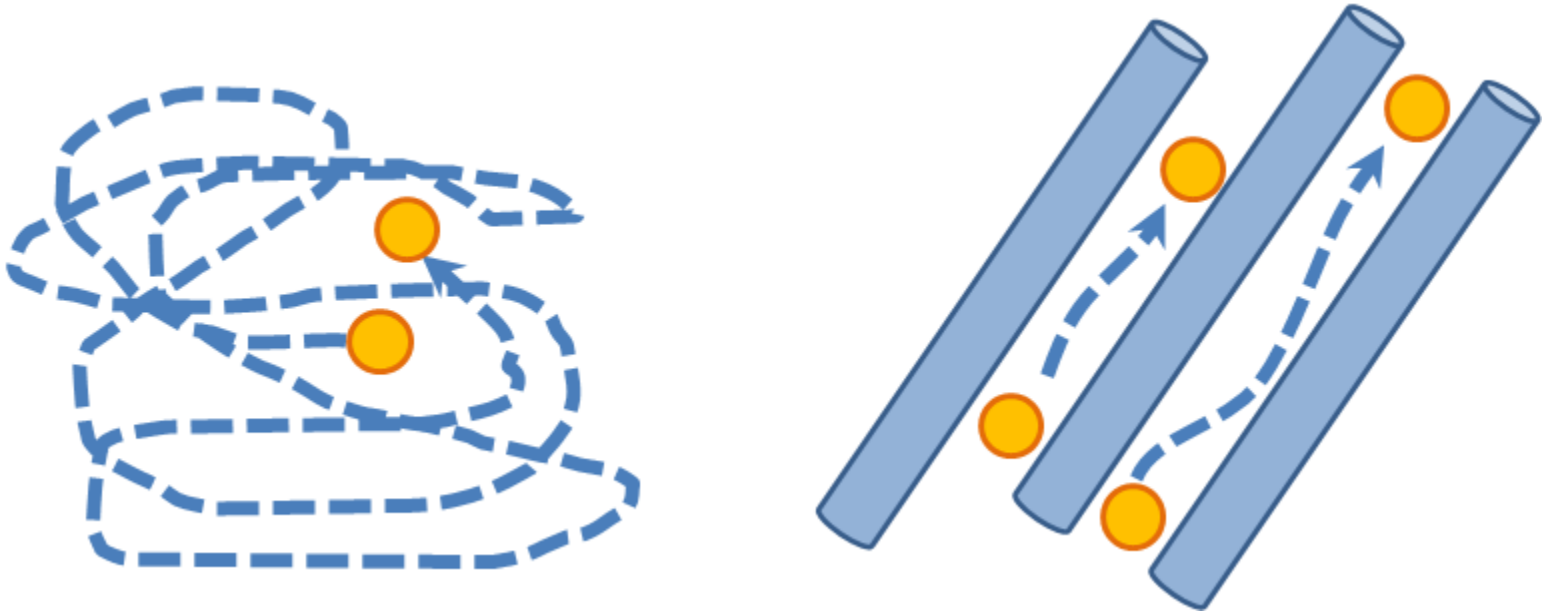




Most of us will go by an existing protocol.
Standard Duke protocol is 36 directions, 2mm isotropic, 1 bvalue. (7mins)
UNC HCP protocol: 1.5mm isotropic, 4 bvals, 64/64/128/128 directions. (80mins)

DWI Background

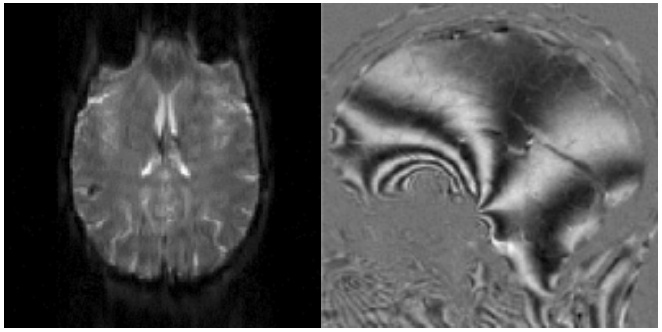
The basis for all these inferences:
Brownian motion (or diffusion) of water molecule



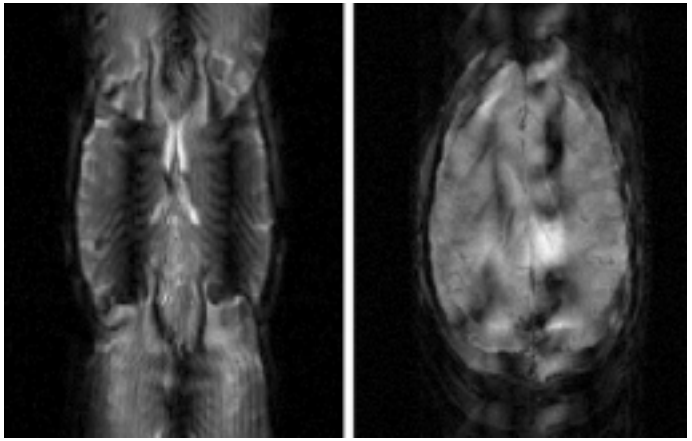
Rosenbloom et al, *NeuroImage*, 1999

DWI Background

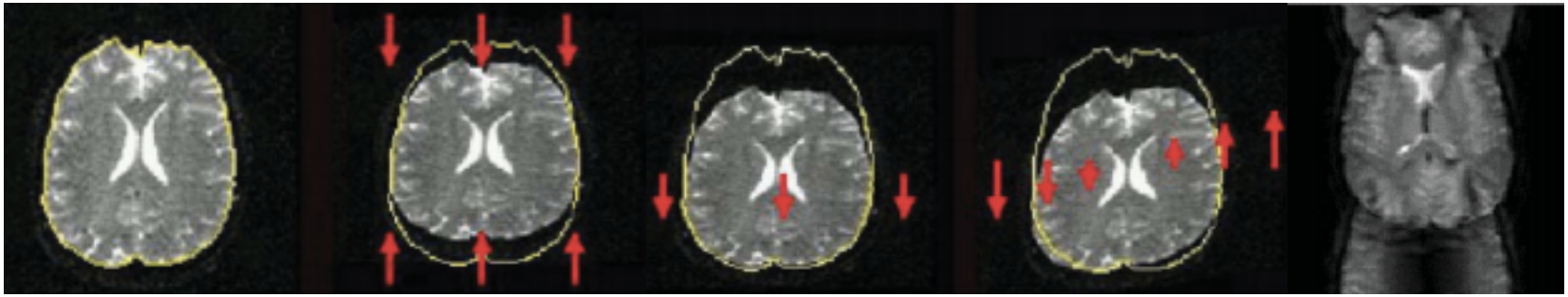
magnetic susceptibility artefacts



motion artefacts

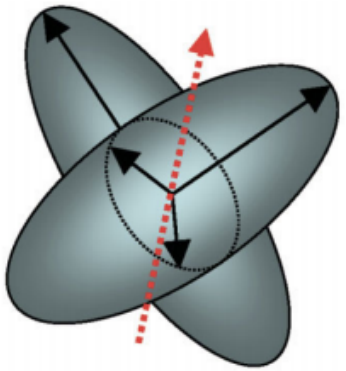


eddy-current artefacts

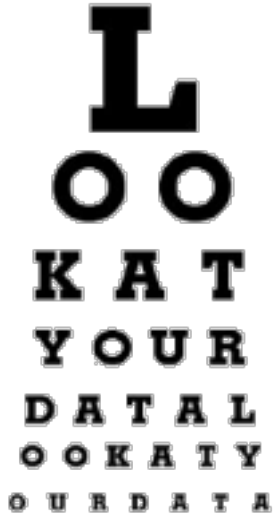


venetian blind artefacts

crossing fibers



DWI Code & QA



Tools:

Processing

- MRTrix

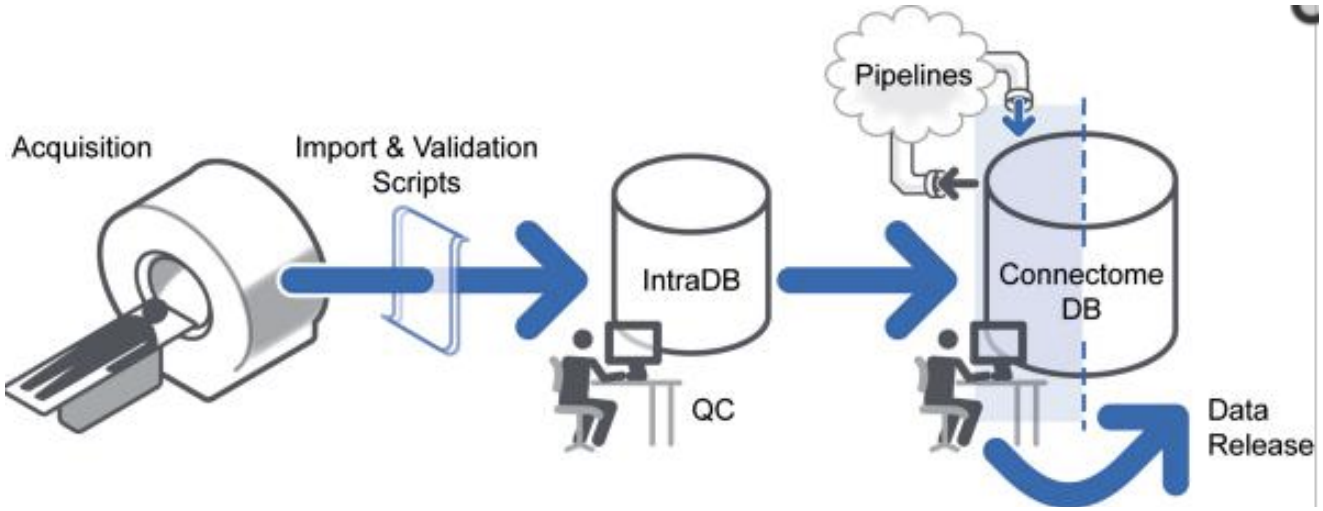
QA

- DTI Prep (Slicer)
- slicedir (FSL)
- fslstats –h –M

- Other good code not examined here
  - ExploreDTI (Alexander Leemans)
  - Processed Connectomes Project Quality Assessment Protocol (Cameron Craddock)

DWI Code & QA

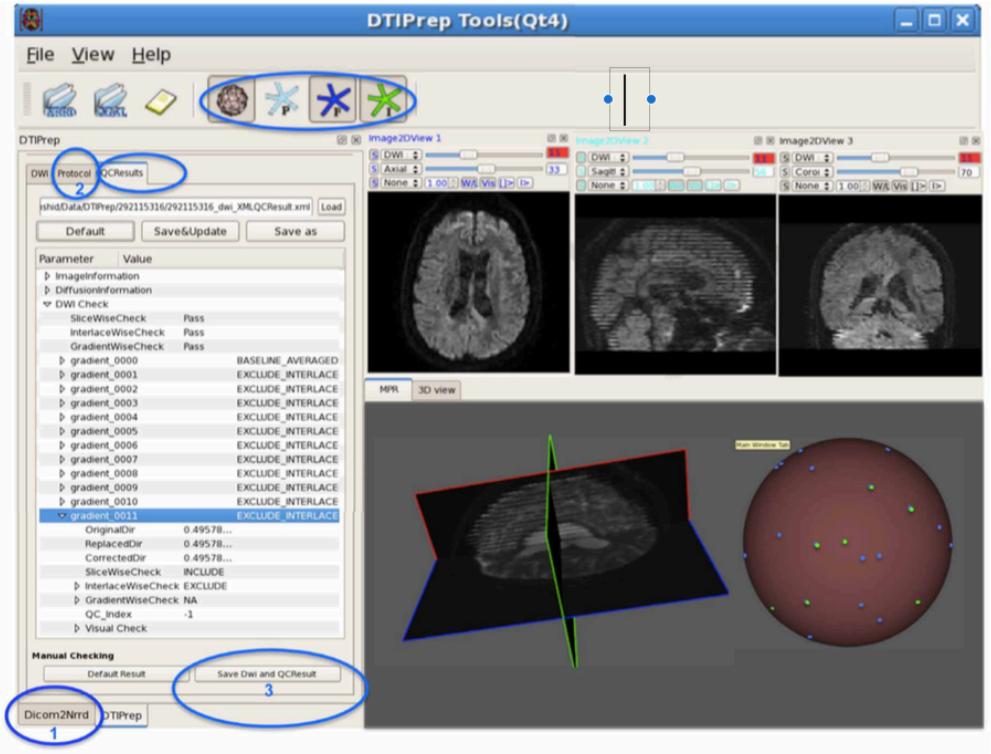
QC in the Human Connectome Project

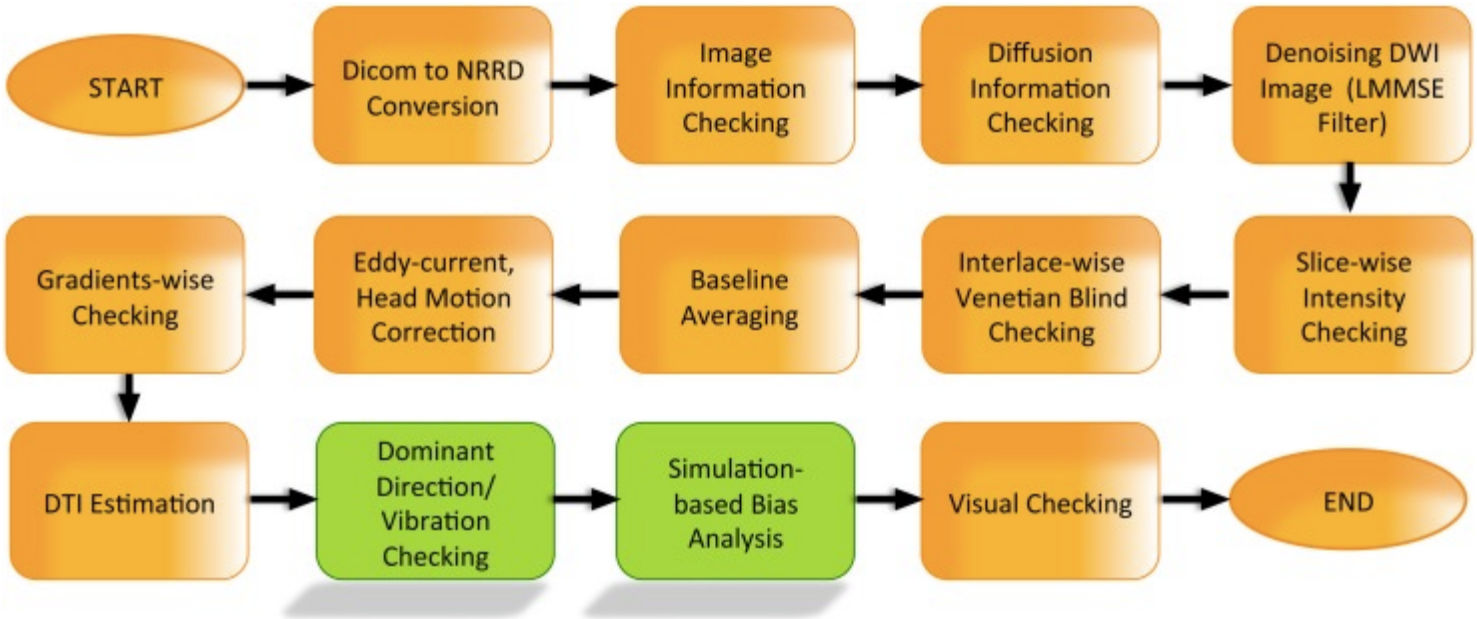


DWI Code & QA

DTIPrep

- Component of Slicer
- Customize protocol files
- Should be done first in order to remove bad b-values, directions, acquisition artifacts





Connectome Pipeline

BIAC scanning

Preprocessing / QA (motion, SNR)

Response functions for CSF, WM, GM

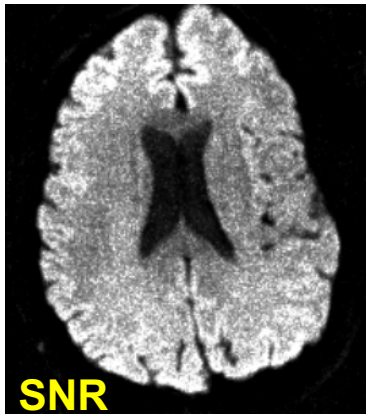
SIFT

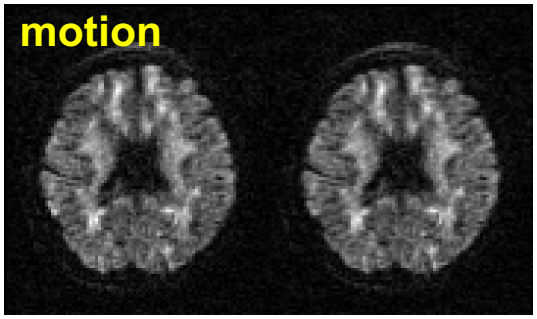
(Spherical-deconvolution Informed Filtering of Tractograms)

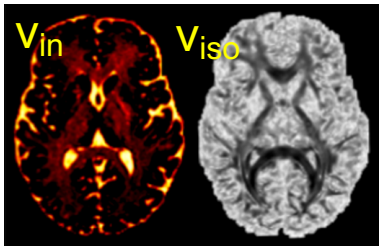
ACT

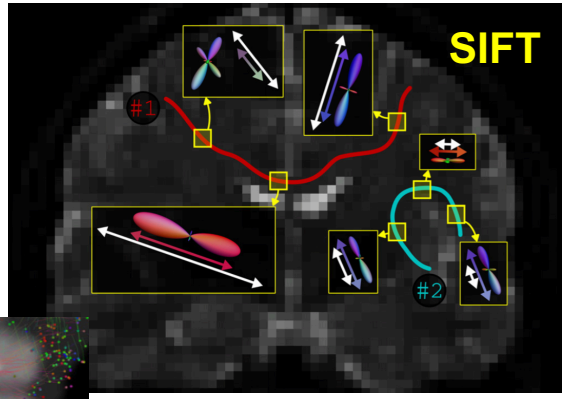
(Anatomically Constrained Tractography)

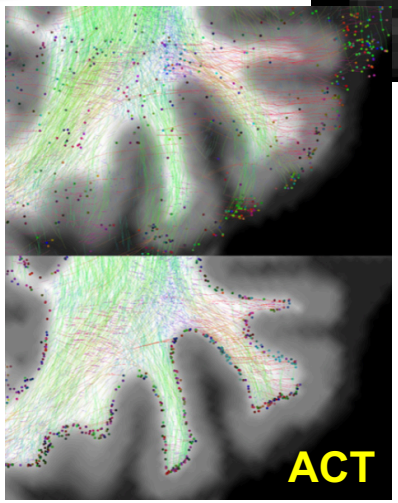
Connectome

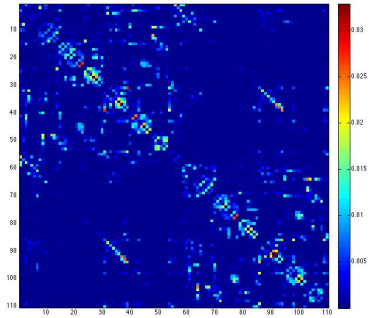












DWI Code & QA

some basic code

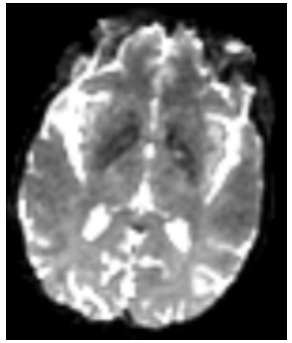
```
# denoise original files
dwidenoise data.nii.gz denoise_output.nii.gz -noise
noise_output.nii.gz
```

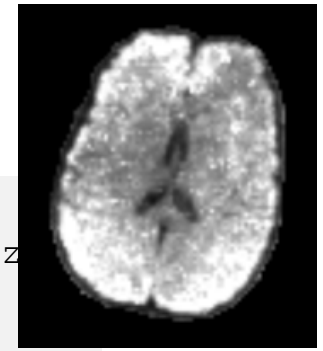
```
# skull strip denoised DWI
bet denoise_output.nii.gz denoise_output2.nii.gz -f 0.1 -F
```

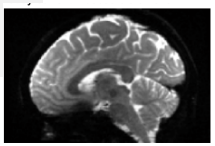
```
# first step in calculating mean b values to get SNR
fslroi denoise_output2.nii.gz denoise_output3.nii.gz 1 25
```

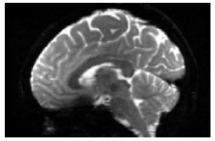
```
# calculate mean b values to get SNR
fslmaths -dt input denoise_output3.nii.gz -Tmean mean_b_vals.nii.gz
odt input
# calculate SNR
fslmaths -dt input mean_b_vals.nii.gz -div noise_output.nii.gz
SNR_output
```

```
# dwipreprocess
dwipreproc denoise_output2.nii.gz preproc_output.nii.gz -
rpe_none -pe_dir AP -fslgrad bvecs bvals -export_grad_fsl
new_bvecs new_bvals
```





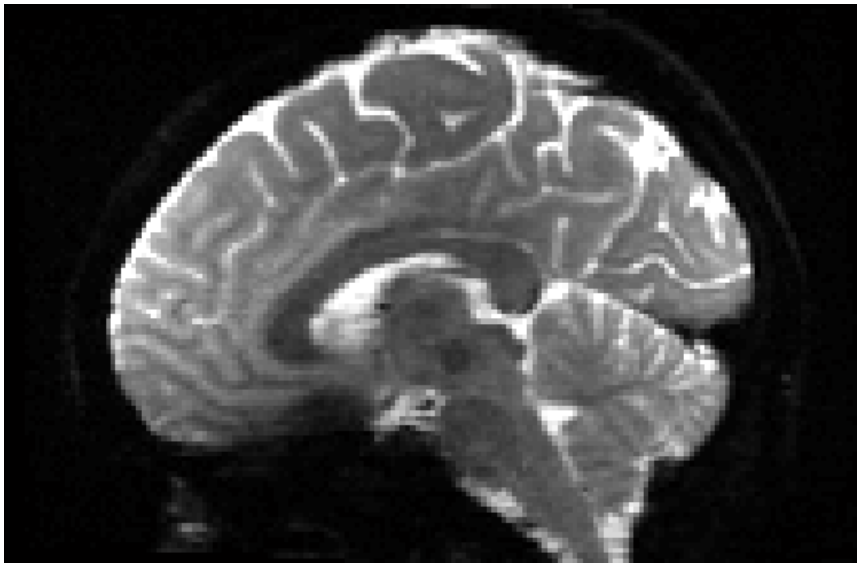




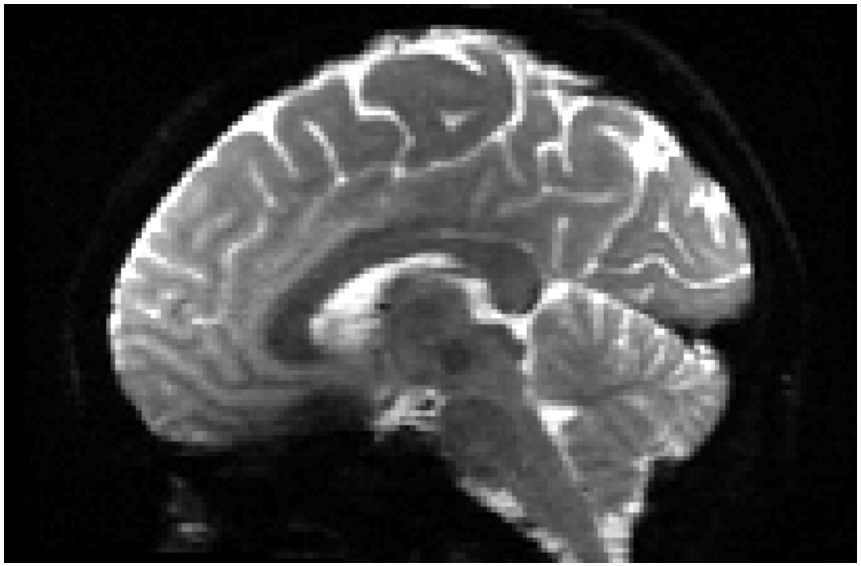
DWI Code & QA

Correction for subject motion and eddy current induced distortions

Before dwipreproc



After dwipreproc

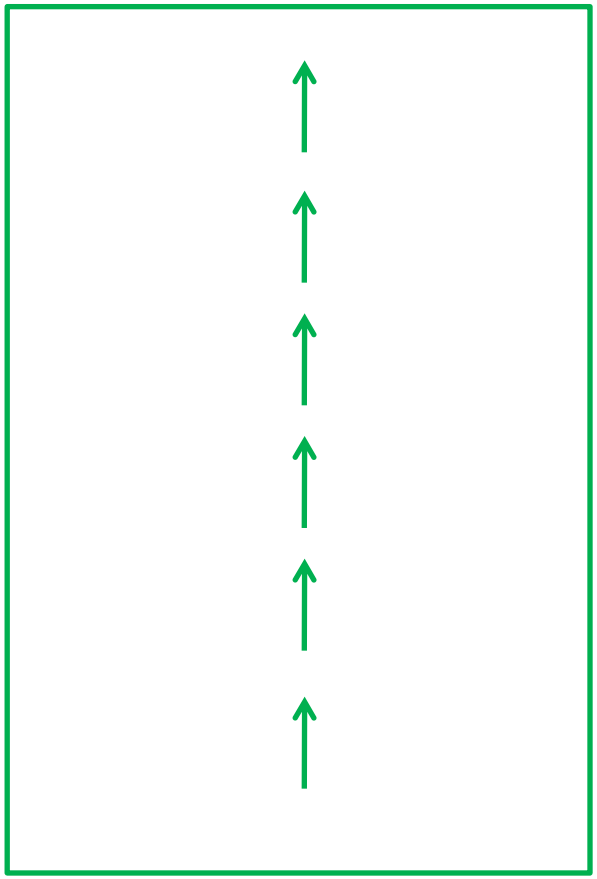


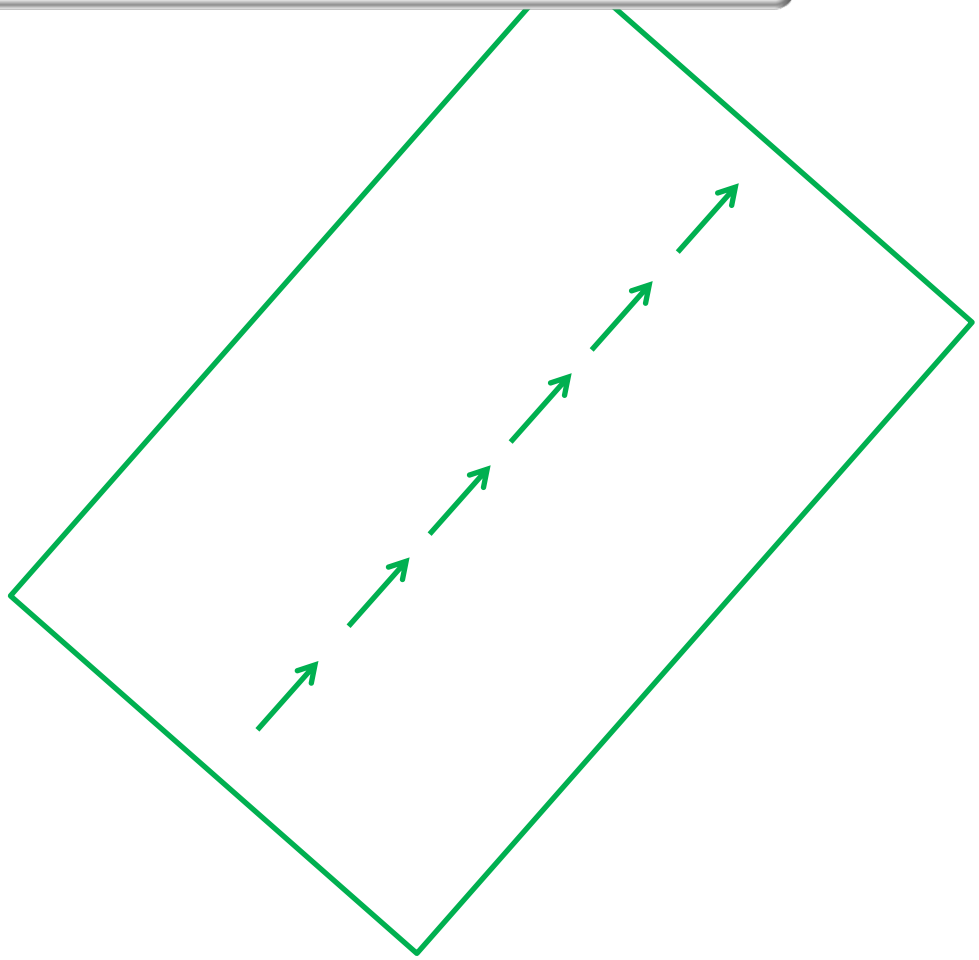
DWI Code & QA

Magnetic Resonance in Medicine 61:1336–1349 (2009)

The *B*-Matrix Must Be Rotated When Correcting for Subject Motion in DTI Data

Alexander Leemans* and Derek K. Jones



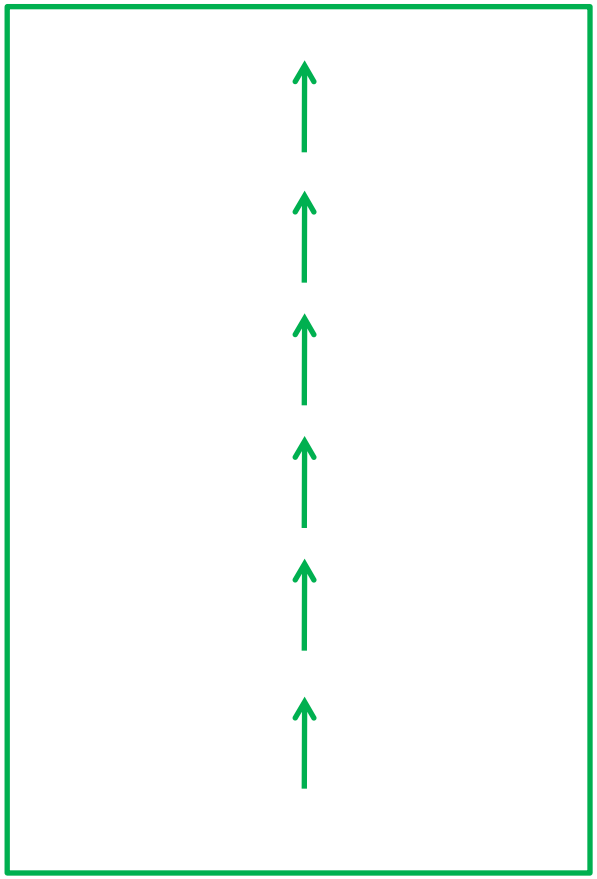


"Reference image"

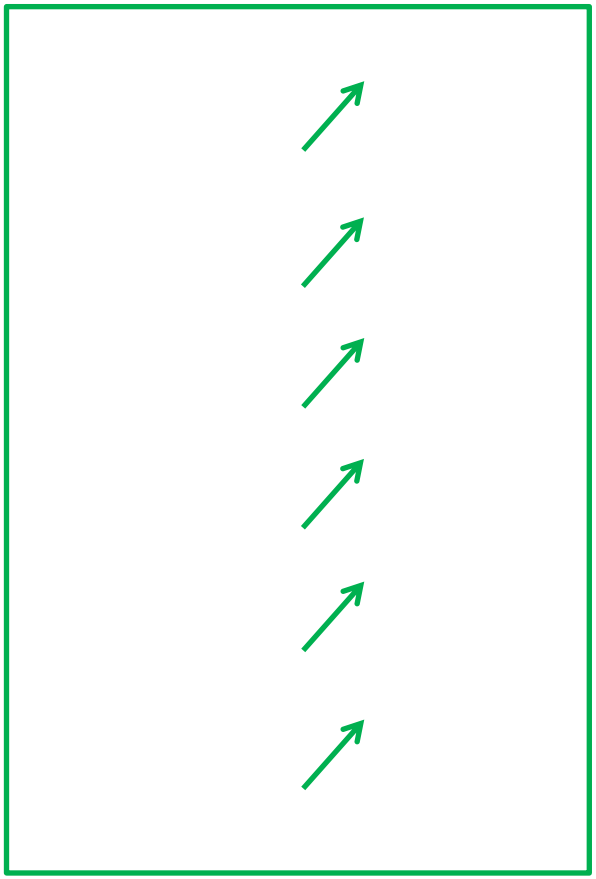
"Image with subject motion"

DWI Code & QA

Correction for subject motion and eddy current induced distortions

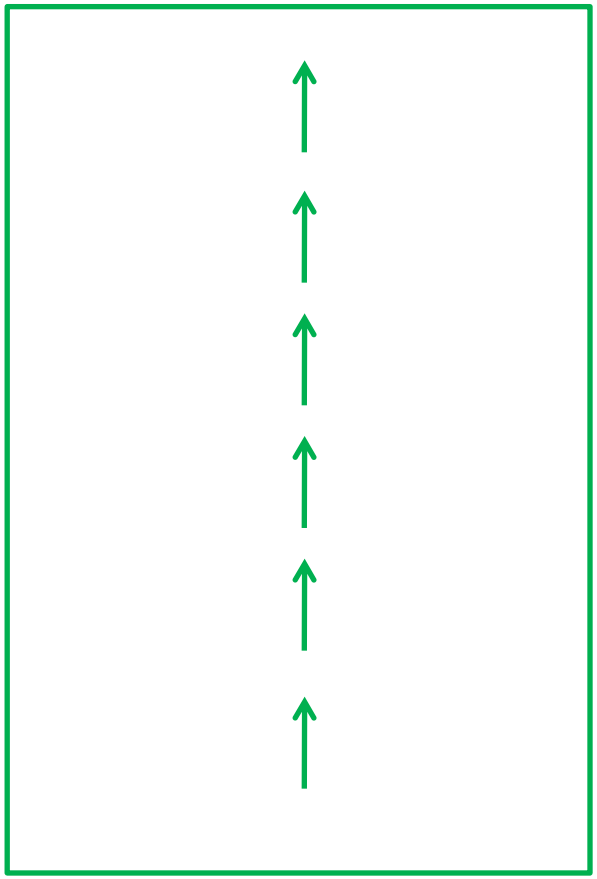


"Reference image"

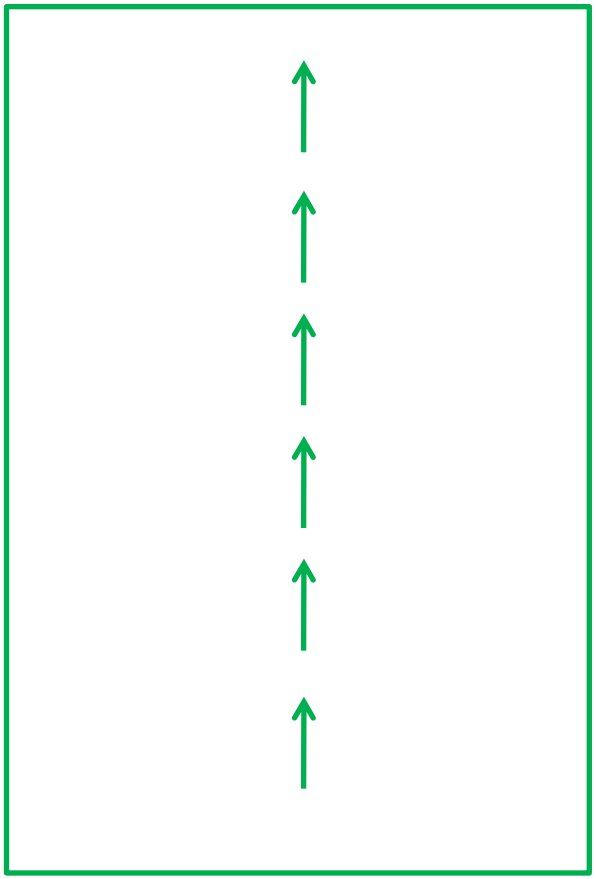


"Corrected image"
(**no** B-matrix rotation)

Correction for subject motion and eddy current induced distortions

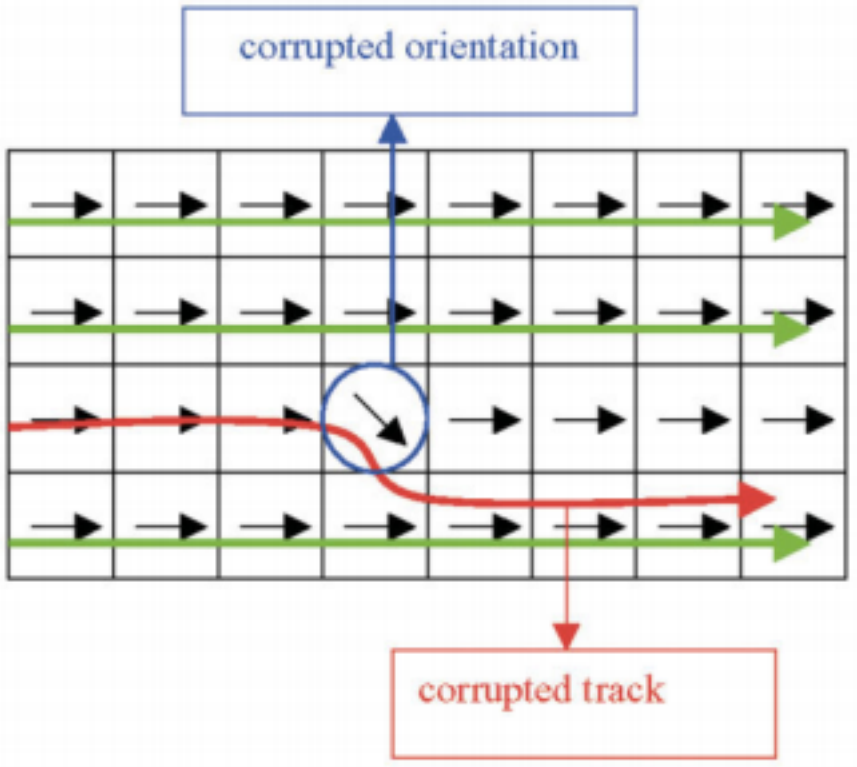


“Reference image”



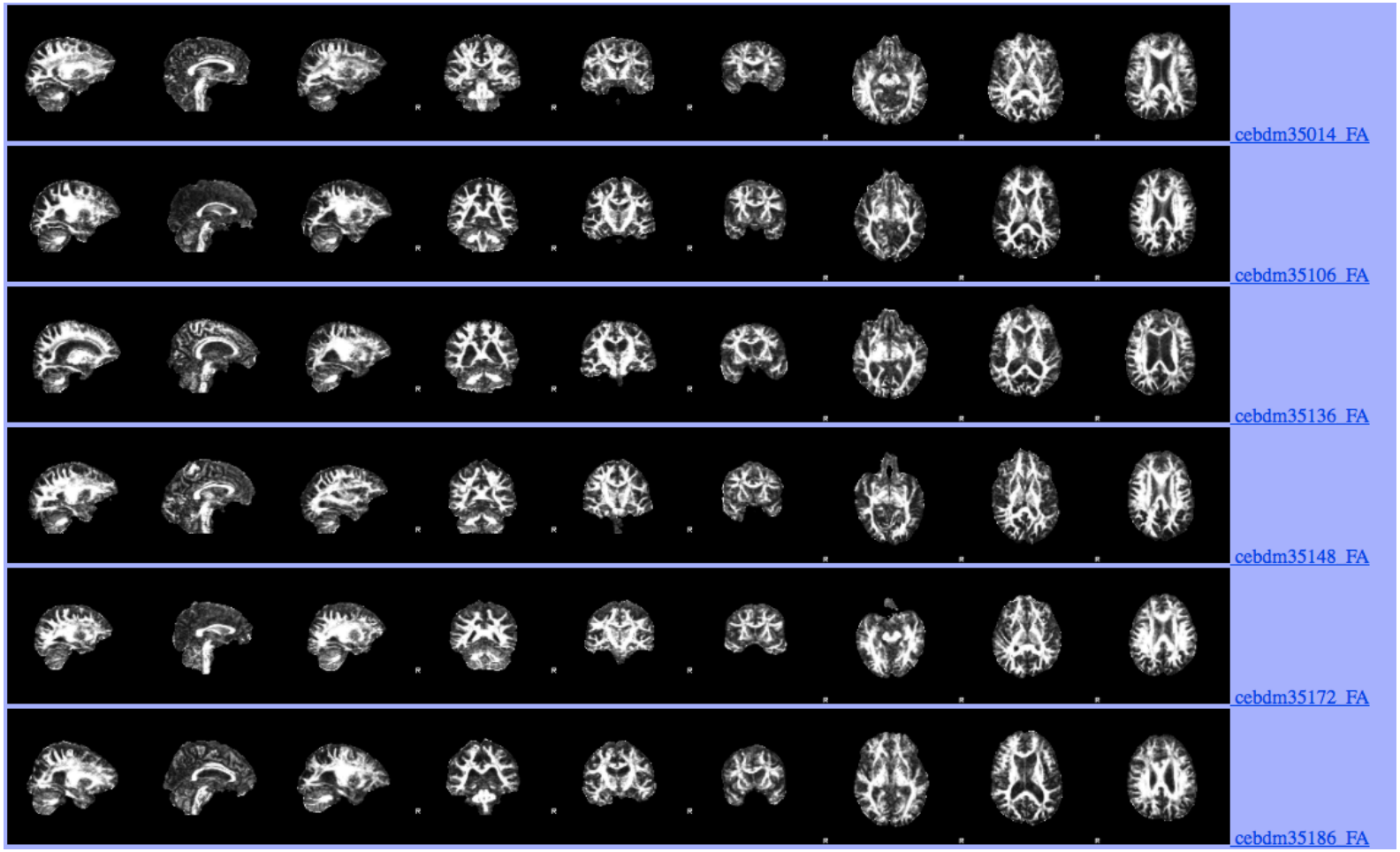
“Corrected image”
(**with** B-matrix rotation)

DWI Code & QA

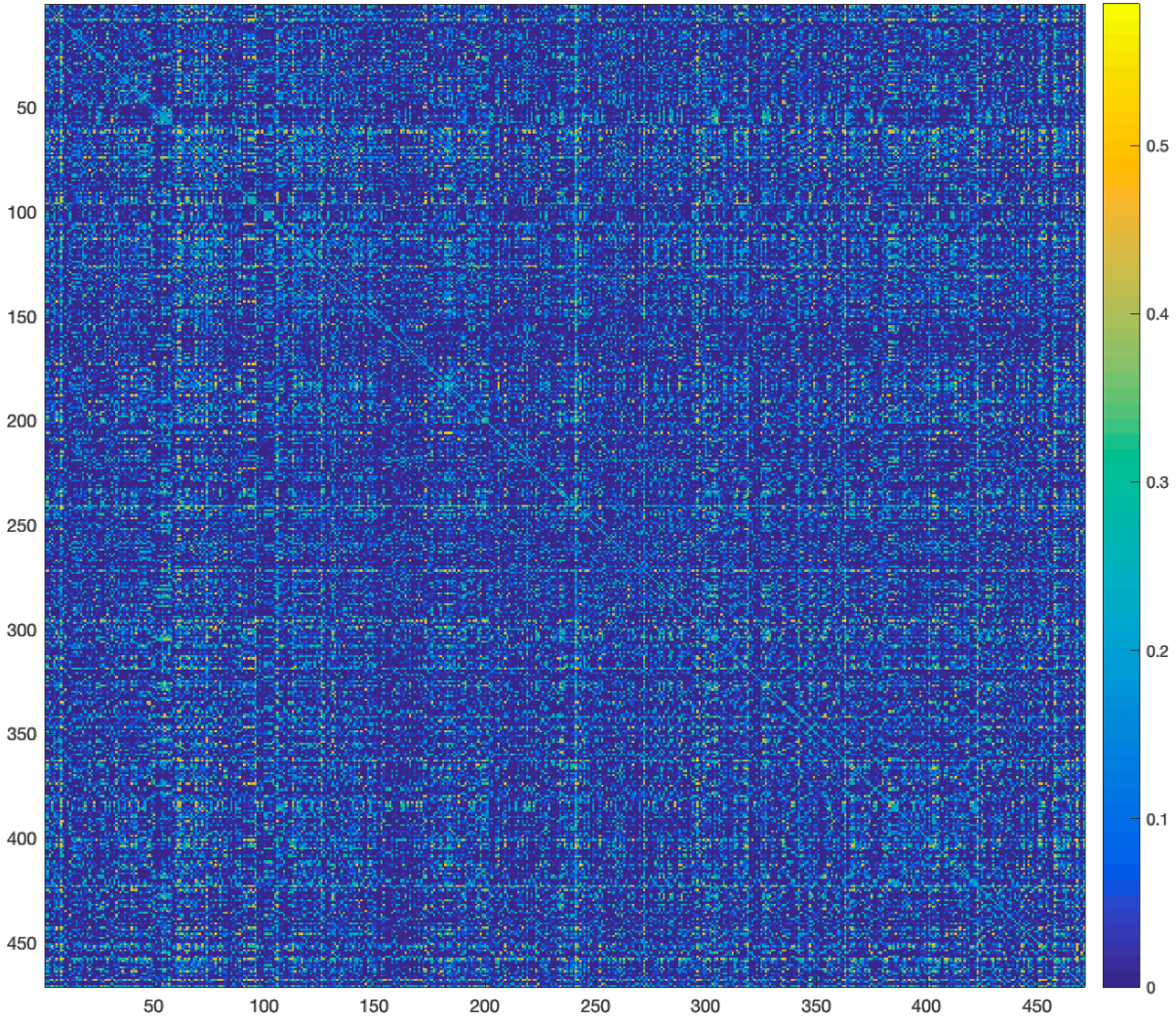


DWI Code & QA

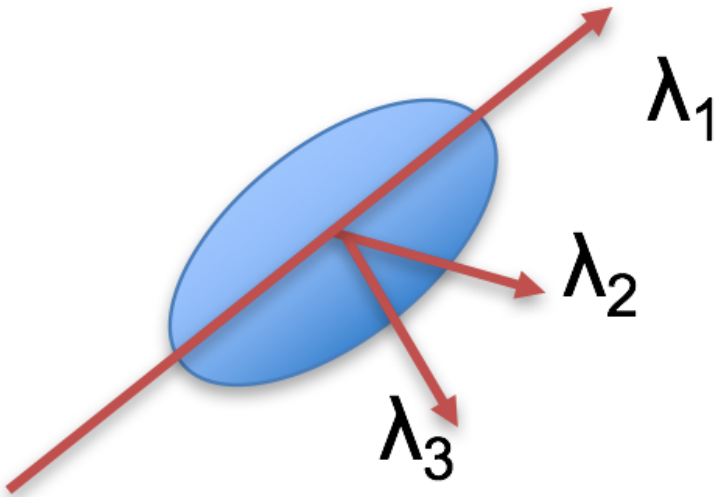
```
# QA with slicesdir
slicesdir *.nii.gz
```



Structural Connectome Background



DTI: The Tensor Model



We use the data reconstructed from diffusion-weighted images to make models of what we think that diffusion means.

The tensor matrix and the ellipsoid can be described by the:

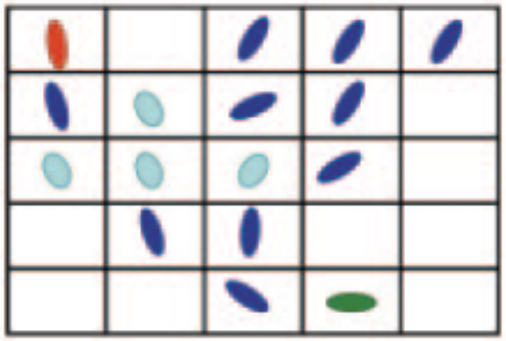
1. Size of the principles axes = Eigenvalue
2. Direction of the principles axes = Eigenvector

- These are represented by

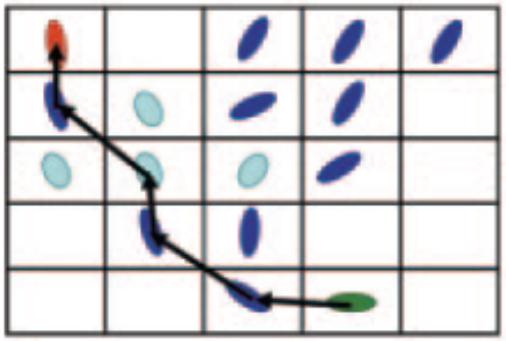
$$(\lambda_1, \lambda_2, \lambda_3)$$

Structural Connectome Background

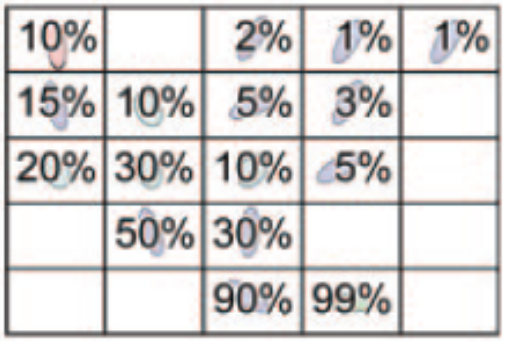
Tractography – General Techniques



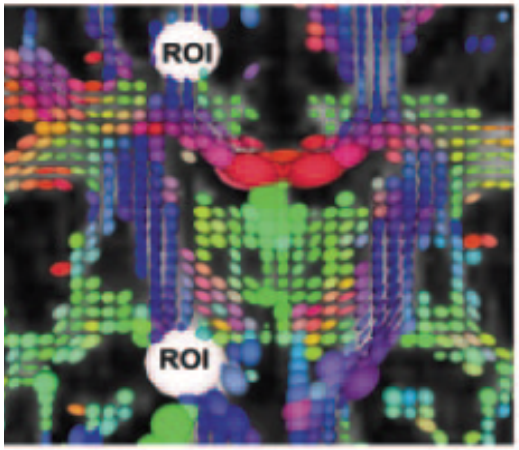
Degree of anisotropy

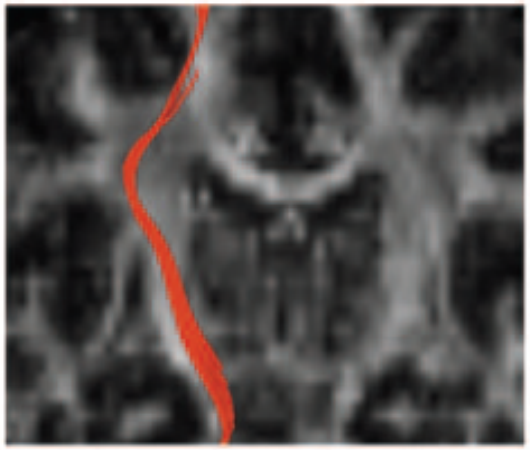


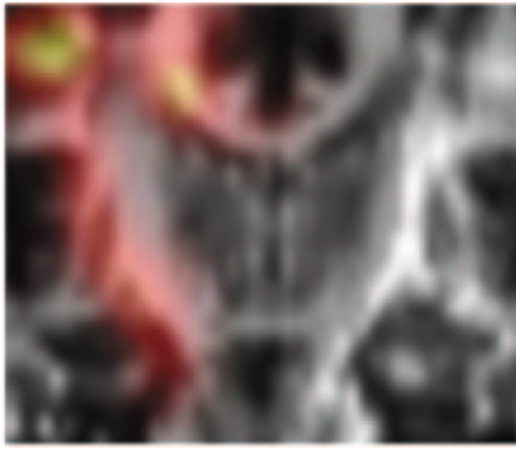
Streamline tractography



Probabilistic tractography







Nucifora et al. *Radiology*, 2007

Structural Connectome Background

Decisions in connectome construction	relevant outcomes
Decisions in Tractography	
Angular threshold	fewer false positive tracts, at the risk of cutting out bendy tracts like the unicate fasciculus, U-fibers
FA threshold	Higher FA threshold increases the rate of False Negatives (you miss genuine fiber pathways), and decreases the rate of False Positives (more confidence in the reconstructed pathways)
Basis function (CSD, probabilistic, tensor)	Lots of potential differenences…
Decisions in Connectome Character	
Binary v. Weighted	Graph properties were developed on binary graphs…but structural connections have a wide range.
FA weighting v. Streamline Counts	more accurate diffusion modeling per voxel
Area-weighting	Larger node is more likely to generate more fibers. Generally aggreed-upon correction for larger ROIs
Length-weighting	Control for the Euclidiean factor
Statistical Corrections	Bonferroni, etc.
Density/Sparsity Corrections	Might help to correct for individual differences in graph density. Often used in binary graphs (e.g., top 20% of connections).

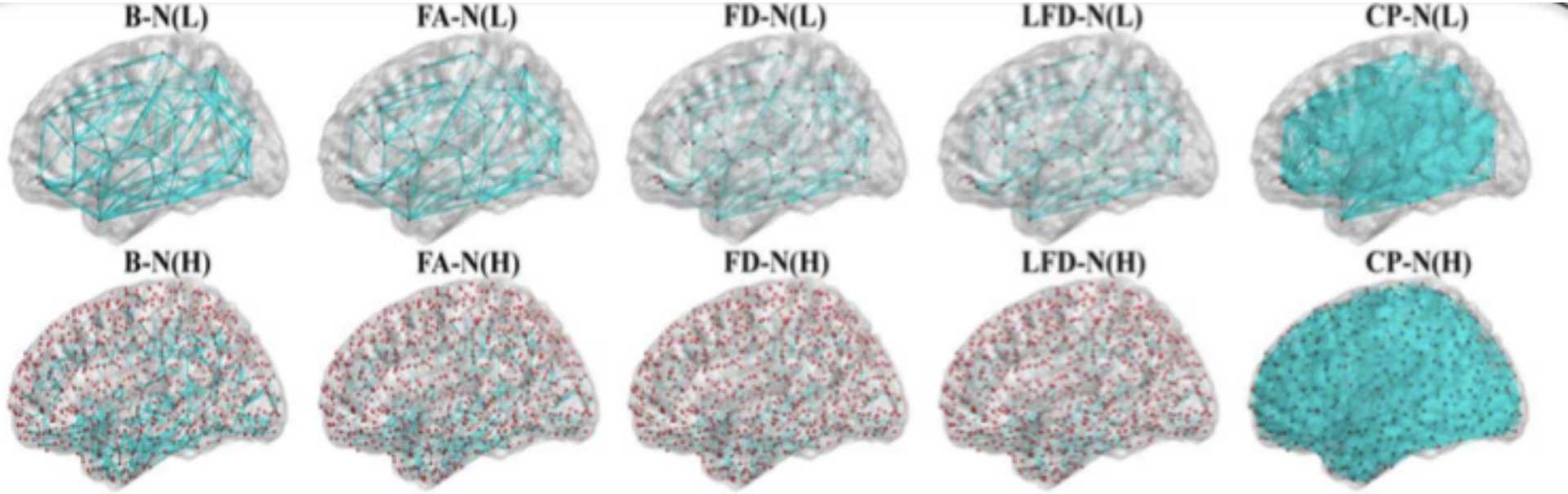
Structural Connectome Background

Convergence and Divergence Across Construction Methods for Human Brain White Matter Networks: An Assessment Based on Individual Differences

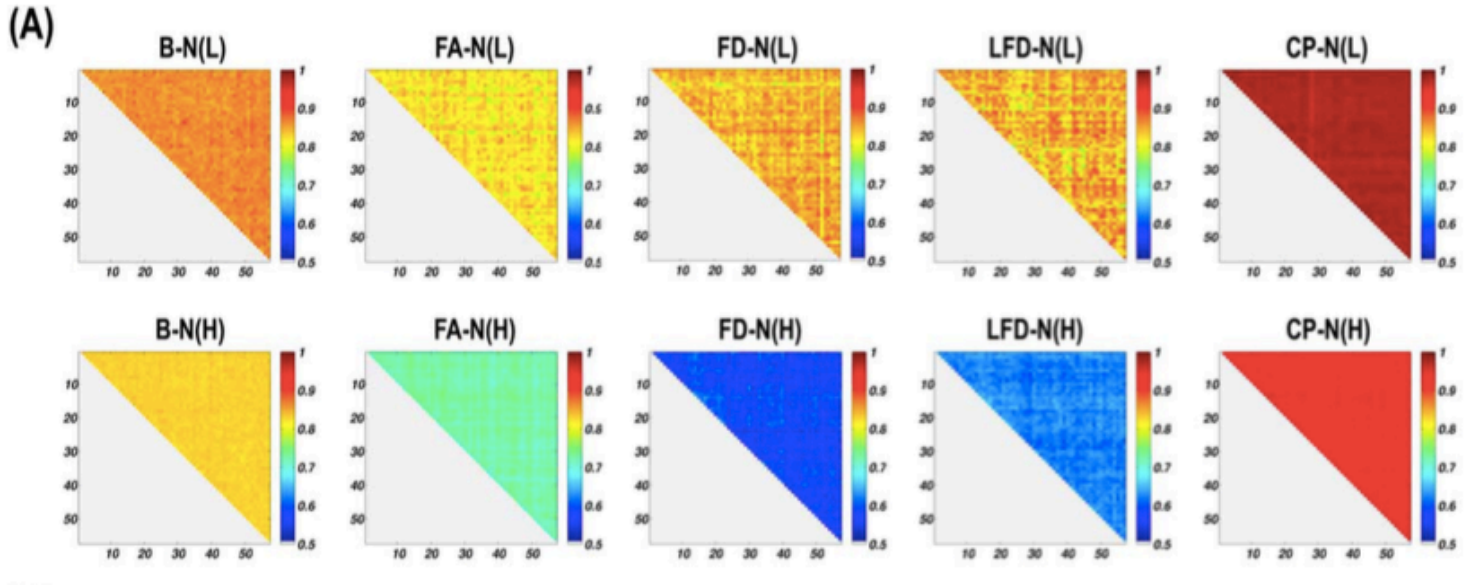
Suyu Zhong, Yong He, and Gaolang Gong*

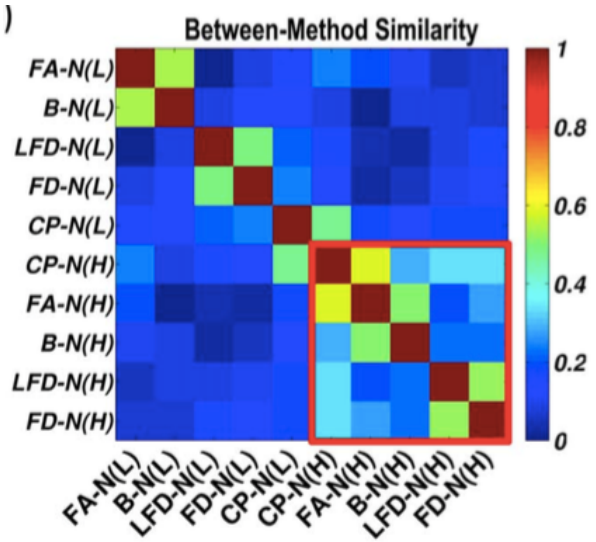
State Key Laboratory of Cognitive Neuroscience and Learning & IDG/McGovern Institute for Brain Research, Beijing Normal University, Beijing, China

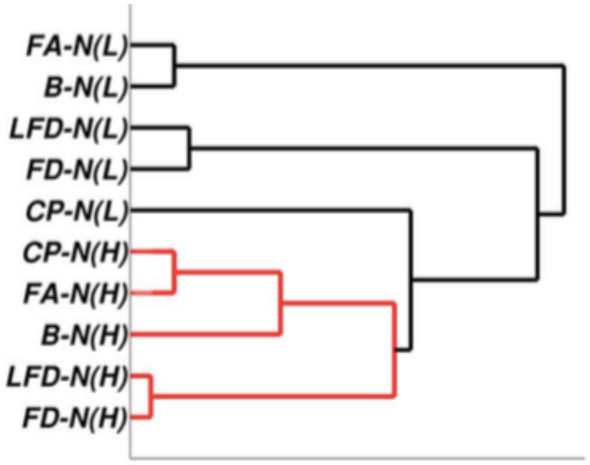
B	Binary
FA	FA-values
FD	FA, weighted by density/area
LFD	FA, weighted by dens. and len.
L	90 ROIs
H	1024 ROIs



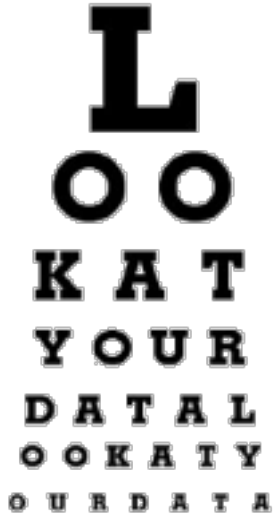
Structural Connectome Background







Connectome Code & QA



Tools:

Processing

- MRTrix

QA

- R-based code
- LiFE

Connectome Pipeline

BIAC scanning

Preprocessing / QA (motion, SNR)

Response functions for CSF, WM, GM

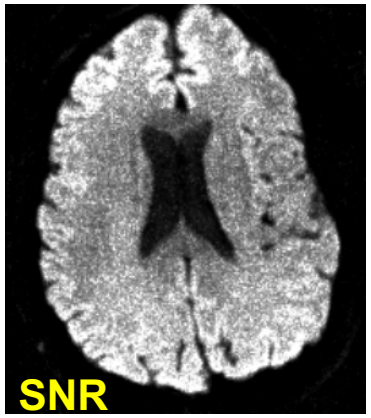
SIFT

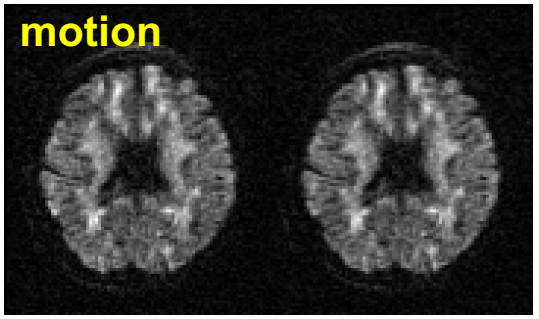
(Spherical-deconvolution Informed Filtering of Tractograms)

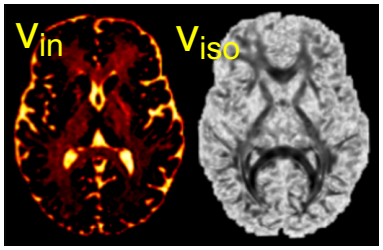
ACT

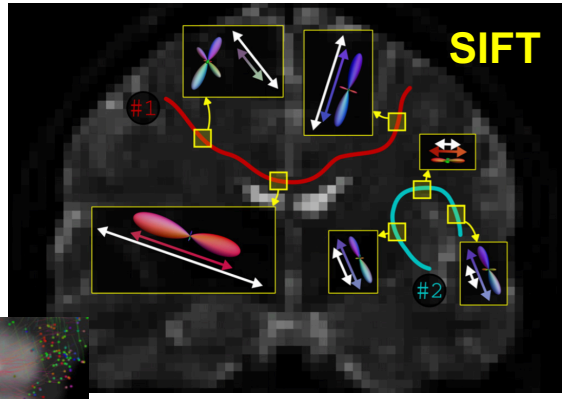
(Anatomically Constrained Tractography)

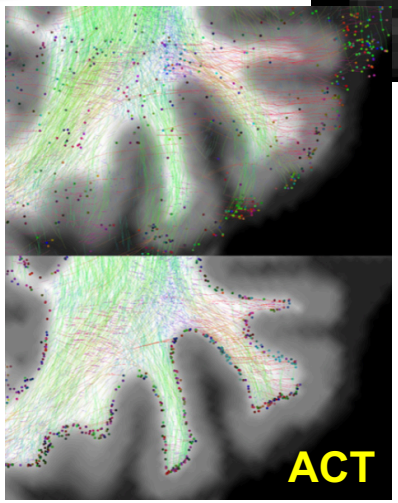
Connectome

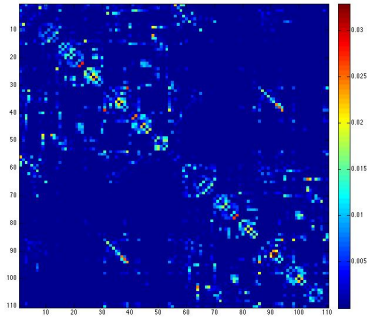






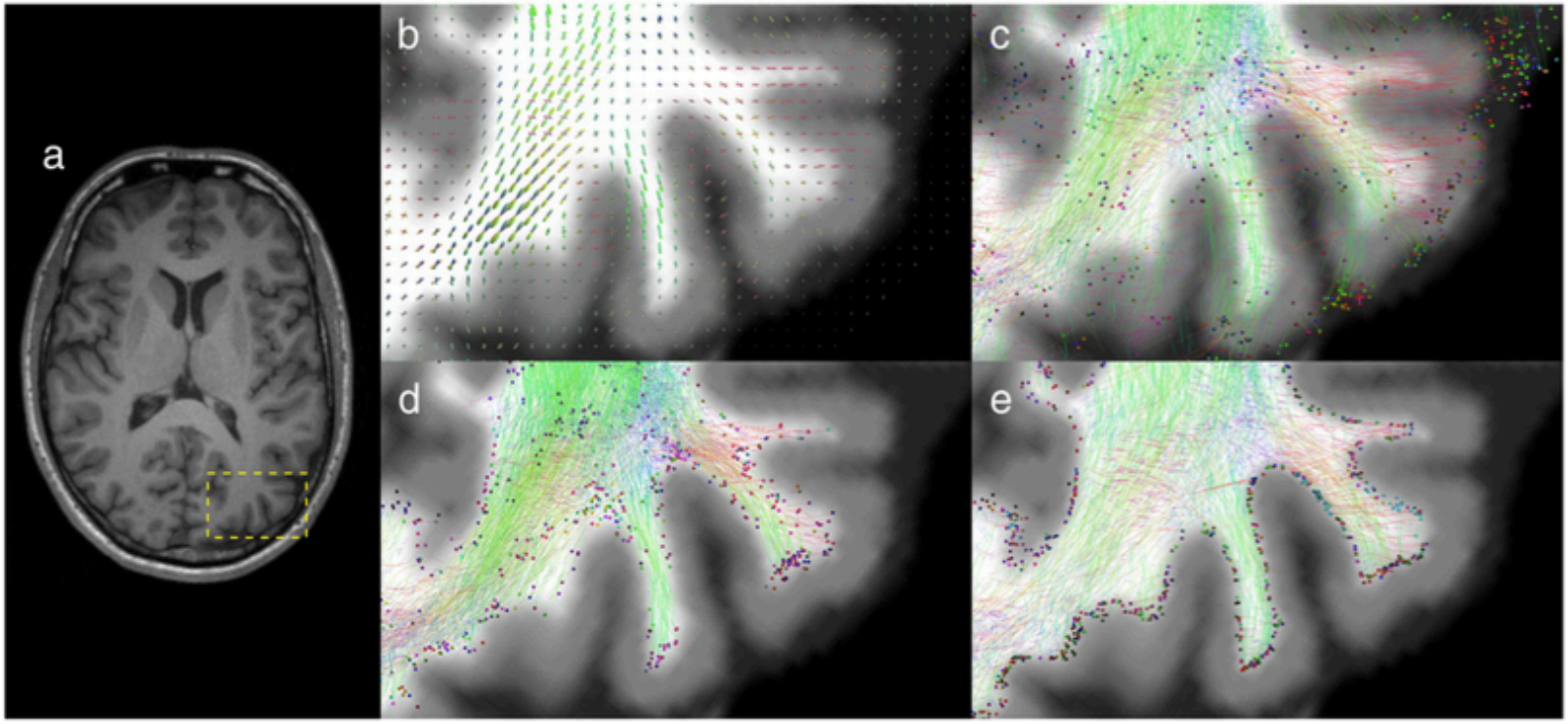






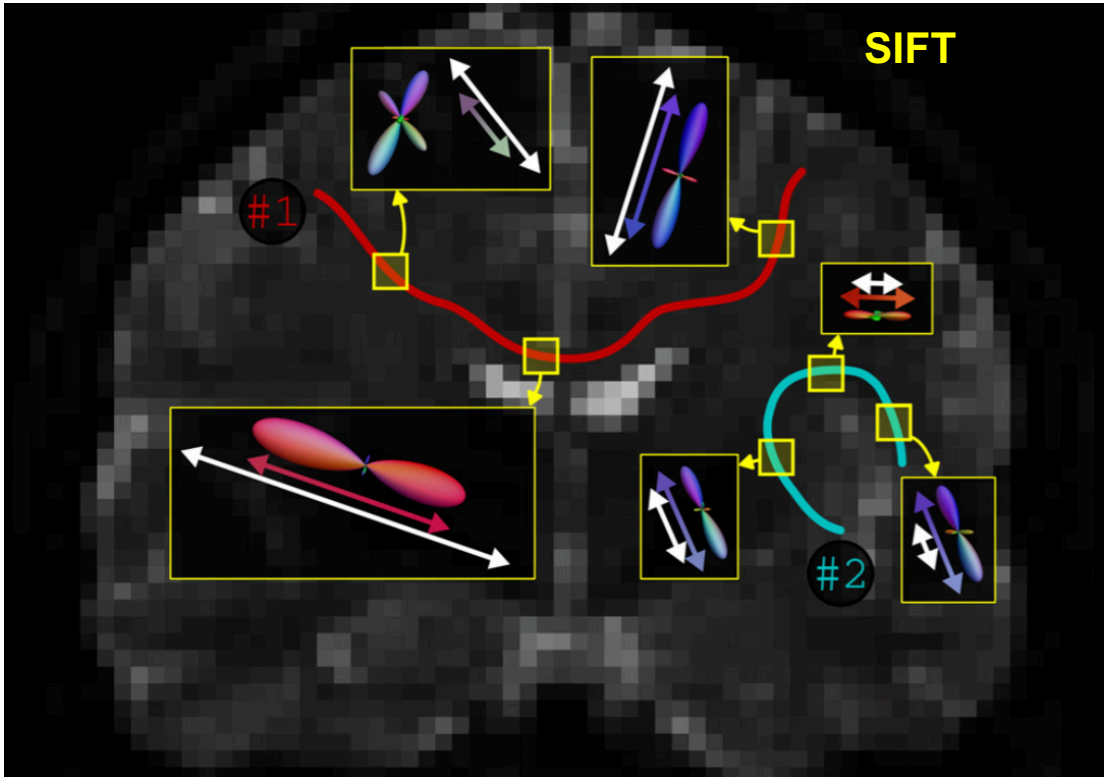
Connectome Code & QA

ACT & SIFT



Connectome Code & QA

ACT & SIFT



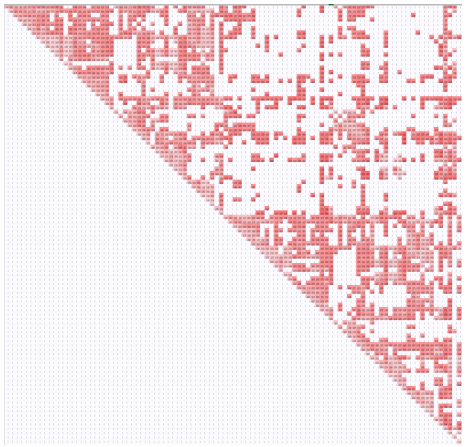
Connectome Code & QA

Electric Dinolab Pipeline

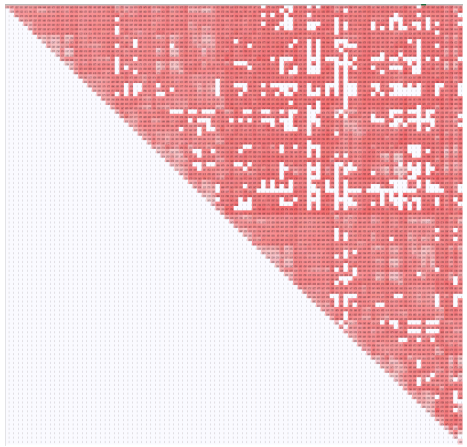
```
# seeding done at random within a mask image
tckgen -seed_image bias_output_mask.nii.gz FOD.nii.gz tracks.tck -select 10M
-maxlength 250 -fslgrad new_bvecs new_bvals -act

tcksift tracks.tck FOD.nii.gz SIFTtracks.tck -term_number 1M -force
```

connectome with SIFT/ACT
based on FA values



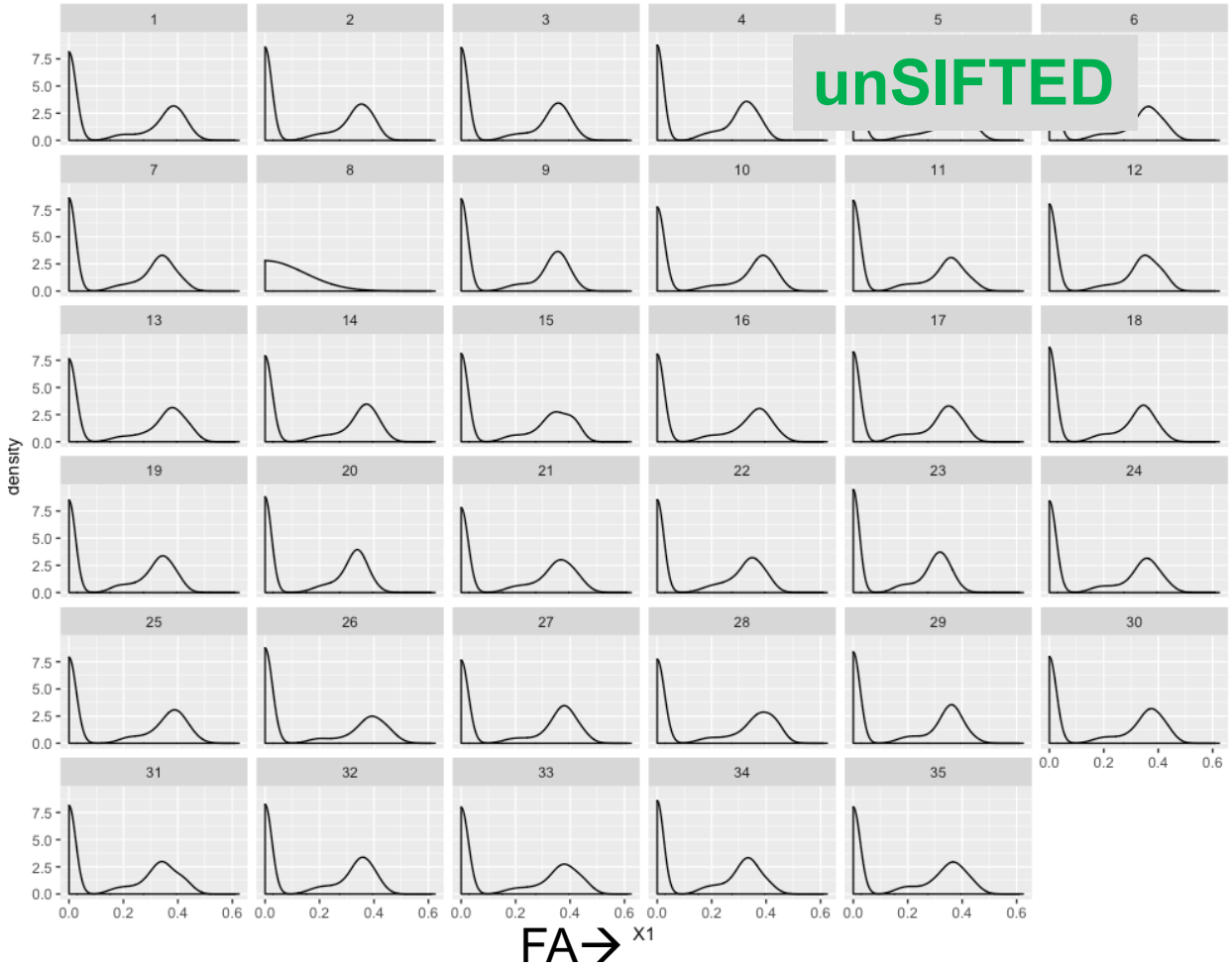
connectome without SIFT/ACT
based on FA values



Connectome Code & QA

Why QA for connectomes?

```
final < readcsv(”connectome.csv" + col_names = FALSE)
tt <- ggplot(final, aes(x=X1))
tt + geom_density(aes(fill=factor(X3))) + facet_wrap(~X2)
```



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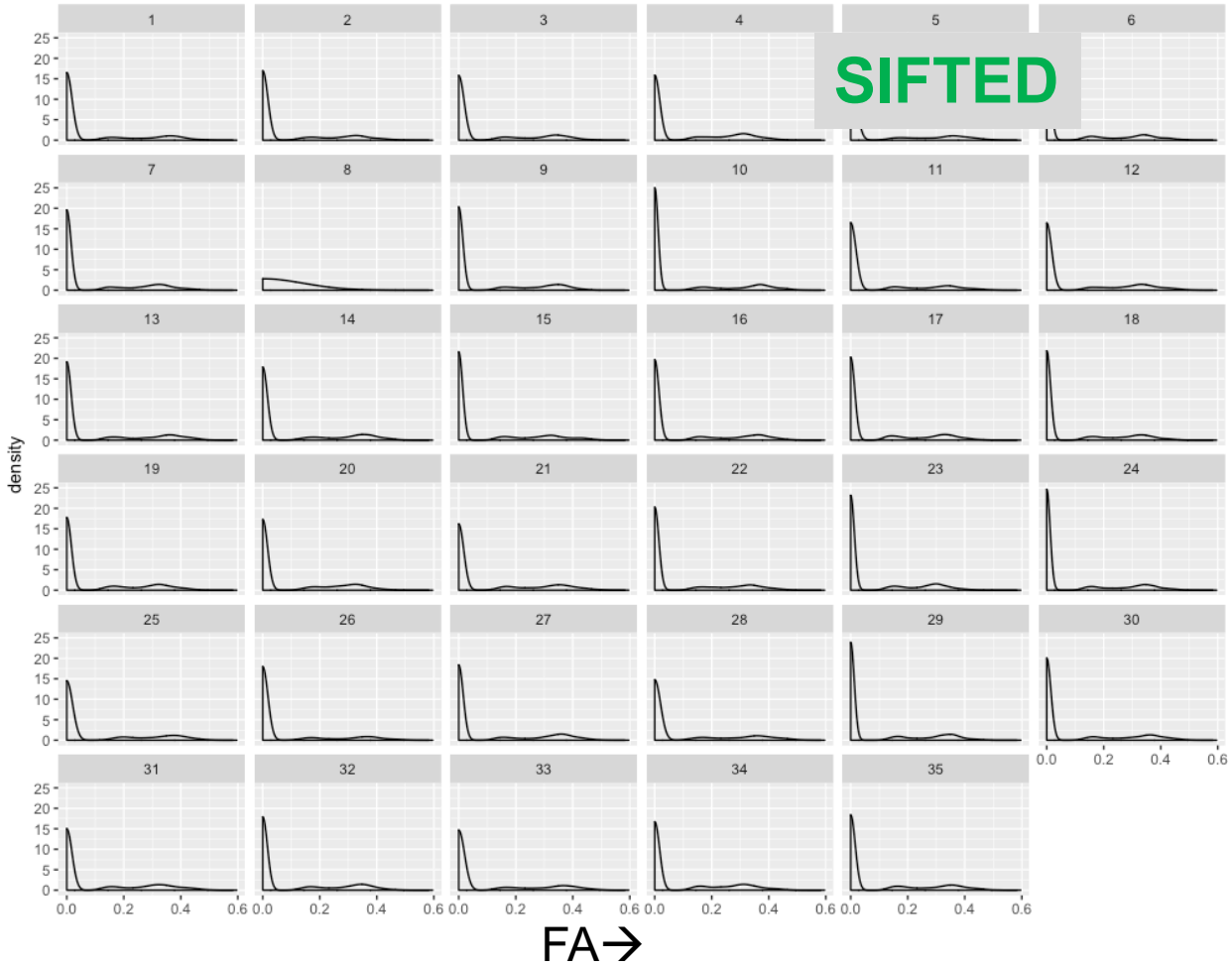


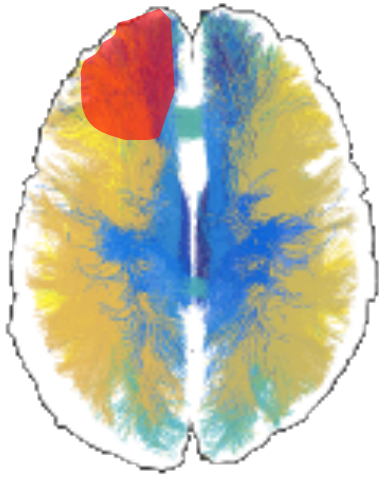
Connectome Code & QA

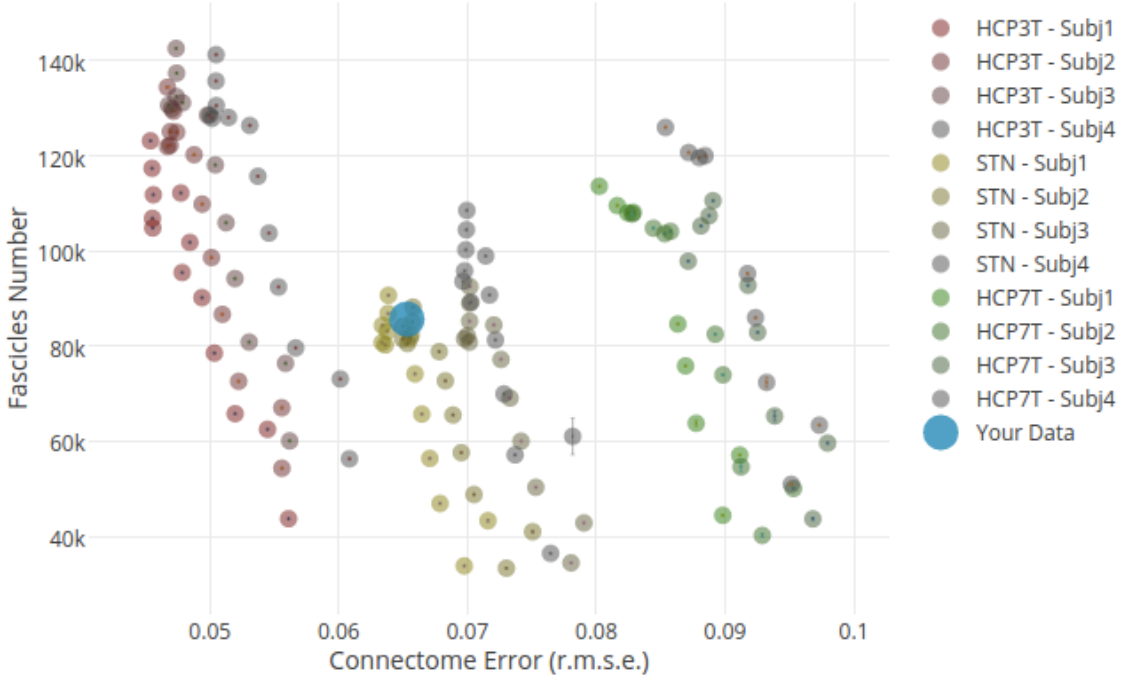
Other Connectome QA: Linear Fascicle Estimation (LiFE)

Evaluation and statistical inference for human connectomes

Franco Pestilli[1], Jason D Yeatman[1], Ariel Rokem[1], Kendrick N Kay[1,2] & Brian A Wandell[1]

Selectively lesion one ROI/bundle of fascicles, and test how well the remaining fibers predict the missing fibers.





Discussion Questions

- *The relationship between structural and functional connectomes is never 1-to-1; what implications does this have for GT metrics based on structure?*

- *What responsibility do papers not focused on methods have to demonstrate the validity of their underlying structural analysis?*

- *How do decisions on preprocessing or the parcellation scheme affect the quality of the structural connectome?*