

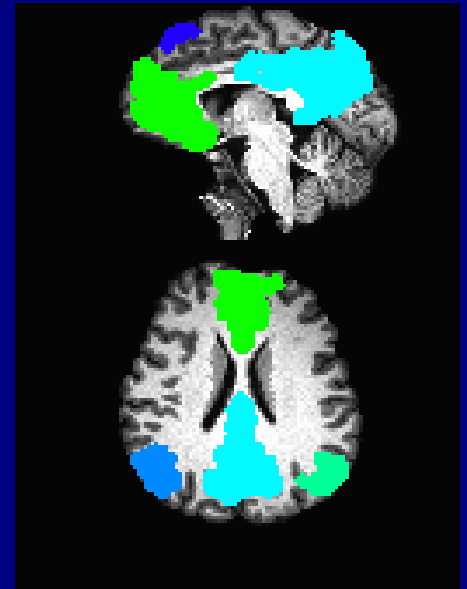
Introduction to
AFNI+SUMA+FATCAT,
Part II

DTI+tractography for data exploration and
complementing functional connectivity

Terminology for tracking in FATCAT

Target: set of voxels with the same integer value, for which we want to find connections (e.g., GM ROI).

Network of targets: set of targets among which we want to find pairwise (AND-logic) or individual (OR-logic) connections (e.g., functional network).



Terminology for tracking in FATCAT

Target: set of voxels with the same integer value, for which we want to find connections (e.g., GM ROI).

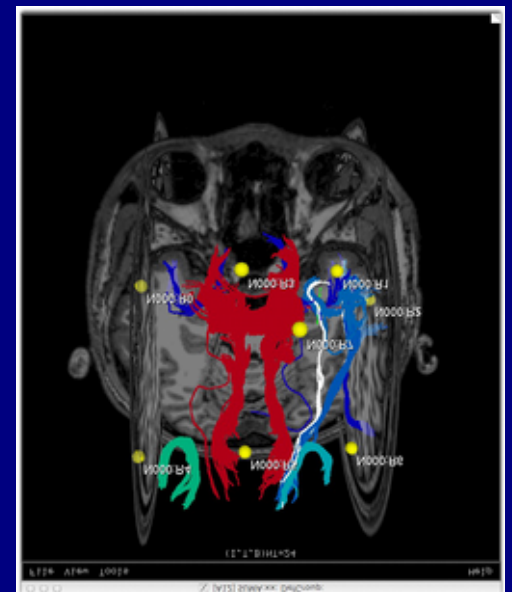
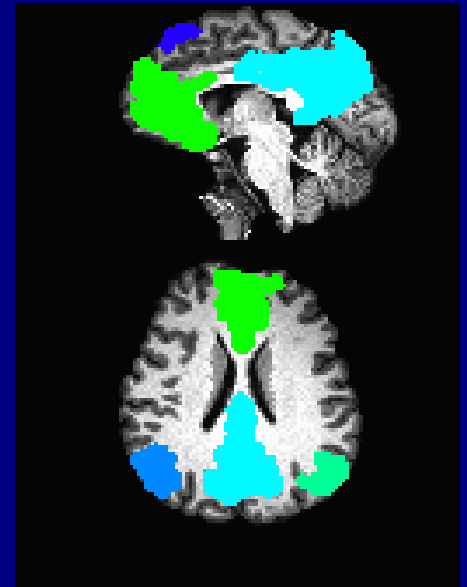
Network of targets: set of targets among which we want to find pairwise (AND-logic) or individual (OR-logic) connections (e.g., functional network).

Tract: set of ordered points in space related to estimated WM trajectory.

Bundle: set of one or more tracts through a single target (OR) or through any pair of targets (AND).

WM ROI: set of voxels through which a bundle passes (possibly after thresholding), useful for quantitative comparisons of average voxel vals.

WM network: set of WM ROIs, likely complementing a given target network

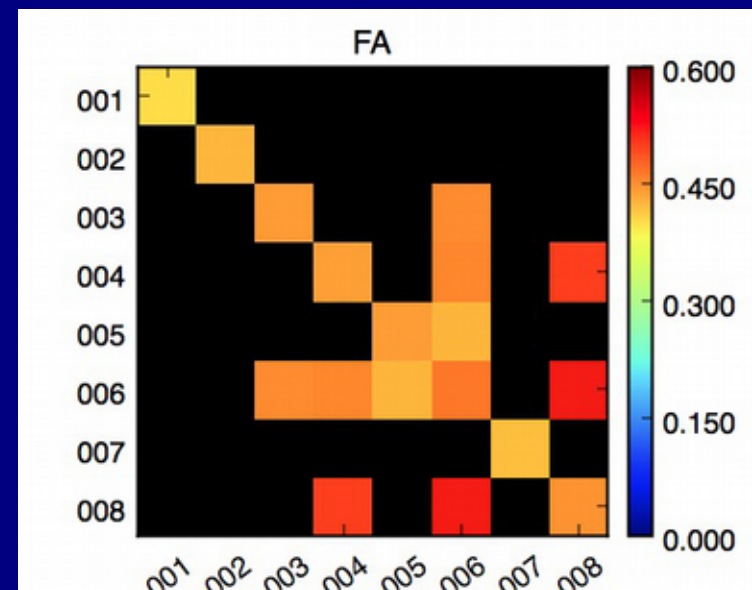
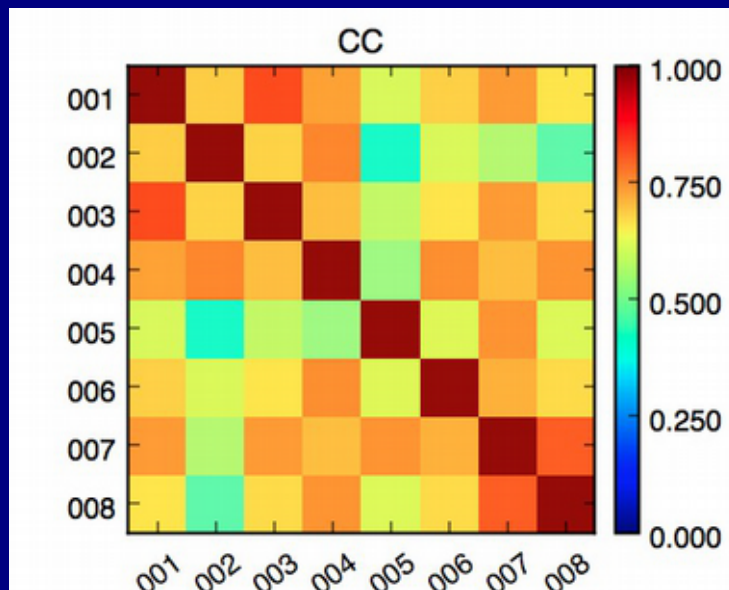


Terminology for tracking in FATCAT

“ $N \times N$ ” connectivity matrices for a network of N targets:

FC matrix: matrix of *functional* properties, such as average correlation between each pair of targets (\rightarrow value stored in each off-diagonal element)

SC matrix: matrix of *structural* properties, such as average FA in a WM ROI connecting two targets (off-diagonal) or WM ROI through single target (on-diagonal)



Question for doing tractography:

where does one go to get the ROIs to try to connect?

Question for doing tractography:

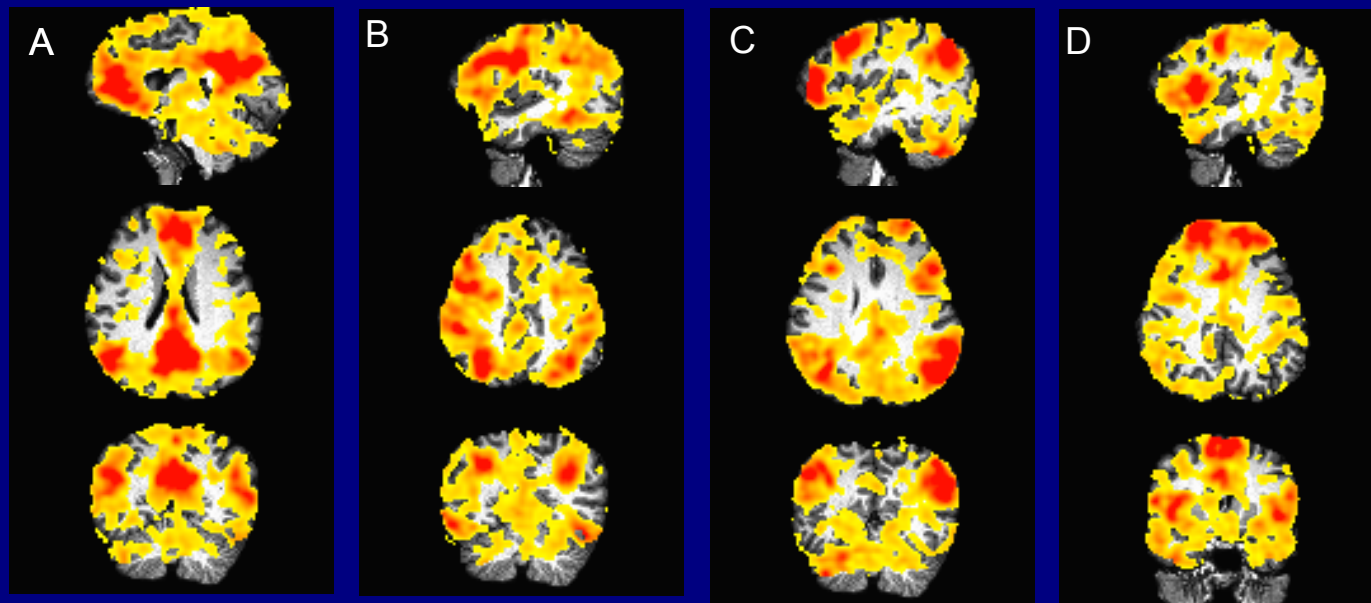
where does one go to get the ROIs to try to connect?

-> could go to atlases and standard maps,
or to exploratory spheres dotted around,

FMRI → networks of target ROIs

- + For example, one can perform ICA on a resting state study, resulting in several functional networks:

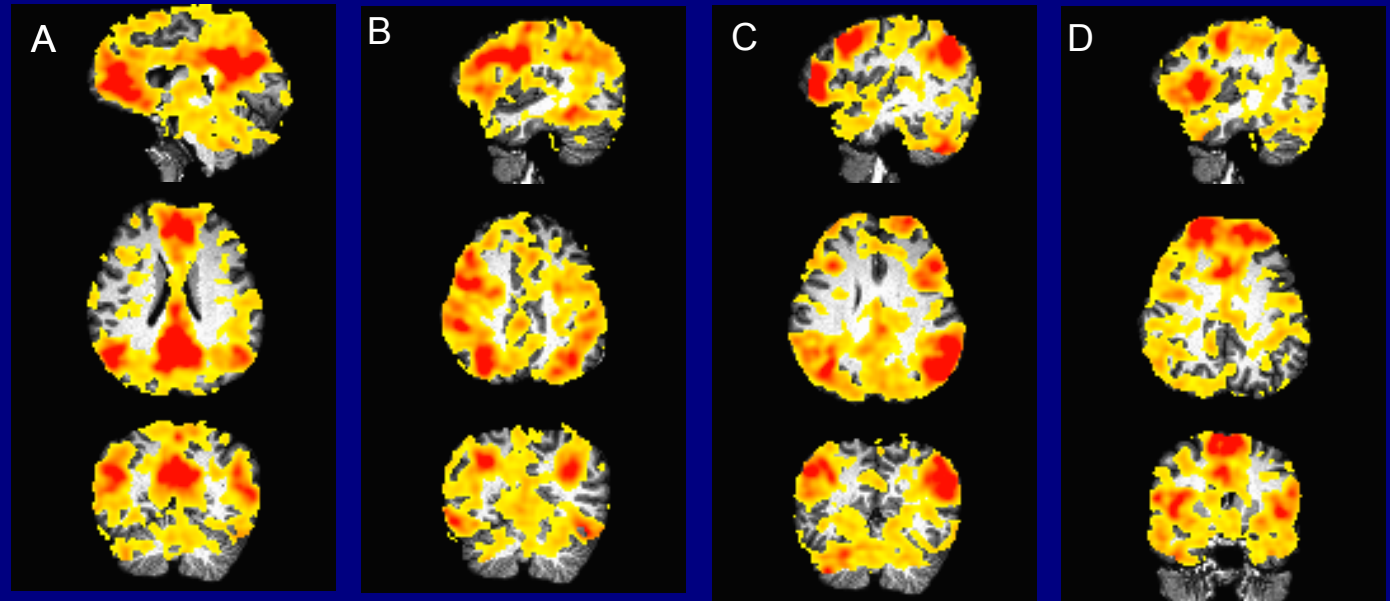
(each IC is map of Z-scores; here, shown for $Z > 0$)



FMRI → networks of target ROIs

- + For example, one can perform ICA on a resting state study, resulting in several functional networks:

(each IC is map of Z-scores; here, shown for $Z > 0$)

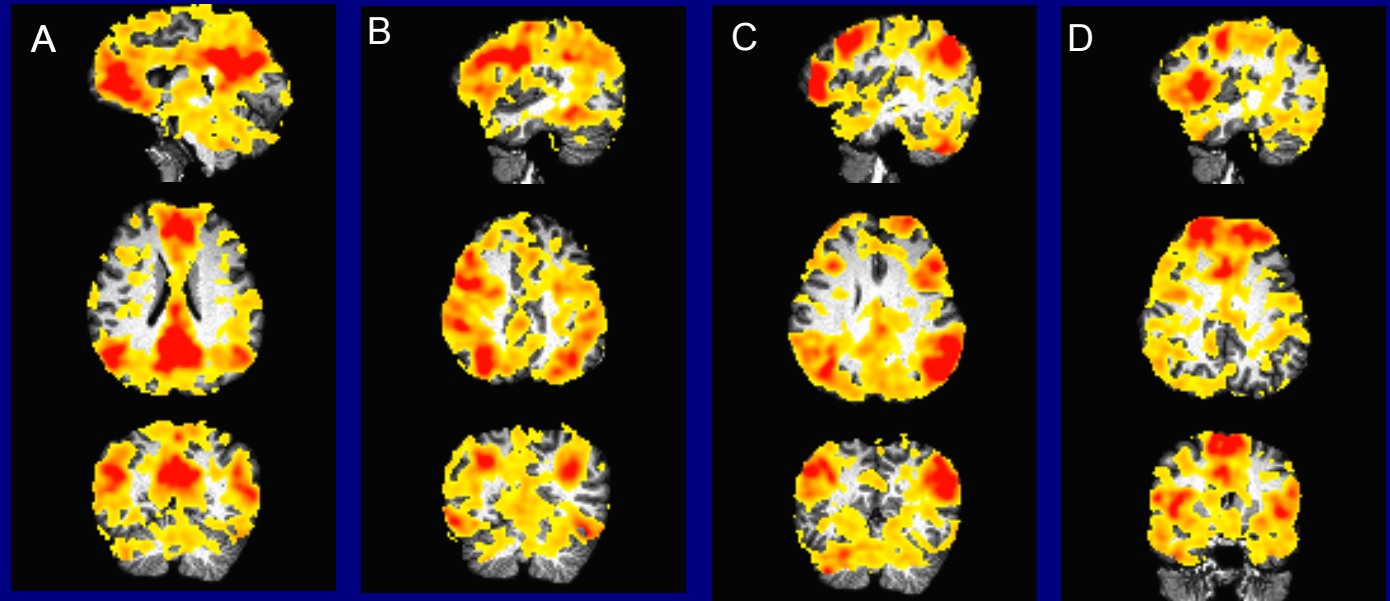


- + want to **isolate GM** ROIs, and then to **expand each** to make sure that they are at least touching nearby (*associated?*) WM voxels to have any hope to connect tracts

FMRI → networks of target ROIs

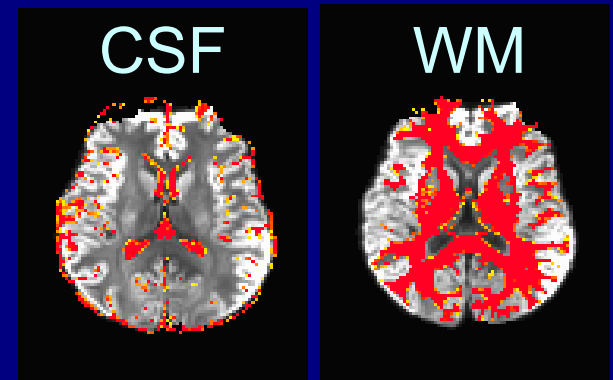
- + For example, one can perform ICA on a resting state study, resulting in several functional networks:

(each IC is map of Z-scores; here, shown for $Z > 0$)



- + **3dROIMaker** can parcellate into GM ROIs based on:

- thresholding **voxel values**
- thresholding **cluster size**
- subtract away CSF and WM voxels from segmentation maps
- **expand** each GM ROI to location of WM (don't want to *overexpand* unphysically)



FMRI → networks of target ROIs

Example case for ICA networks:

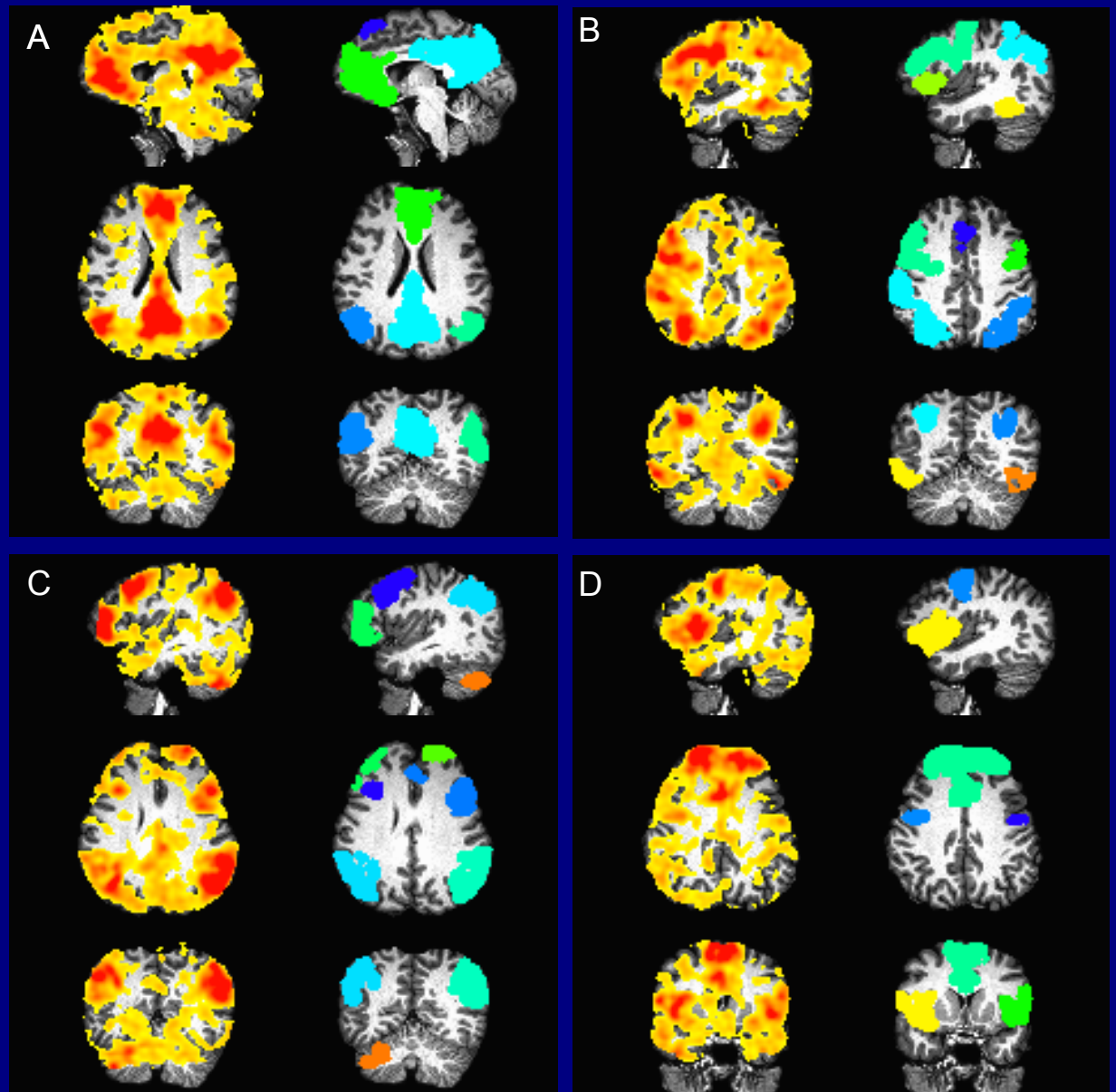
thresholded $Z > 3.0$

cluster volume > 130 voxels

expand clusters +2 voxels

limit expansion with WM map

(NB: this involved mapping FMRI data of ICs and T1 tissue segmentation results into DWI space; used 3dAllineate)



FMRI → networks of target ROIs

Example case for ICA networks:

thresholded $Z > 3.0$

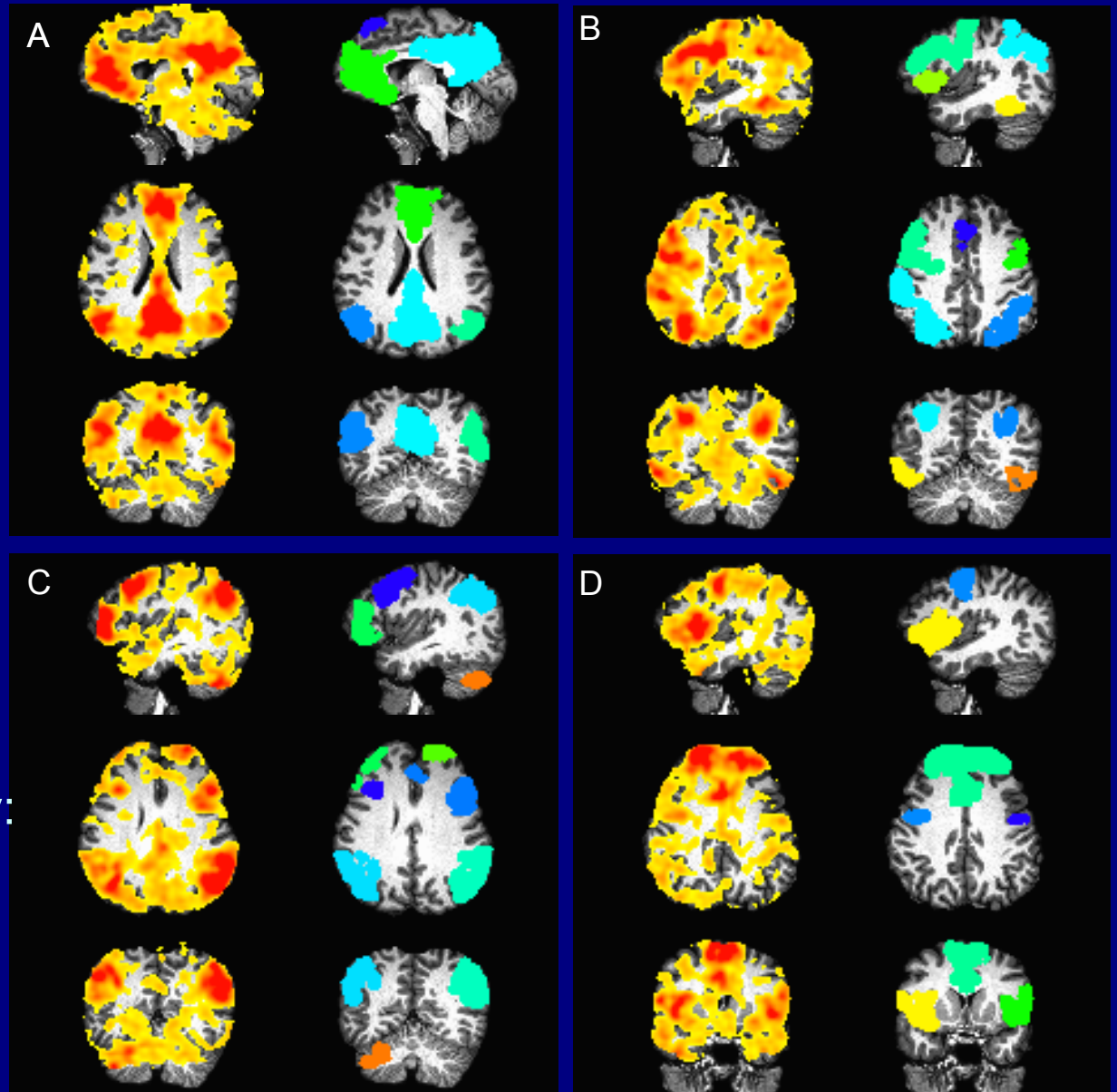
cluster volume > 130 voxels

expand clusters +2 voxels

limit expansion with WM map

(NB: this involved mapping FMRI data of ICs and T1 tissue segmentation results into DWI space; used 3dAllineate)

Also, for efficiency, can process multiple networks simultaneously:
use a multibrick file, with each network processed separately in each brick



FMRI → networks of target ROIs

Example case for ICA networks:

thresholded $Z > 3.0$

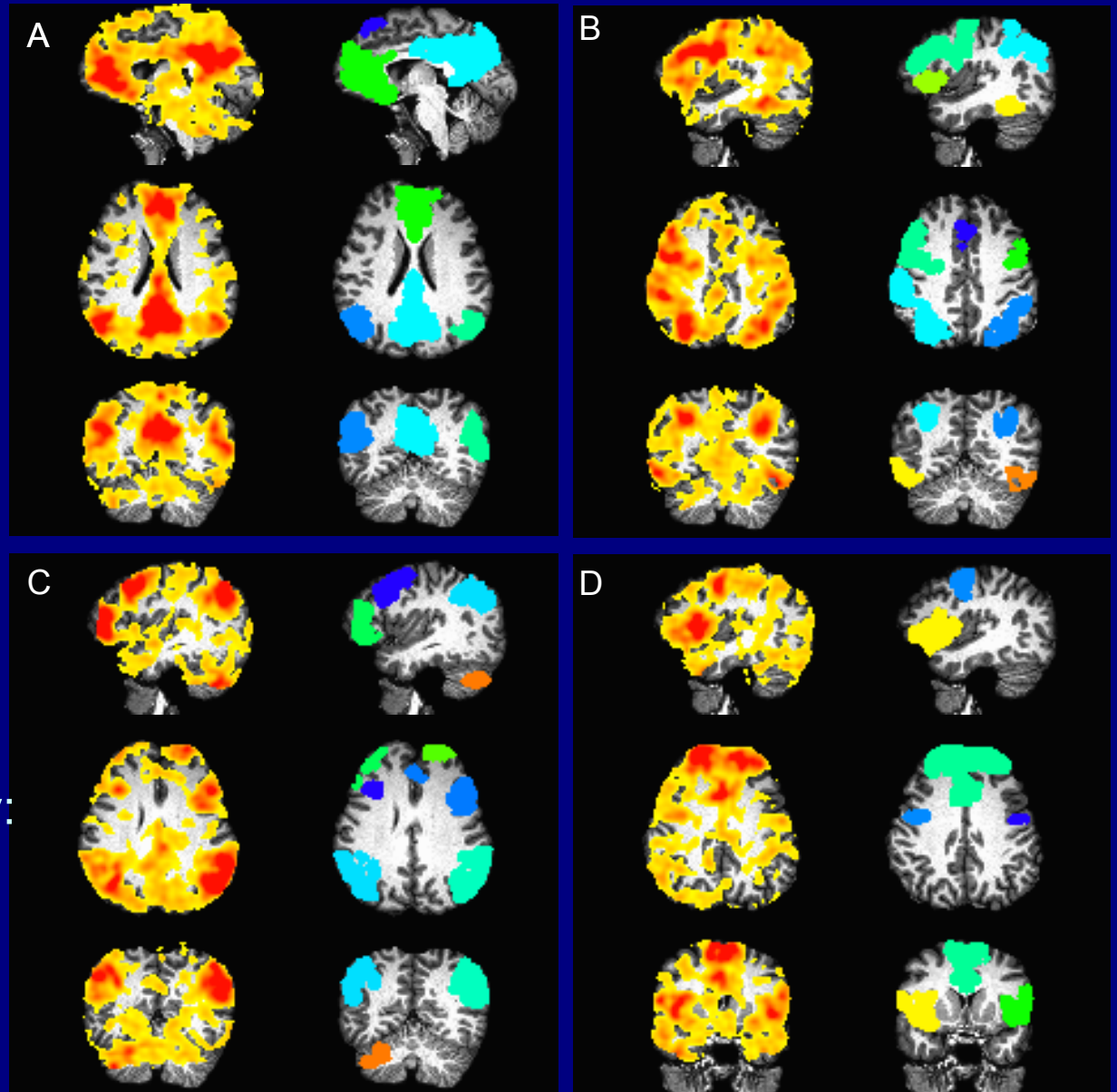
cluster volume > 130 voxels

expand clusters +2 voxels

limit expansion with WM map

(NB: this involved mapping FMRI data of ICs and T1 tissue segmentation results into DWI space; used 3dAllineate)

Also, for efficiency, can process multiple networks simultaneously:
use a multibrick file, with each network processed separately in each brick



And, can use a single reference data set to have same labels across group.

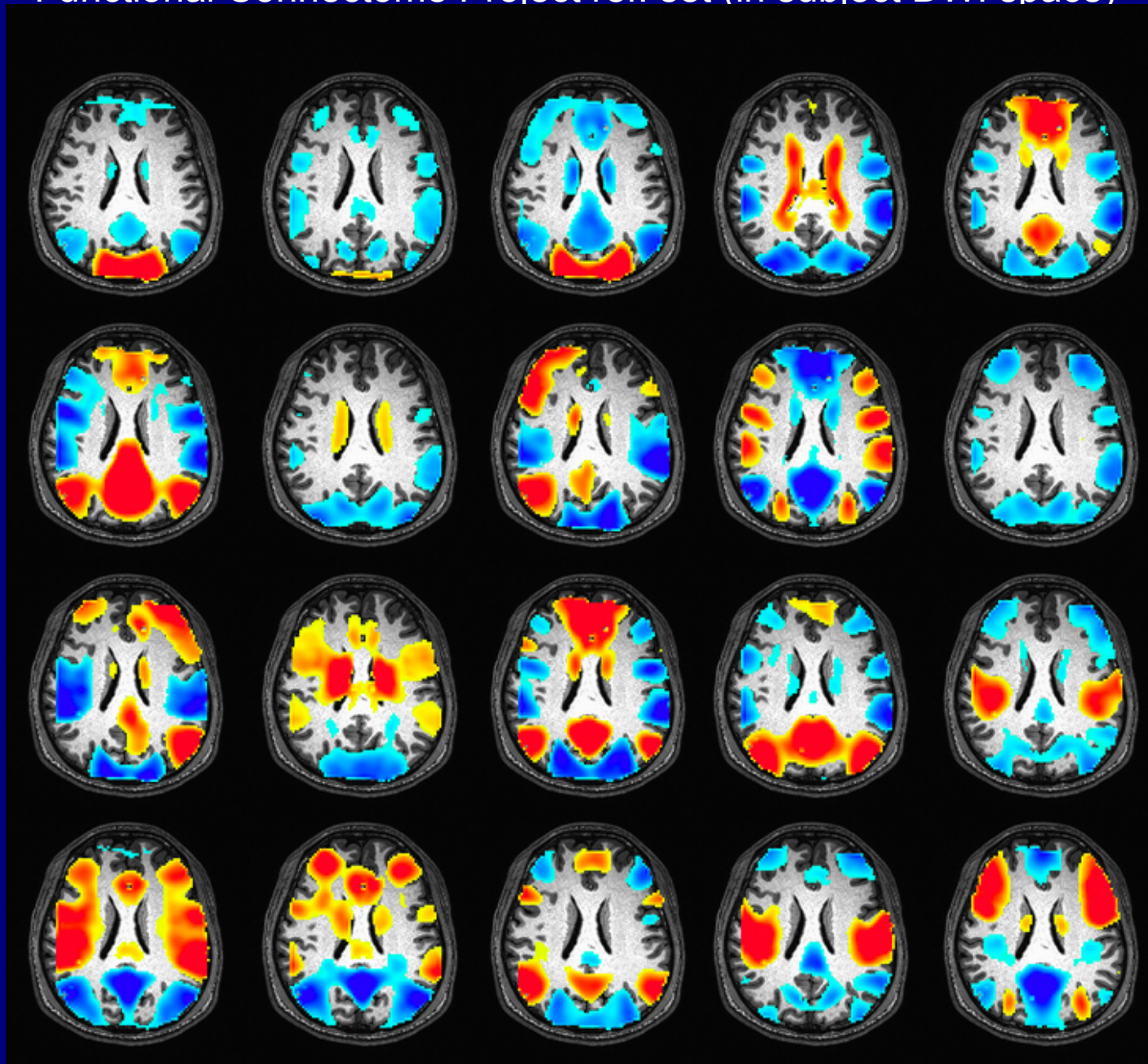
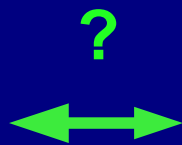
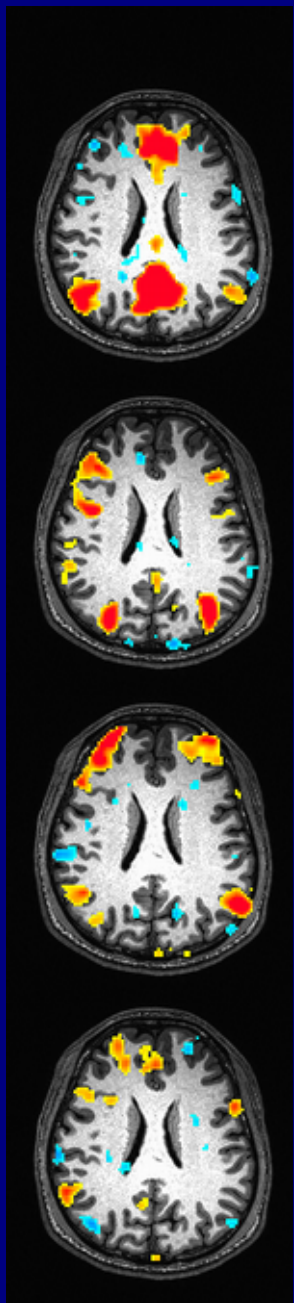
Sidenote:

***How to identify network maps, or
match them with reference/group set?***

Matching Network maps

Some Z-score

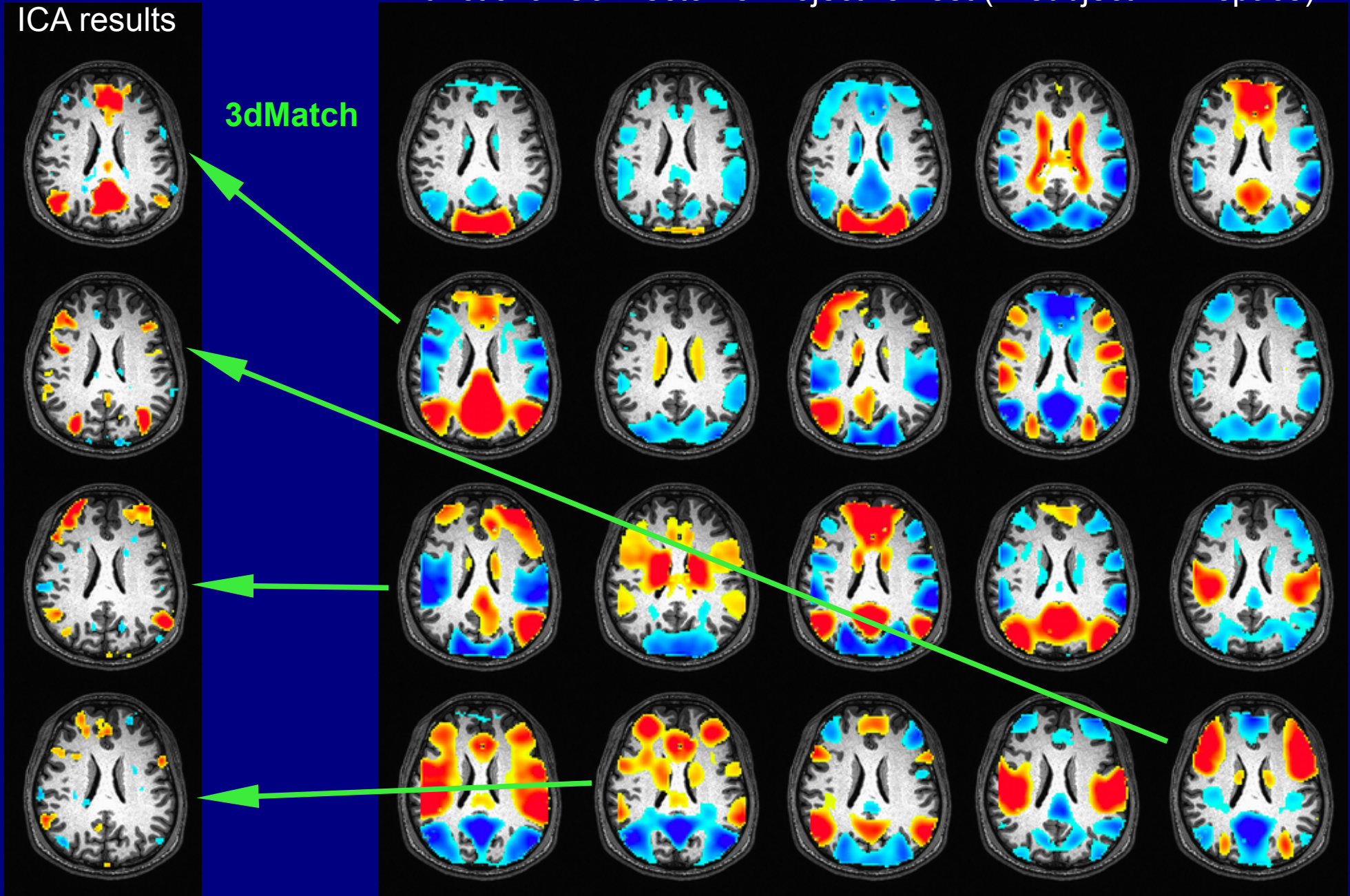
Functional Connectome Project ref. set (in subject DWI space)



Matching Network maps

Some Z-score
ICA results

Functional Connectome Project ref. set (in subject DWI space)



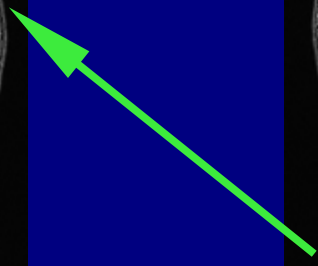
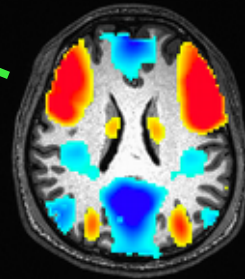
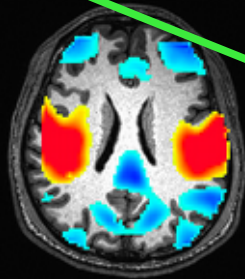
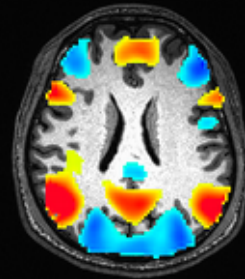
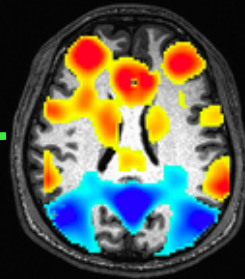
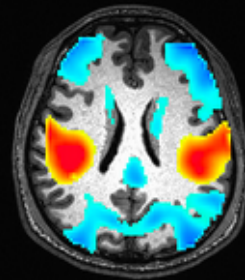
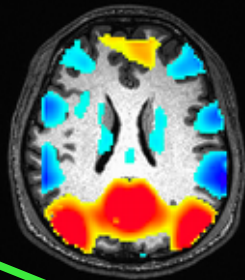
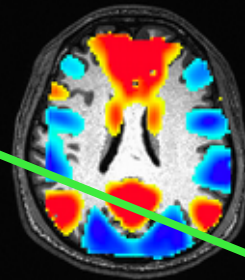
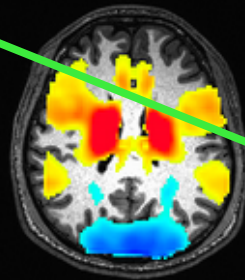
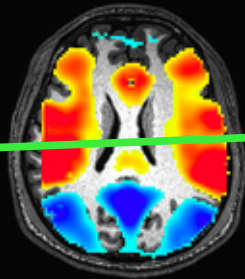
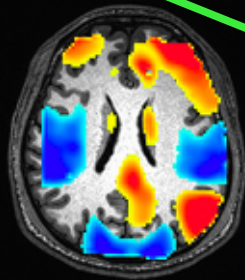
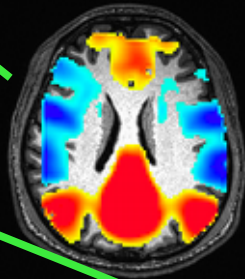
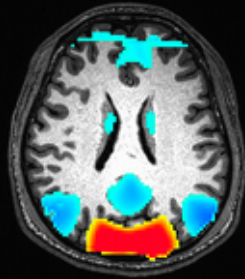
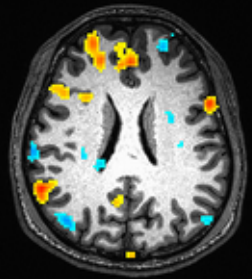
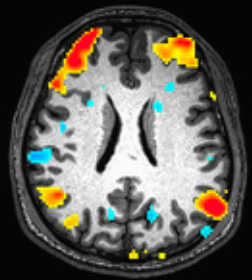
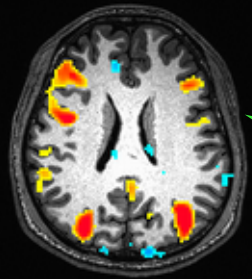
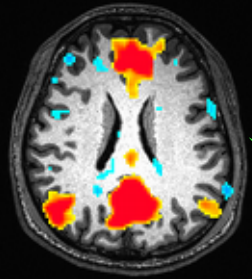
Matching Network maps

Some Z-score
ICA results

Functional Connectome Project ref. set (in subject DWI space)

3dMatch

- + **3dMatch** using spatial correlation
- + Can use separate min/max thresholds on input and reference set
- + Calculate Dice coefficient as well
- + Find best fit of reference to input, and vice versa



Tractography: overview of flavors

All tracking done via 3dTrackID (name change from original FATCAT paper).

Modes of tracking:

DET

(deterministic):

- tract/bundle files
- WM ROI files
- SC (*.grid) files

- + fast estimates
- + view tracts in 3D
(AND or OR logic)

PROB

(probabilistic)

- WM ROI files
- SC (*.grid) files

- + slow(er)
- + uses DT uncertainty
info for robustness
- + no tract viewing

Tractography: overview of flavors

All tracking done via 3dTrackID (name change from original FATCAT paper).

Modes of tracking:

DET

(deterministic):

- tract/bundle files
- WM ROI files
- SC (*.grid) files

- + fast estimates
- + view tracts in 3D
(AND or OR logic)

PROB

(probabilistic)

- WM ROI files
- SC (*.grid) files

- + slow(er)
- + uses DT uncertainty
info for robustness
- + no tract viewing

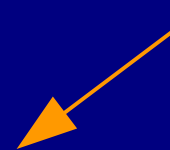
MINIP

(mini-probabilistic)

- tract/bundle files
- WM ROI files
- SC (*.grid) files

- + fast estimates
- + uses DT uncertainty
info for robustness
- + view tracts in 3D
(AND or OR logic)

NEW



Tractography: overview of flavors

All tracking done via 3dTrackID (name change from original FATCAT paper).

Modes of tracking:

DET

(deterministic):

- tract/bundle files
- WM ROI files
- SC (*.grid) files

- + fast estimates
- + view tracts in 3D
(AND or OR logic)

PROB

(probabilistic)

- WM ROI files
- SC (*.grid) files

- + slow(er)
- + uses DT uncertainty
info for robustness
- + no tract viewing

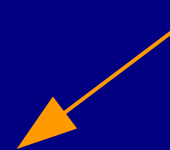
MINIP

(mini-probabilistic)

- tract/bundle files
- WM ROI files
- SC (*.grid) files

- + fast estimates
- + uses DT uncertainty
info for robustness
- + view tracts in 3D
(AND or OR logic)

NEW



In each case, multiple target networks can be tracked simultaneously for greater efficiency, using a multibrick '-netrois' file, one network per brick.

Deterministic tractography

+ 3dTrackID -mode DET -logic { OR | AND }

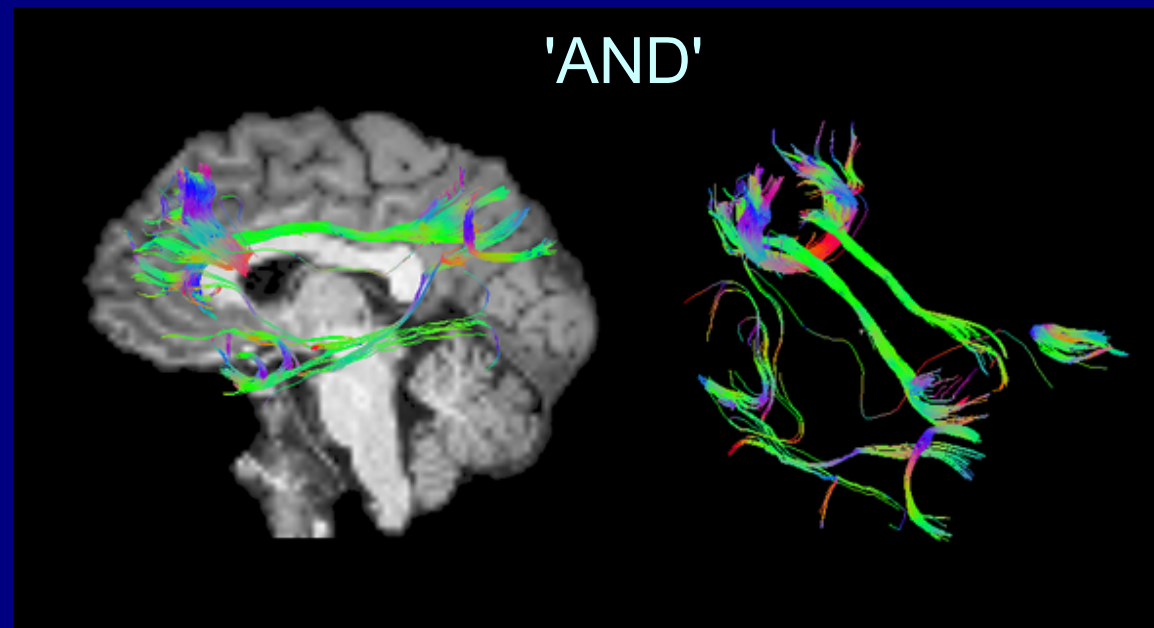
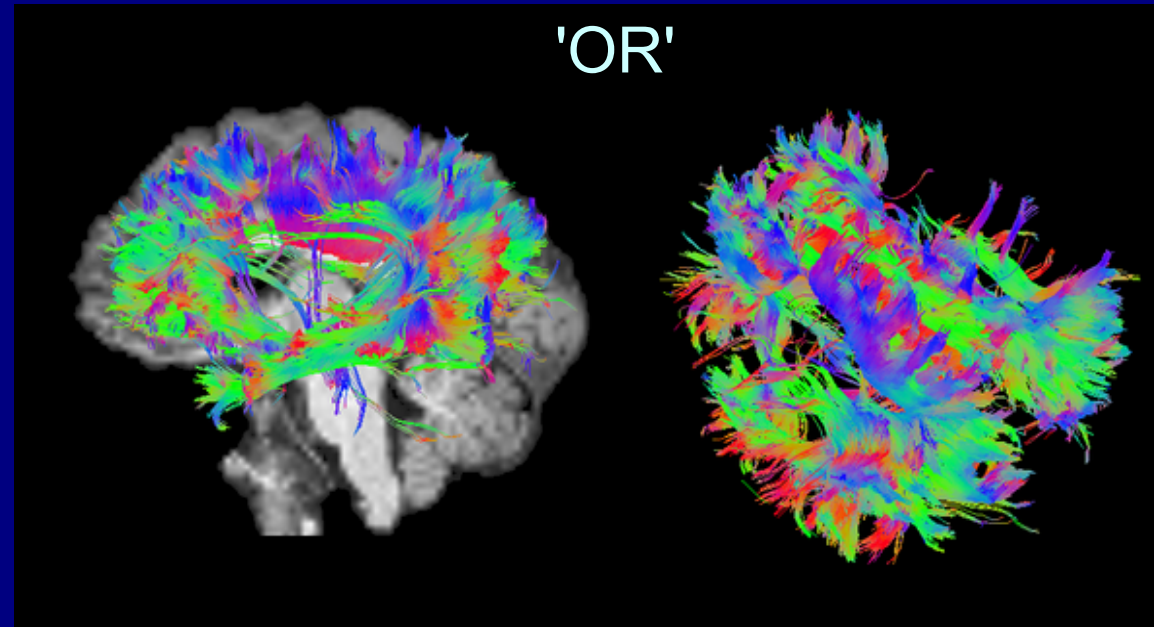
+ uses FACTID

+ good for exploratory
analysis and visualization
of results

ex.: DMN network tractography
results using ROIs from

3dROIMaker

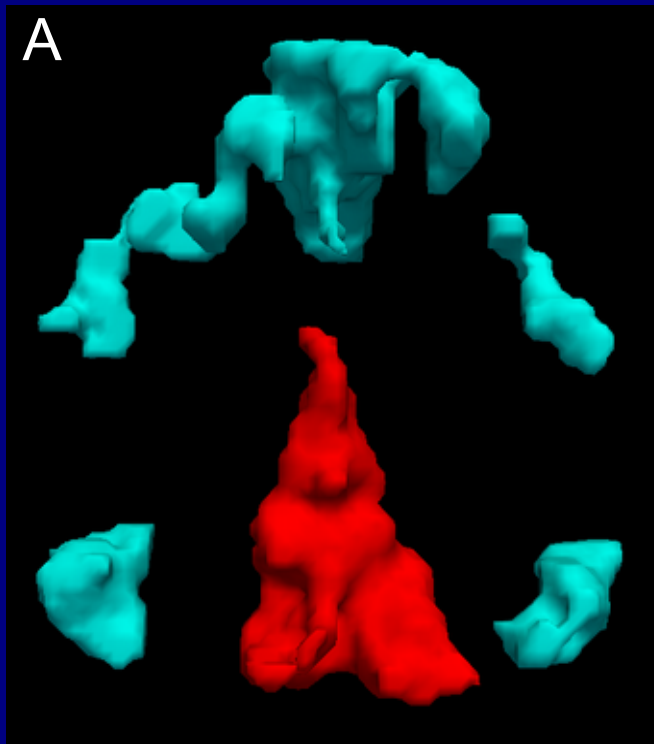
($FA > 0.2$; max angle 60deg;
8 seeds/voxel)



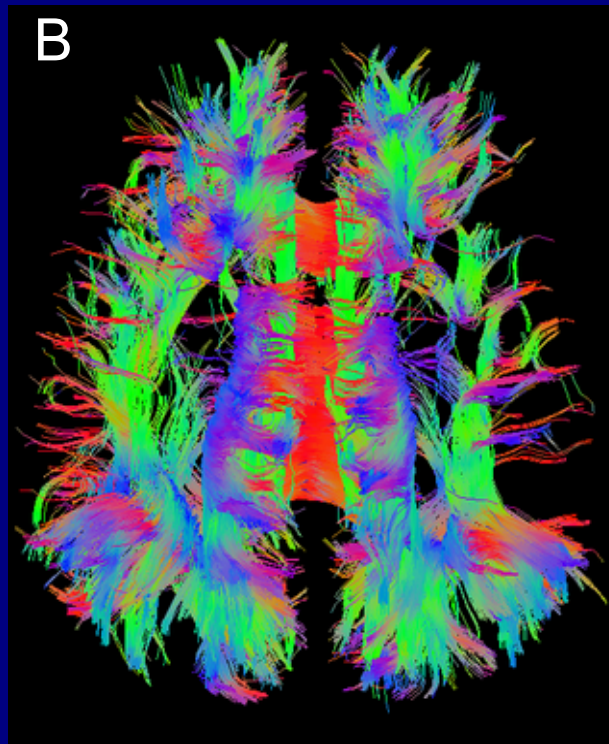
Deterministic tractography

+ 3dTrackID -mode DET -logic { OR | AND }

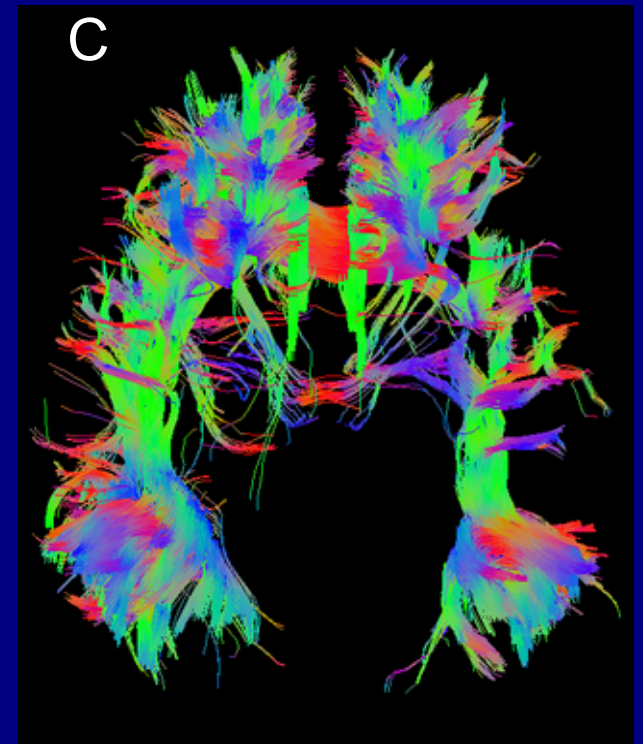
Control track propagation with `anti-mask' regions,
simply defined by voxels =-1:



ROIs: blue >0 , red <0



results when:
all ROIs >0
(no anti-mask)



results when:
blue >0 , red <0
(using anti-masks)

Deterministic tractography

+ 3dTrackID -mode DET -logic { OR | AND }

+ Automatic quantification per network in produced PREFIX.grid files.

SC matrices of WM ROI parameters such as:
mean/std of FA, MD, RD, L1, numbers of tracts, volume of tracts (and options for scaling tract-stats by ROI volumes)

+ possible to load in other files for automatic statistics, also.

→ Will use in group stats later...

```
# 8 # Number of network ROIs
# 17 # Number of grid matrices
# WITH_ROI_LABELS
      001      002      003      004      005
      1        2        3        4        5
# NT
      1529         0         0         2         0
      0        3219         70         8         0
      0         70        1313         0         0
      2         8         0        15776         0
      0         0         0         0        5734
      0         0         40        1234        203
      0         0         16         0         0
      0         0         0        1134         0
# fNT
5.614388e-03 0.000000e+00 0.000000e+00 7.343869e-06 0.000000e+00
0.000000e+00 1.181996e-02 2.570354e-04 2.937548e-05 0.000000e+00
0.000000e+00 2.570354e-04 4.821250e-03 0.000000e+00 0.000000e+00
7.343869e-06 2.937548e-05 0.000000e+00 5.792844e-02 0.000000e+00
0.000000e+00 0.000000e+00 0.000000e+00 0.000000e+00 2.105487e-02
0.000000e+00 0.000000e+00 1.468774e-04 4.531167e-03 7.454027e-04
0.000000e+00 0.000000e+00 5.875095e-05 0.000000e+00 0.000000e+00
0.000000e+00 0.000000e+00 0.000000e+00 4.163974e-03 0.000000e+00
# PV
9.496000e+03 0.000000e+00 0.000000e+00 2.720000e+02 0.000000e+00
0.000000e+00 1.768800e+04 1.408000e+03 4.800000e+02 0.000000e+00
0.000000e+00 1.408000e+03 1.473600e+04 0.000000e+00 0.000000e+00
2.720000e+02 4.800000e+02 0.000000e+00 5.078400e+04 0.000000e+00
0.000000e+00 0.000000e+00 0.000000e+00 0.000000e+00 2.095200e+04
0.000000e+00 0.000000e+00 1.520000e+03 7.784000e+03 1.648000e+03
0.000000e+00 0.000000e+00 4.640000e+02 0.000000e+00 0.000000e+00
0.000000e+00 0.000000e+00 0.000000e+00 6.600000e+03 0.000000e+00
# fNV
7.036951e-03 0.000000e+00 0.000000e+00 2.015639e-04 0.000000e+00
0.000000e+00 1.310758e-02 1.043390e-03 3.557010e-04 0.000000e+00
0.000000e+00 1.043390e-03 1.092002e-02 0.000000e+00 0.000000e+00
2.015639e-04 3.557010e-04 0.000000e+00 3.763317e-02 0.000000e+00
0.000000e+00 0.000000e+00 0.000000e+00 0.000000e+00 1.552635e-02
0.000000e+00 0.000000e+00 1.126386e-03 5.768285e-03 1.221240e-03
0.000000e+00 0.000000e+00 3.438443e-04 0.000000e+00 0.000000e+00
0.000000e+00 0.000000e+00 0.000000e+00 4.890889e-03 0.000000e+00
```

Deterministic tractography

+ 3dTrackID -mode DET -logic { OR | AND }

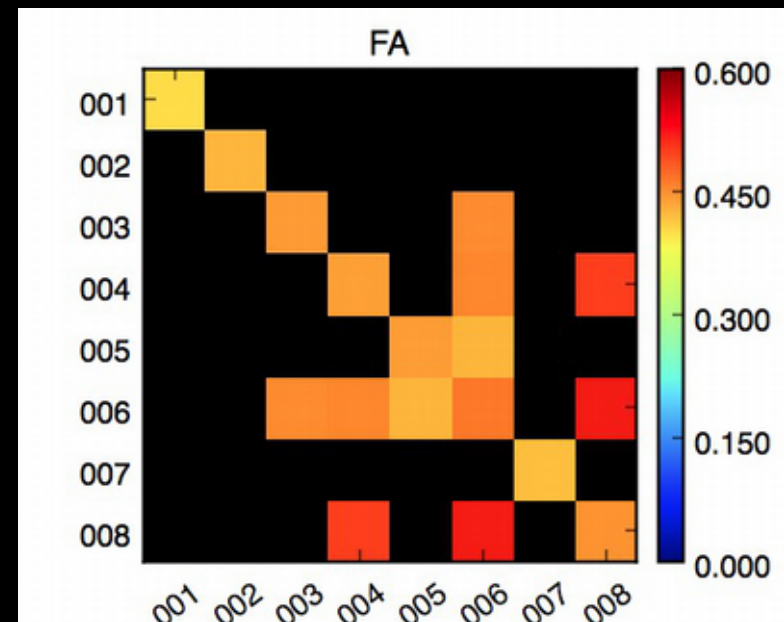
+ Automatic quantification per network in produced PREFIX.grid files.

SC matrices of WM ROI parameters such as:
mean/std of FA, MD, RD, L1, numbers of tracts, volume of tracts (and options for scaling tract-stats by ROI volumes)

+ possible to load in other files for automatic statistics, also.

→ Will use in group stats later...

+ fat_mat_plot.py: command line tool to visualize each SC matrix:



+ can control font, colors, ranges, DPI, etc.

```
0.000000e+00 0.000000e+00 3.438443e-04 0.000000e+00 0.000000e+00
0.000000e+00 0.000000e+00 0.000000e+00 4.890889e-03 0.000000e+00
o.NETS_AND_000.grid Top L4 (Fundamental)
```


Deterministic tractography

+ 3dTrackID -mode DET -logic { OR | AND }

+ uses FACTID

+ good for exploratory analysis and visualization of results

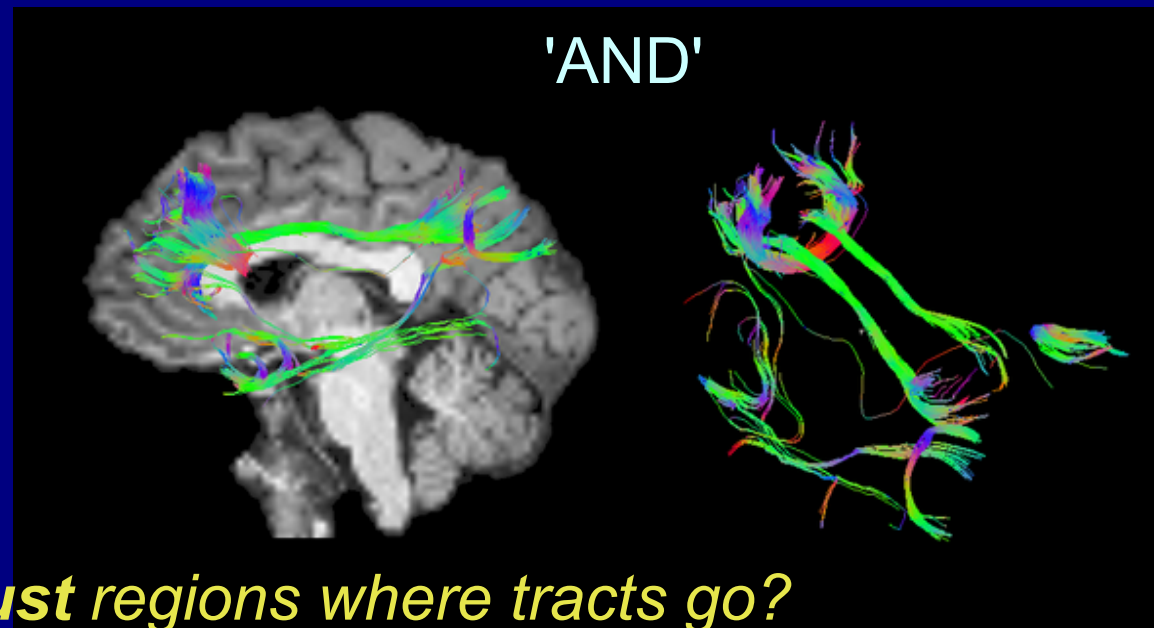
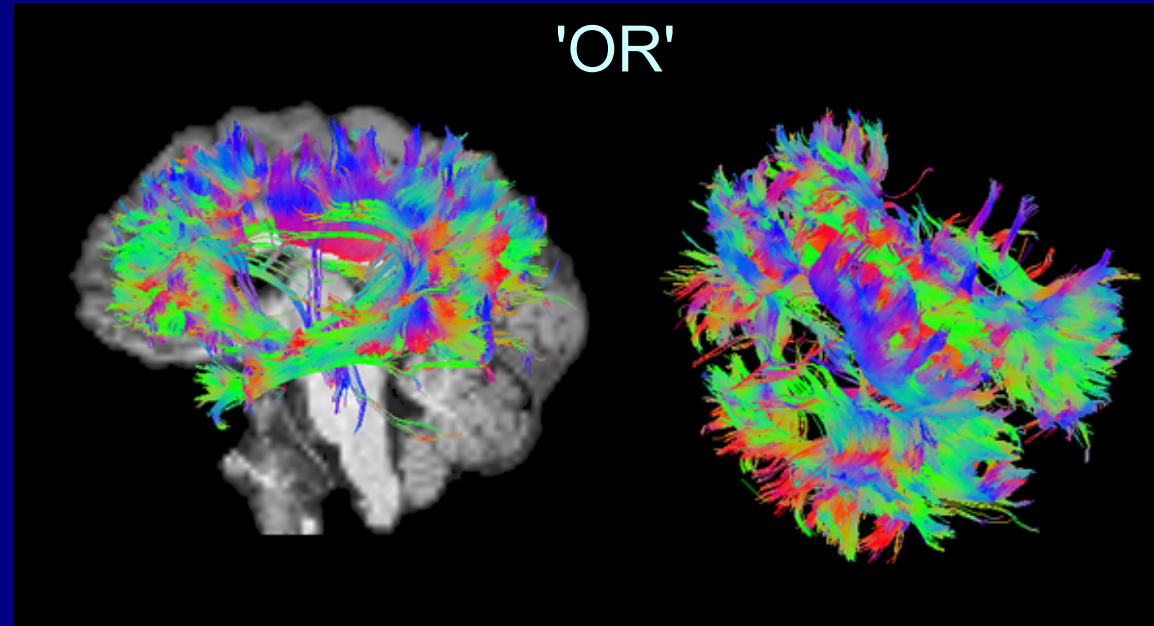
ex.: DMN network tractography results using ROIs from

3dROIMaker

($FA > 0.2$; max angle 60deg; 8 seeds/voxel)

*Tract results may seem 'fine', but is **noise** affecting them?*

*Are these the **most likely/robust** regions where tracts go?*



Brings up next question for doing tractography:

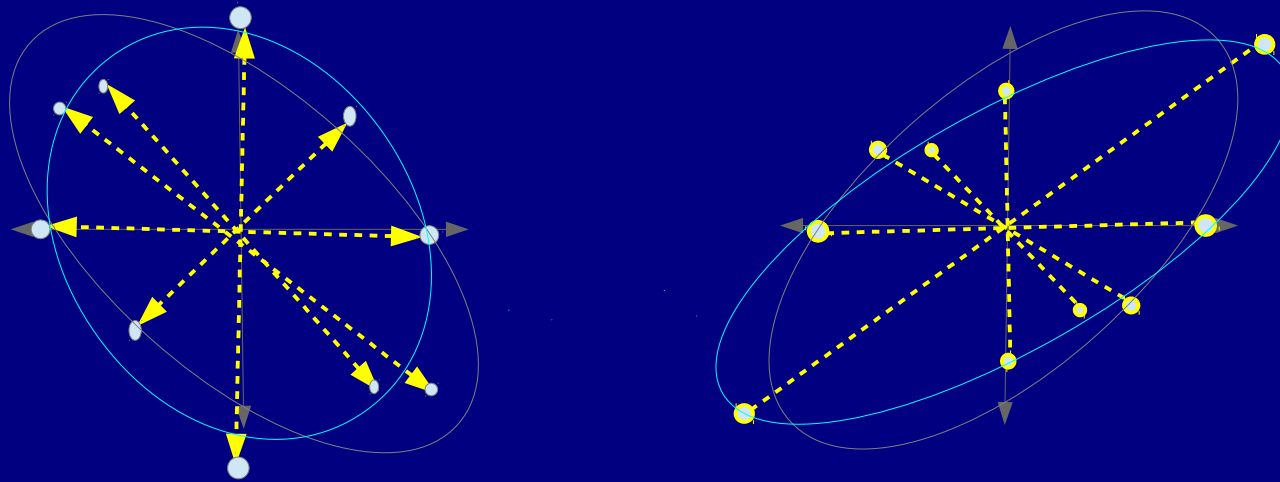
***How do we estimate tensor parameter
noise/uncertainty?***

Noise in DW signals

MRI signals have additive noise

$$S_i = S_0 e^{-b \mathbf{g}_i^T \mathbf{D} \mathbf{g}_i} + \varepsilon,$$

where ε is (Rician) noise, with the effect of leading to errors in surface fit, equivalent to *rotations* and *rescalings* of ellipsoids:



'Un-noisy' vs perturbed/noisy fit

EPI distortions, subject motion, et al. also warp ellipsoids.

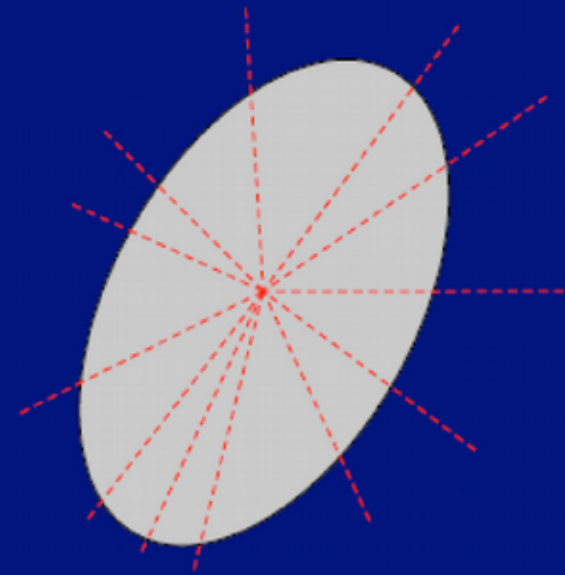
DTI Uncertainty

- We use jackknife resampling (e.g., Efron 1982)
 - Other studies have used bootstrapping (e.g., Jones 2003), or theoretical estimates (Jeong & Anderson 2008)
 - Jackknifing is efficient (just need one data set unlike bootstrap), simpler than theory, since, e.g., SNR is likely not constant across voxels

Jackknifing

- Basically, take M acquisitions

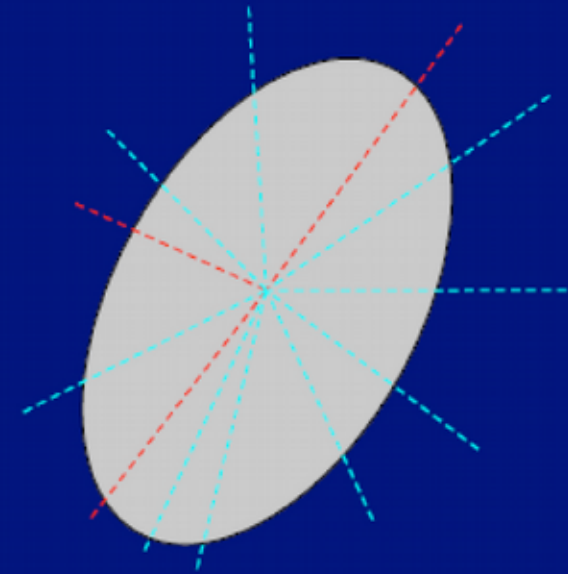
e.g., $M=12$



Jackknifing

- Basically, take M acquisitions
- Randomly select $M_J < M$ to use to calculate quantity of interest
 - standard nonlinear fits

e.g., $M=12$
 $M_J=9$

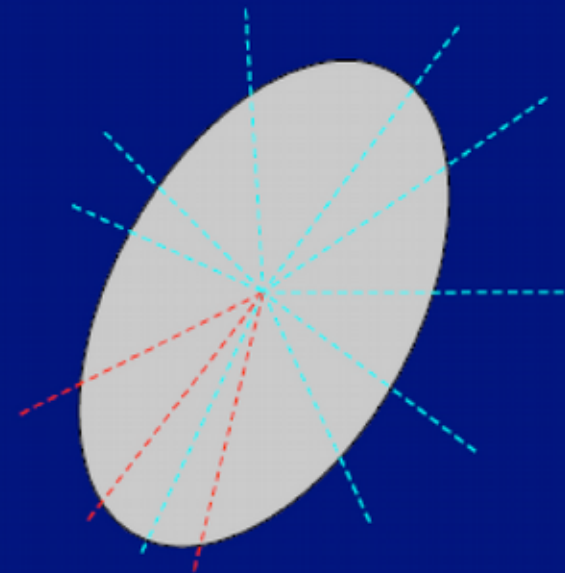


$$[D_{11} \ D_{22} \ D_{33} \ D_{12} \ D_{13} \ D_{23}] = \dots$$

Jackknifing

- Basically, take M acquisitions
- Randomly select $M_J < M$ to use to calculate quantity of interest
 - standard nonlinear fits
- Repeatedly subsample large number ($\sim 10^3$ - 10^4 times)

e.g., $M=12$
 $M_J=9$

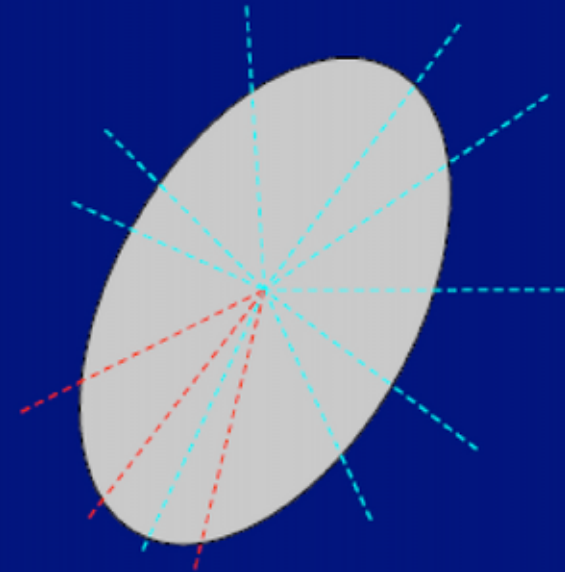


$$\begin{aligned} [D_{11} \ D_{22} \ D_{33} \ D_{12} \ D_{13} \ D_{23}] &= \dots \\ [D_{11} \ D_{22} \ D_{33} \ D_{12} \ D_{13} \ D_{23}] &= \dots \\ [D_{11} \ D_{22} \ D_{33} \ D_{12} \ D_{13} \ D_{23}] &= \dots \\ &\dots \end{aligned}$$

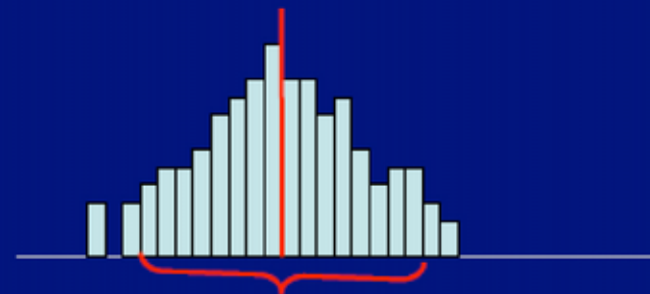
Jackknifing

- Basically, take M acquisitions
- Randomly select $M_J < M$ to use to calculate quantity of interest
 - standard nonlinear fits
- Repeatedly subsample large number ($\sim 10^3$ - 10^4 times)
- Analyze distribution of values for estimator (mean) and confidence interval
 - sort/%iles
 - (not so efficient)
 - if Gaussian, e.g. $\mu \pm 2\sigma$
 - simple

e.g., $M=12$
 $M_J=9$

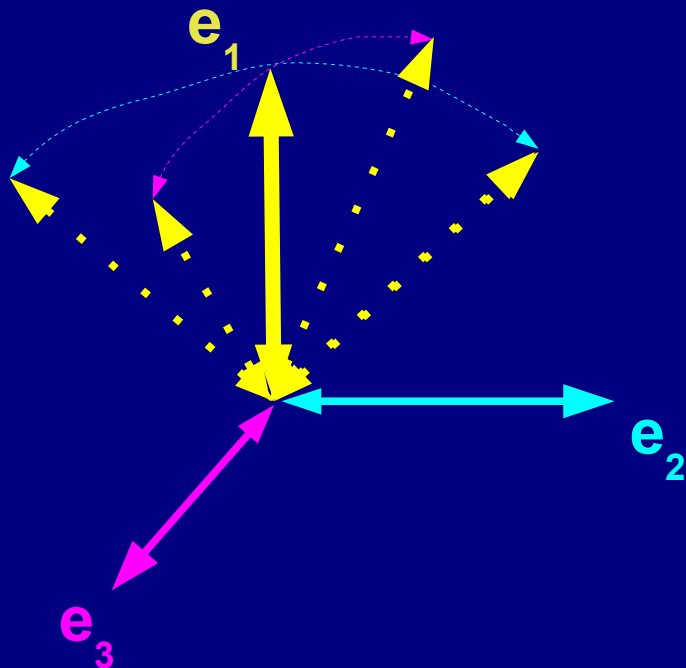


$$\begin{aligned} [D_{11} \ D_{22} \ D_{33} \ D_{12} \ D_{13} \ D_{23}] &= \dots \\ [D_{11} \ D_{22} \ D_{33} \ D_{12} \ D_{13} \ D_{23}] &= \dots \\ [D_{11} \ D_{22} \ D_{33} \ D_{12} \ D_{13} \ D_{23}] &= \dots \\ &\dots \end{aligned}$$



Uncertainty estimation

+ **3dDWUncert** estimates bias and σ of first eigenvector \mathbf{e}_1 (main direction of diffusion), based on how much it could tip toward either \mathbf{e}_2 or \mathbf{e}_3 :



.... and the bias and σ of FA

1) Obtain M DWIs.



1b) Estimate DT and parameters from M DWIs.

$\hat{\mathbf{D}}, \hat{\mathbf{F}}\hat{\mathbf{A}}, \dots$

2) Make N_j subsets of M_j DWIs.



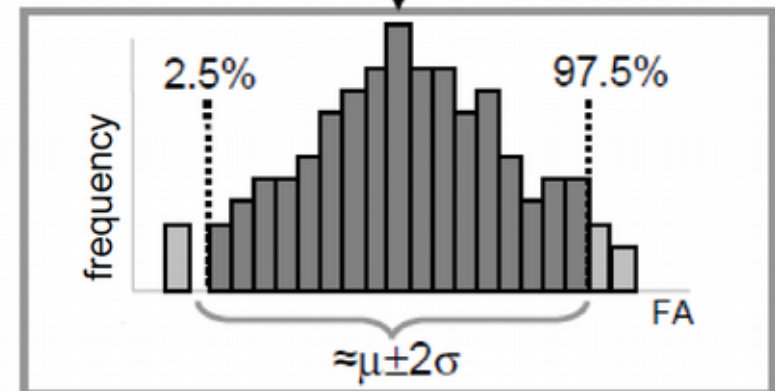
3) Estimate N_j DTs.

\mathbf{D}_1^* \mathbf{D}_2^* ... $\mathbf{D}_{N_j}^*$

4) Estimate set of N_j parameters.

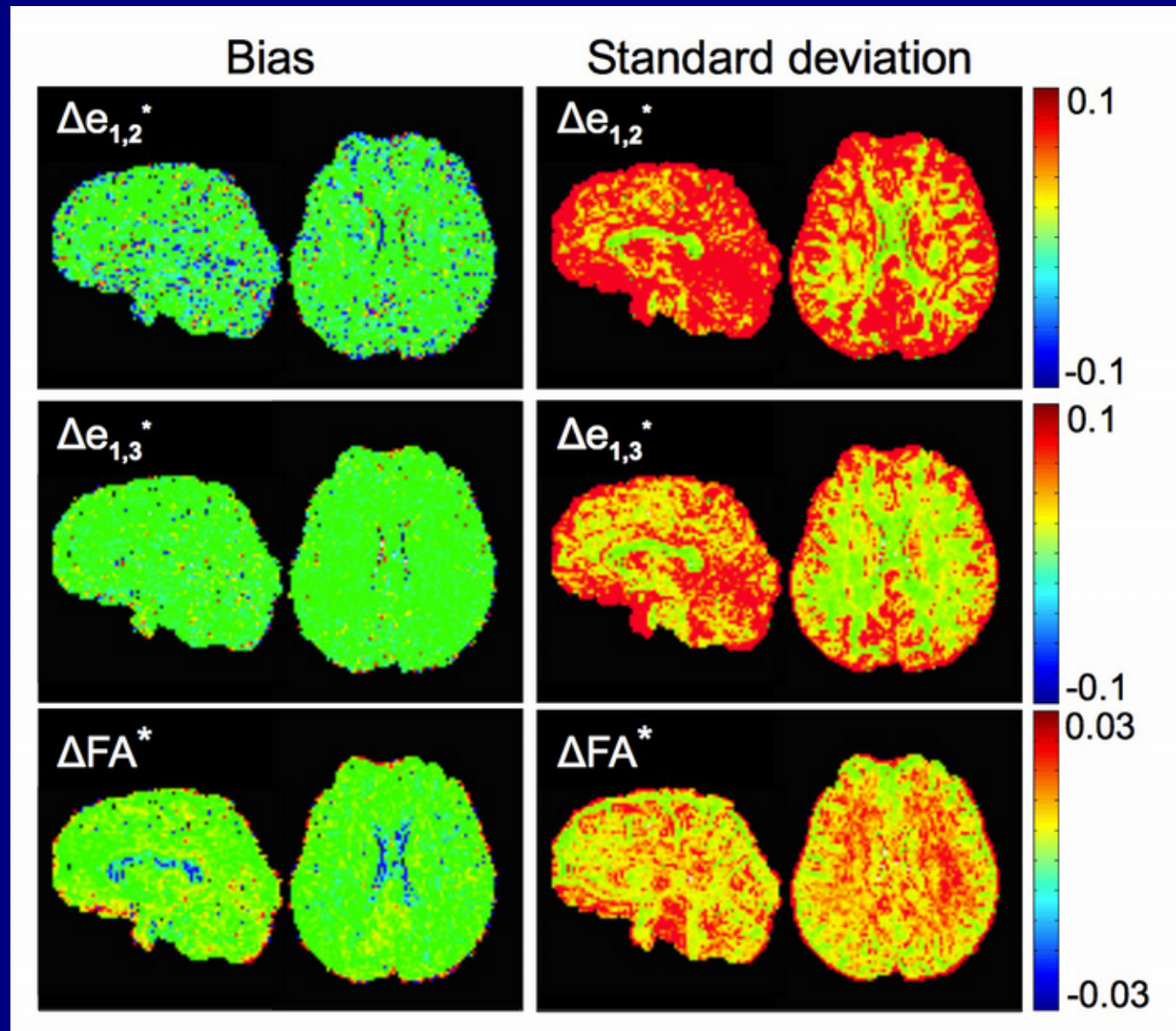
$\{ \mathbf{FA}_1^*, \mathbf{FA}_2^*, \dots, \mathbf{FA}_{N_j}^* \}, \{ (\Delta \mathbf{e}_{1,2})_i \}, \dots$

5) Find confidence intervals.



Uncertainty example

- + Can see difference in e1 uncertainty along e2 and e3
- + Tissue-dependent differences in FA uncertainty



Next question for doing tractography:

***How do we take into account
noise/uncertainty during tracking?***

Probabilistic Tractography

- We know that estimates of DTI ellipsoids are not exactly representing tracts/bundles
 - Size scale differences between voxel/tracts, multiple tracts, complex structure, signal noise, eddy currents, nonlinear fits, etc.
- How to include errors/uncertainty in interpretation and usage?

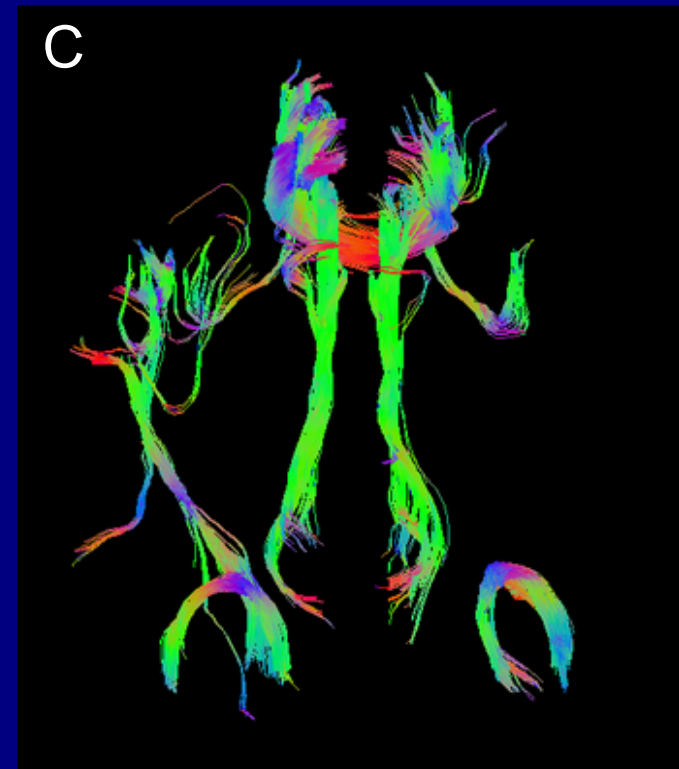
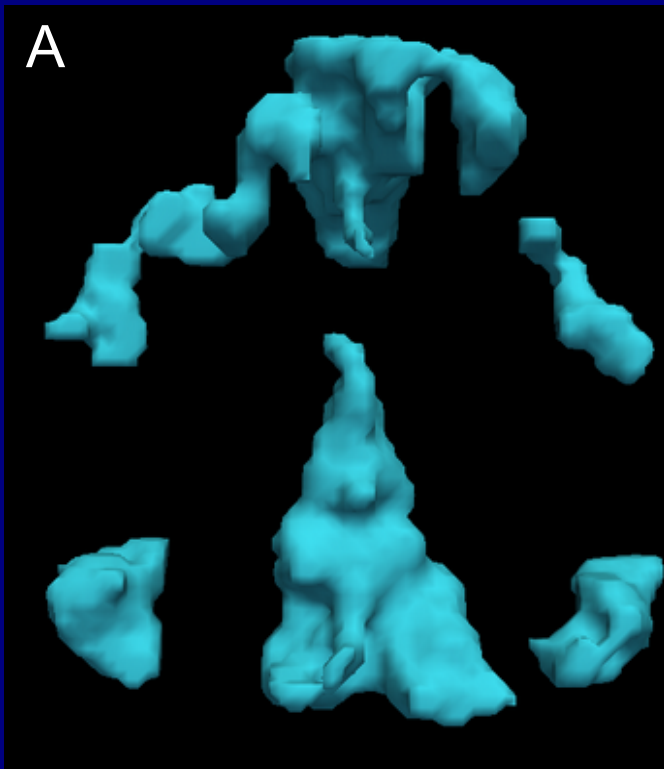
Probabilistic Tractography

- We know that estimates of DTI ellipsoids are not exactly representing tracts/bundles
 - Size scale differences between voxel/tracts, multiple tracts, complex structure, signal noise, eddy currents, nonlinear fits, etc.
- How to include errors/uncertainty in interpretation and usage?
- Probabilistic tractography: use uncertainty in ellipsoid measures with Monte Carlo-esque simulations and build up large ~population of possible trajectories
 - E.g., Parker et al. (2003); Behrens et al. (2003)
 - Do DTI estimates; do whole brain tractography; keep track of number of tracks through relevant voxels; perturb DTI voxel estimates based on uncertainty values; do whole brain tract... [repeat many ~1000 times] ... find voxels which had lots of traffic, define relative 'connectivity' based on traffic

(Side note before continuing with
'full' probabilistic tracking)

Mini-Probabilistic Tracking

- + Full probabilistic methods generate voxelwise brain maps without linear track structure
- + 'Mini-probabilistic' tracking performs a few extra iterations of 'deterministic' tracking on uncertainty-perturbed data sets
 - track structure is retained,
 - results generally exhibit more robust tracks and fewer false negatives than deterministic tracking alone
 - false positives tend to be isolated and visually apparent.



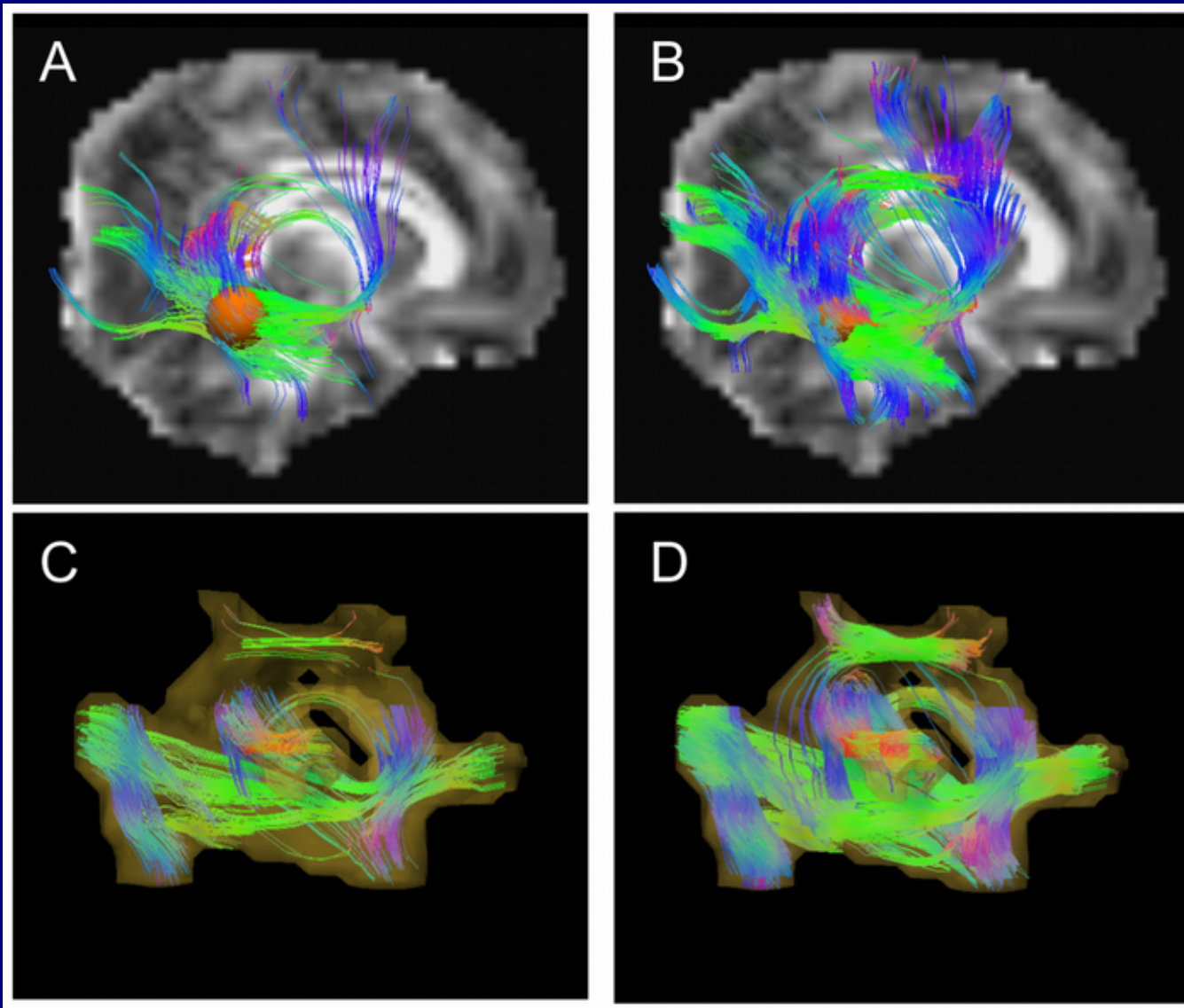
Deterministic (AND)

with '-mini_prob 7'

Mini-Probabilistic Tracking

Deterministic vs mini-Probabilistic

Through
single ROI



AND logic
through
network, cf
with full-prob
results

(Taylor et al., 2014)

Probabilistic Tractography

- Note on interpretation: most reports define a parameter to be the probability of connection between voxels A and X:
 $\Psi(X,A)=\mu(X,A)/N$
 - N: number of iterations
 - μ : number of tracts through voxel X which either start from or pass through A

Probabilistic Tractography

- Note on interpretation: most reports define a parameter to be the probability of connection between voxels A and X:
$$\Psi(X,A)=\mu(X,A)/N$$
 - N: number of iterations
 - μ : number of tracts through voxel X which either start from or pass through A
- While this quantity is somehow relevant in representing what relative 'connectivity' which can be estimated, exact interpretation as 'probability of connectivity' is tricky

Probabilistic Tractography

- Note on interpretation: most reports define a parameter to be the probability of connection between voxels A and X:
$$\Psi(X,A)=\mu(X,A)/N$$
 - N: number of iterations
 - μ : number of tracts through voxel X which either start from or pass through A
- While this quantity is somehow relevant in representing what relative 'connectivity' which can be estimated, exact interpretation as 'probability of connectivity' is tricky
 - > for example, how literally can one equate a numerically-constructed tract through a ~2x2x2mm voxel with a fiber bundle with **orders-of-magnitude** smaller diameter?
 - > or how can one compare this 'connectivity' between **ROIs of different sizes** on equal footing?

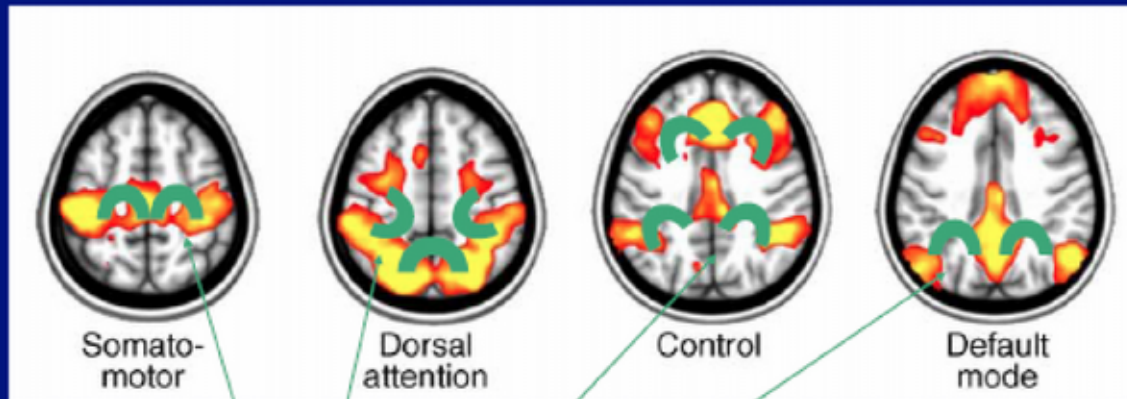
Probabilistic Tractography

- Note on interpretation: most reports define a parameter to be the probability of connection between voxels A and X:
$$\Psi(X,A)=\mu(X,A)/N$$
 - N: number of iterations
 - μ : number of tracts through voxel X which either start from or pass through A
- While this quantity is somehow relevant in representing what relative 'connectivity' which can be estimated, exact interpretation as 'probability of connectivity' is tricky
- Prefer to think of Ψ more loosely as a probability of that voxel being a part of WM volume related to the two ROI-voxels.
 - Not probability of *connectivity* of A and X, but more *likelihood of a voxel being part of associated WM*

Probabilistic Tractography

- This interpretation more useful for working with GM networks. Recall interest:

GM ROIs network:

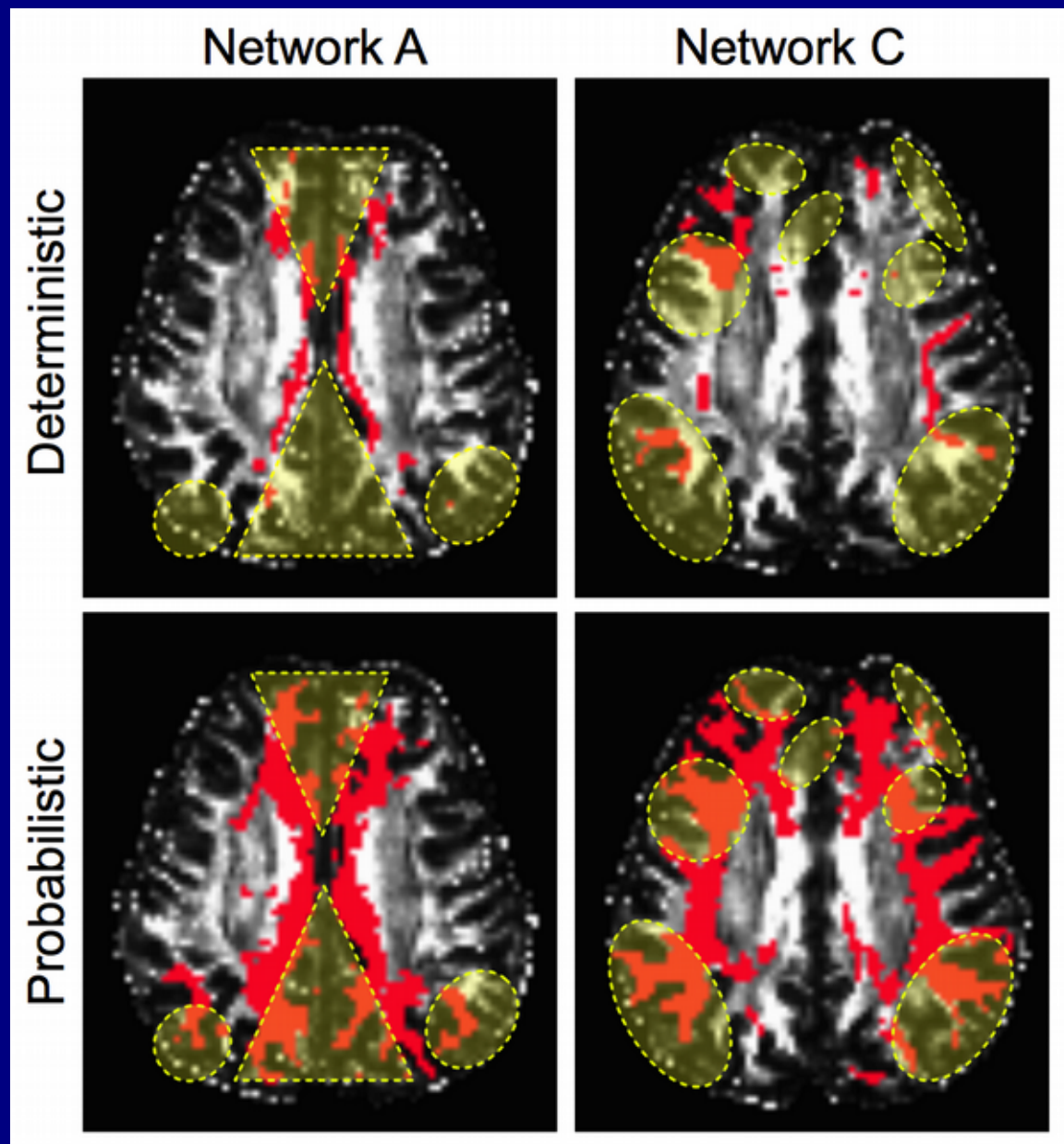


Associated WM ROIs

- Threshold Ψ per voxel after probabilistic tracking, use to define WM ROI between GM ROIs

Deterministic vs Probabilistic

- + NB: coverage and connectivity differences between tractography types
- + Deterministic can be useful for initial investigations, but is more susceptible to noise/errors and truncation



Probabilistic tractography

- + with networks of ROIs from **3dROIMaker** and uncertainty from **3dDWUncert** (as well as tensor estimates from, e.g., 3dDWItoDT), can finally do probabilistic tractography
- + **3dTrackID -mode PROB**
 - does lots of **Monte Carlo simulations**: wholebrain tractography -> perturb FA & e1 based on uncertainty -> wholebrain tracking -> perturb -> wholebrain tracking -> etc.

Probabilistic tractography

- + with networks of ROIs from **3dROIMaker** and uncertainty from **3dDWUncert** (as well as tensor estimates from, e.g., 3dDWItoDT), can finally do probabilistic tractography
- + **3dTrackID -mode PROB**
 - does lots of Monte Carlo simulations: wholebrain tractography -> perturb FA & e1 based on uncertainty -> wholebrain tracking -> perturb -> wholebrain tracking -> etc.
 - at each iteration, checks for **connections** between any pair of ROIs
 - can **trim** saved tracts to only keep voxels *between* 2 ROIs (i.e., no overrunners in the 'connection' ROIs)

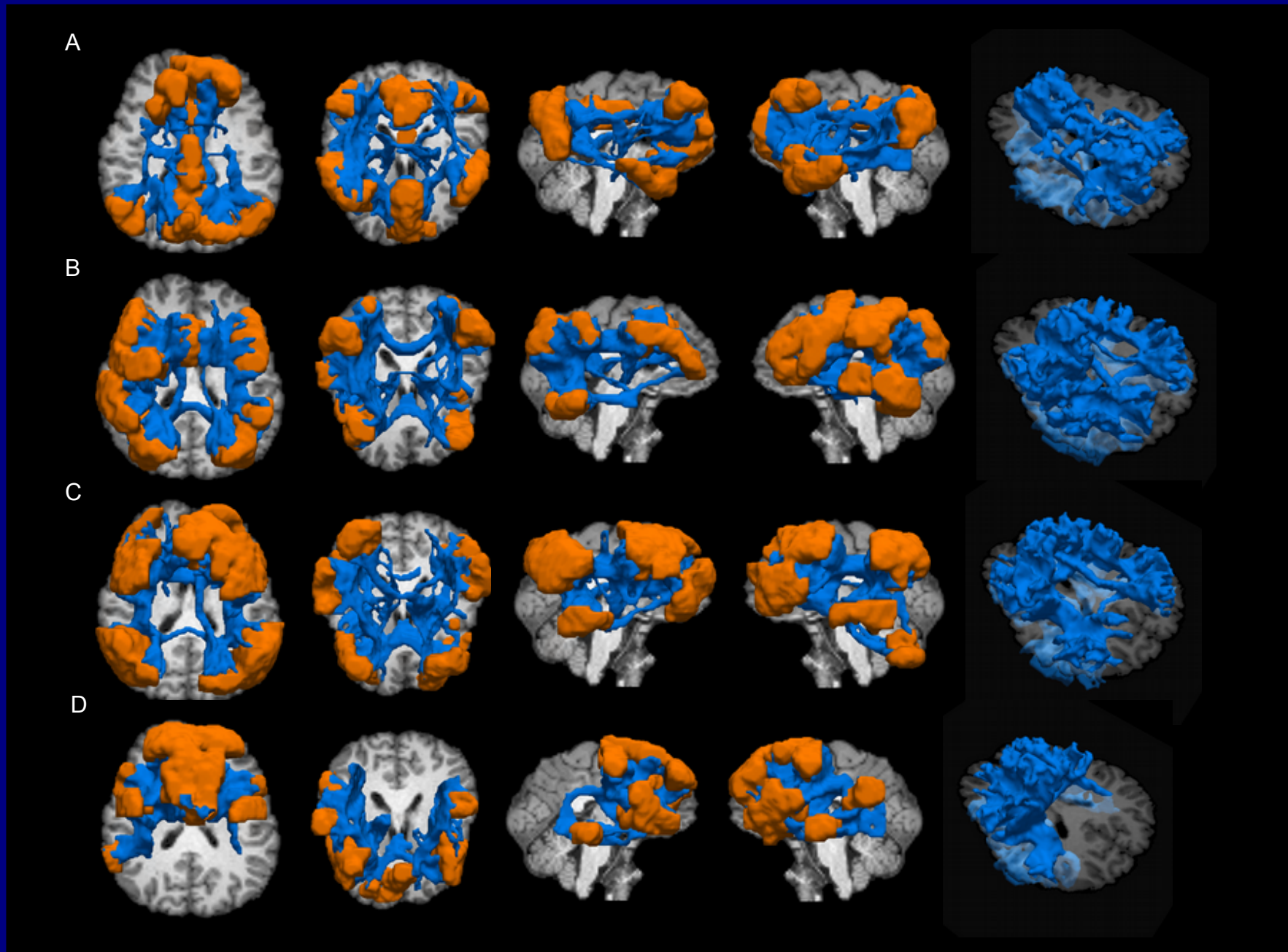
Probabilistic tractography

- + with networks of ROIs from **3dROIMaker** and uncertainty from **3dDWUncert** (as well as tensor estimates from, e.g., 3dDWItoDT), can finally do probabilistic tractography
- + **3dTrackID -mode PROB**
 - does lots of Monte Carlo simulations: wholebrain tractography -> perturb FA & e1 based on uncertainty -> wholebrain tracking -> perturb -> wholebrain tracking -> etc.
 - at each iteration, checks for connections between any pair of ROIs
 - can trim saved tracts to only keep voxels *between* 2 ROIs (i.e., no overrunners in the 'connection' ROIs)
 - also finds tracts through each individual ROI
 - to find WM region connecting, say, ROI 1 and 2: keep voxels through which Ntracks which intersected both ROI1 and ROI2 is greater than a user-defined threshold

Probabilistic tractography

- + with networks of ROIs from **3dROIMaker** and uncertainty from **3dDWUncert** (as well as tensor estimates from, e.g., 3dDWItoDT), can finally do probabilistic tractography
- + **3dTrackID -mode PROB**
 - does lots of Monte Carlo simulations: wholebrain tractography -> perturb FA & e1 based on uncertainty -> wholebrain tracking -> perturb -> wholebrain tracking -> etc.
 - at each iteration, checks for connections between any pair of ROIs
 - can trim saved tracts to only keep voxels *between* 2 ROIs (i.e., no overrunners in the 'connection' ROIs)
 - also finds tracts through each individual ROI
 - to find WM region connecting, say, ROI 1 and 2:
 - keep voxels through which Ntracks which intersected both ROI1 and ROI2 is greater than a user-defined threshold
 - calculate stats on final WM ROIs found
 - analyze multiple networks **simultaneously** for efficiency (i.e., very little extra cost)

3dTrackID: Probabilistic tractography

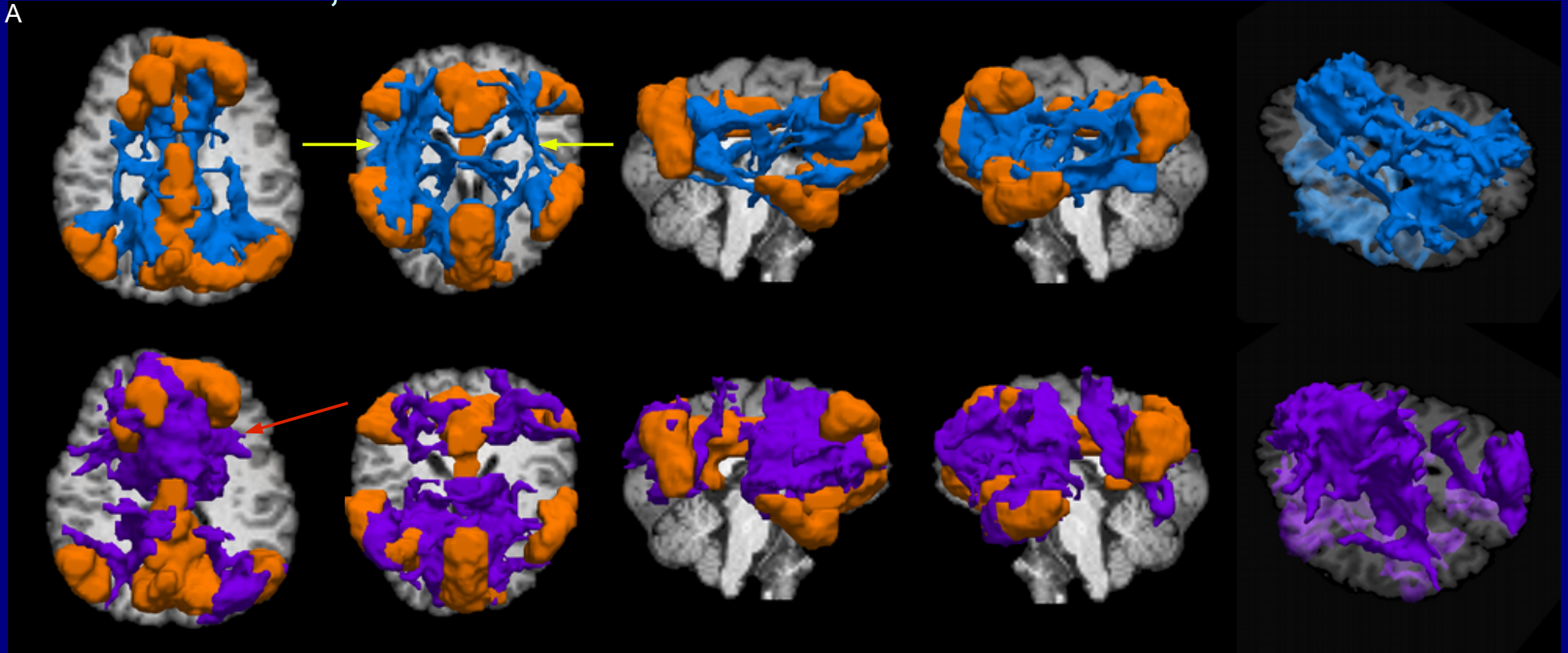


(orange is ROI; blue is set of WM regions with tracts connecting)

3dTrackID: Probabilistic tractography

+ compare with existing algorithms:

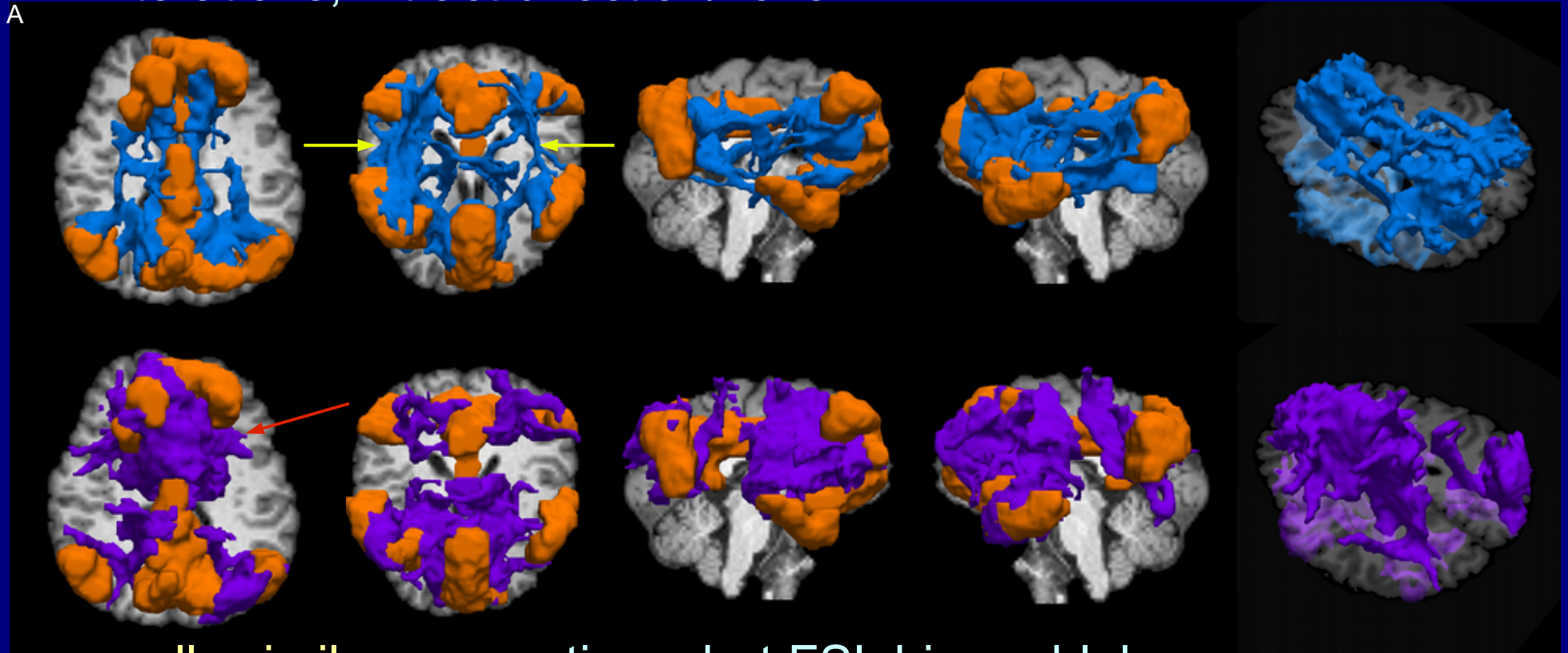
- purple: FSL-probtrackX (and FSL-bedpostX for uncertainty)
- same parameters: $FA > 0.2$, max angle 60deg, 5000 Monte Carlo iterations; 1 tract direction/voxel



3dTrackID: Probabilistic tractography

+ compare with existing algorithms:

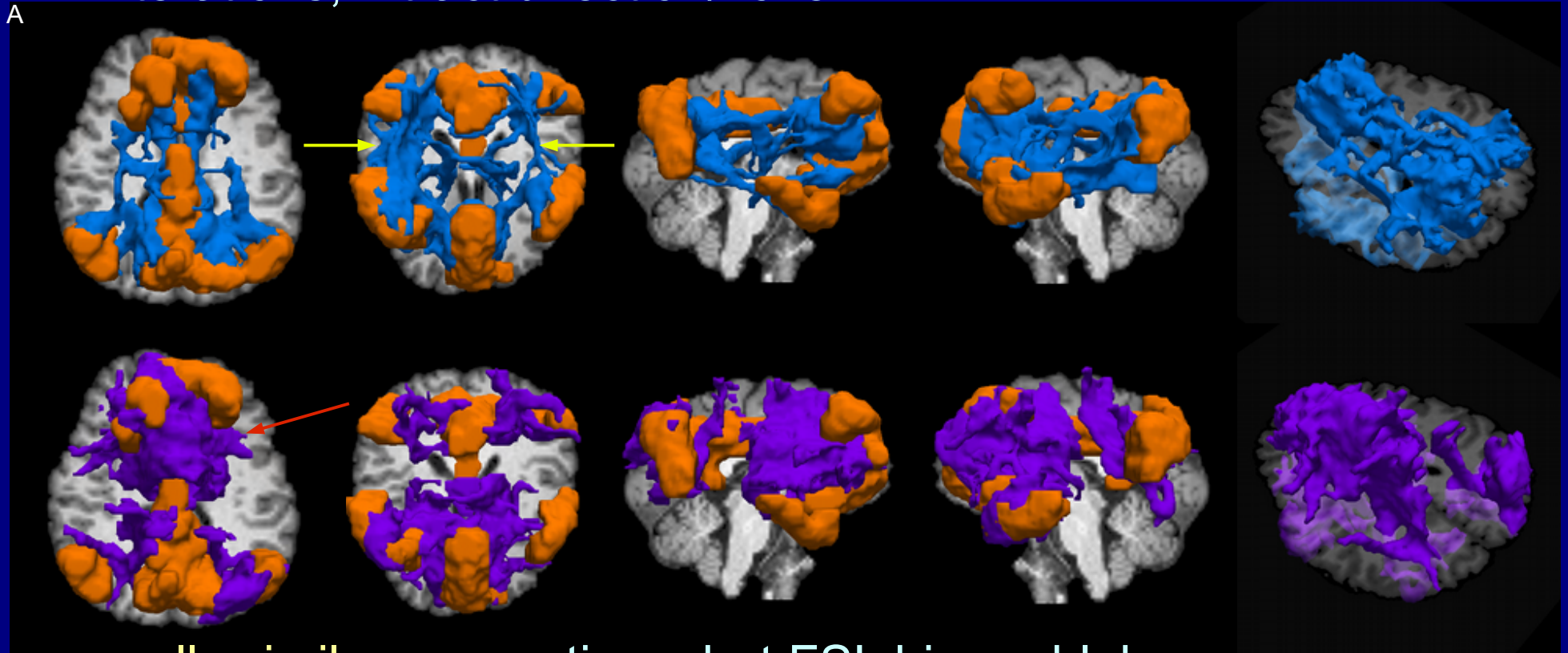
- purple: FSL-probtrackX (and FSL-bedpostX for uncertainty)
- same parameters: $FA > 0.2$, max angle 60deg, 5000 Monte Carlo iterations; 1 tract direction/voxel



+ generally similar connections, but FSL bigger blobs

3dTrackID: Probabilistic tractography

- + compare with existing algorithms:
 - purple: FSL-probtrackX (and FSL-bedpostX for uncertainty)
 - same parameters: $FA > 0.2$, max angle 60deg, 5000 Monte Carlo iterations; 1 tract direction/voxel

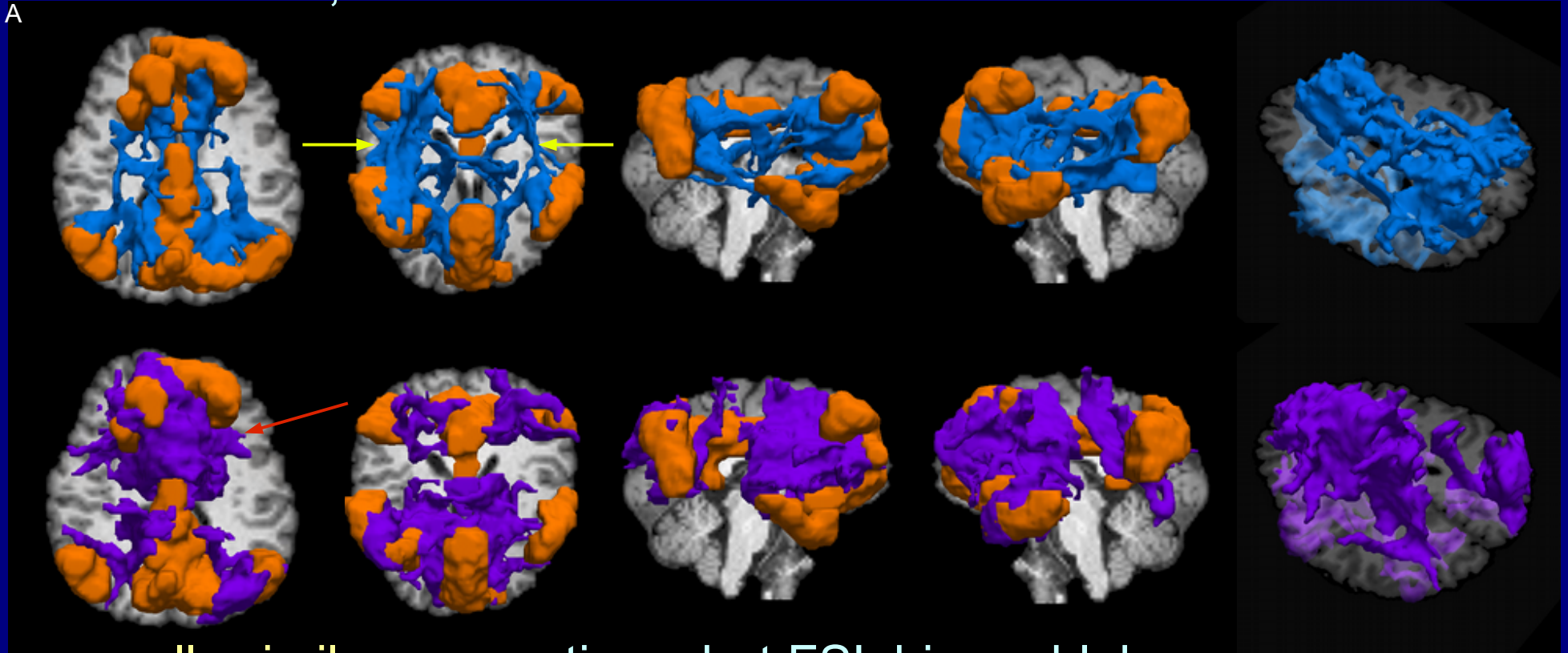


- + generally similar connections, but FSL bigger blobs
- + FSL took **several hours** for uncertainty, and then **>24 hours** for tracking this single network (and had to run 4 for this study)

3dTrackID: Probabilistic tractography

+ compare with existing algorithms:

- purple: FSL-probtrackX (and FSL-bedpostX for uncertainty)
- same parameters: $FA > 0.2$, max angle 60deg, 5000 Monte Carlo iterations; 1 tract direction/voxel



+ generally similar connections, but FSL bigger blobs

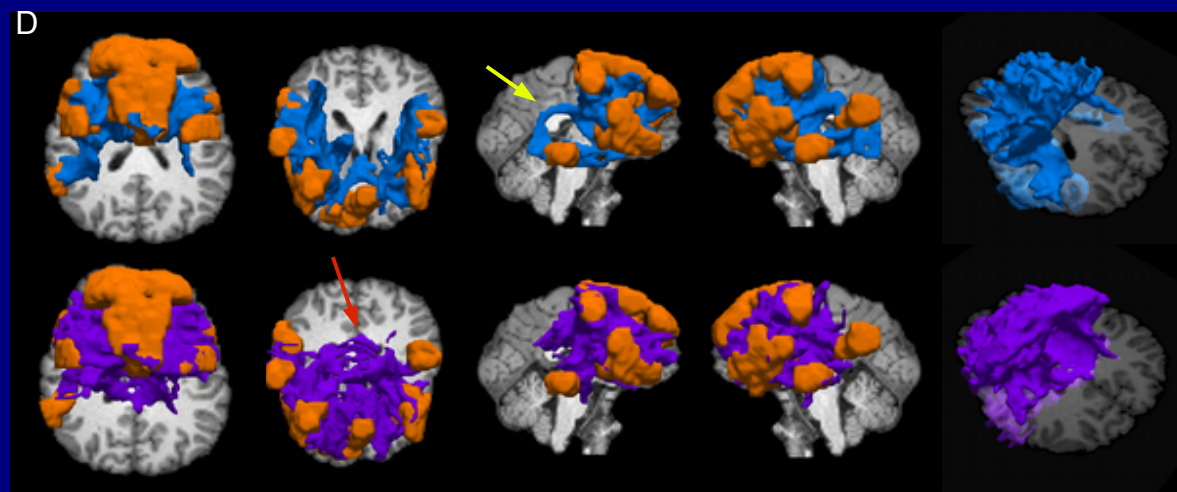
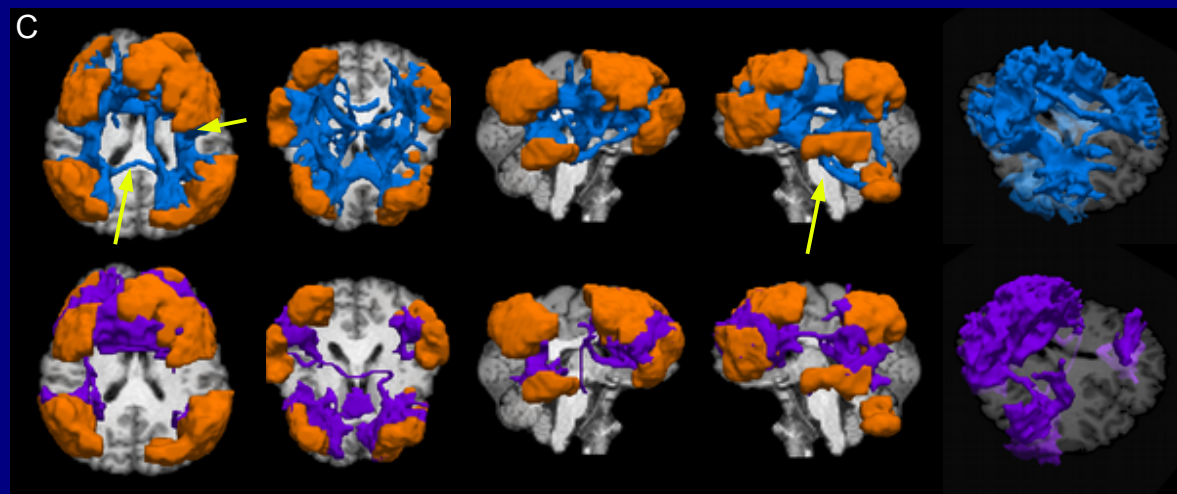
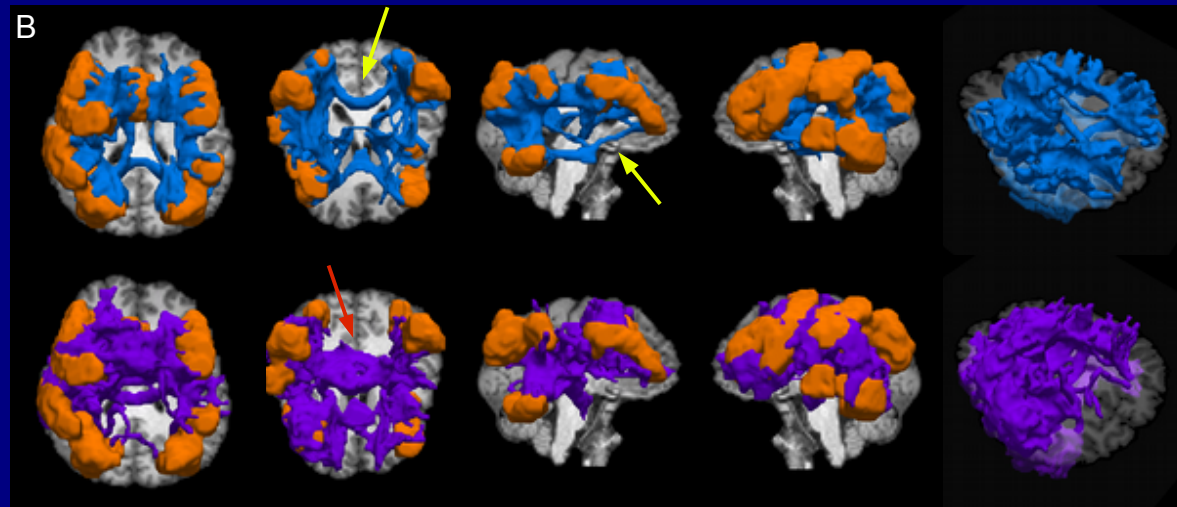
+ FSL took **several hours** for uncertainty, and then **>24 hours** for tracking this single network (and had to run 4 for this study)

+ **3dDWUncert** took **7min**; **3dTrackID** took **25mins** total for 4 netw.

3dTrackID:

(other networks show similar results in terms of:

- narrow/wide regions of tracts;
- broadly similar locations;
- each program shows some tracks which the other doesn't)

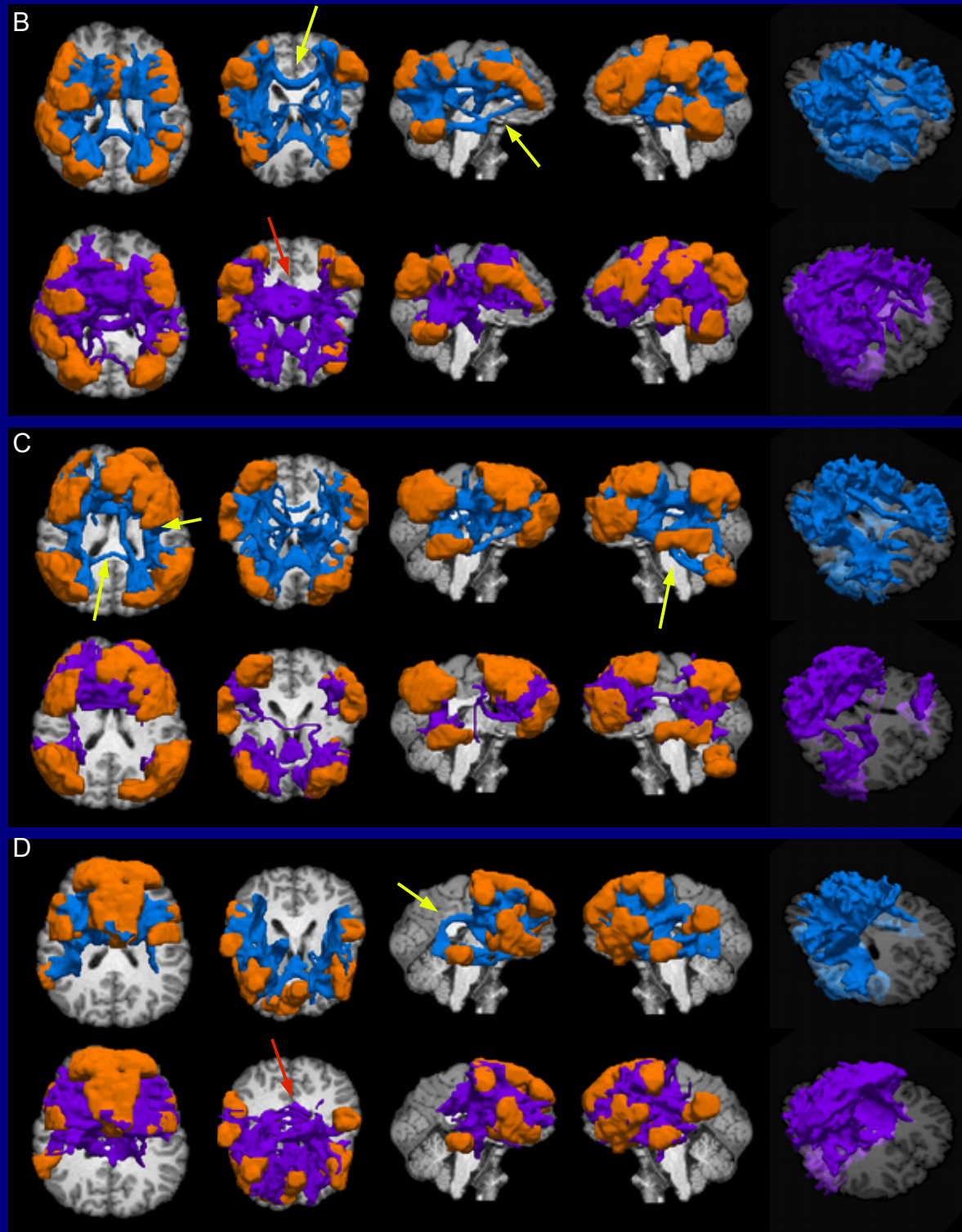


3dTrackID:

(other networks show similar results in terms of:

- narrow/wide regions of tracts;
- broadly similar locations;
- each program shows some tracks which the other doesn't)

(3dTrackID automatically creates *.grid files for probabilistic files, as well.)

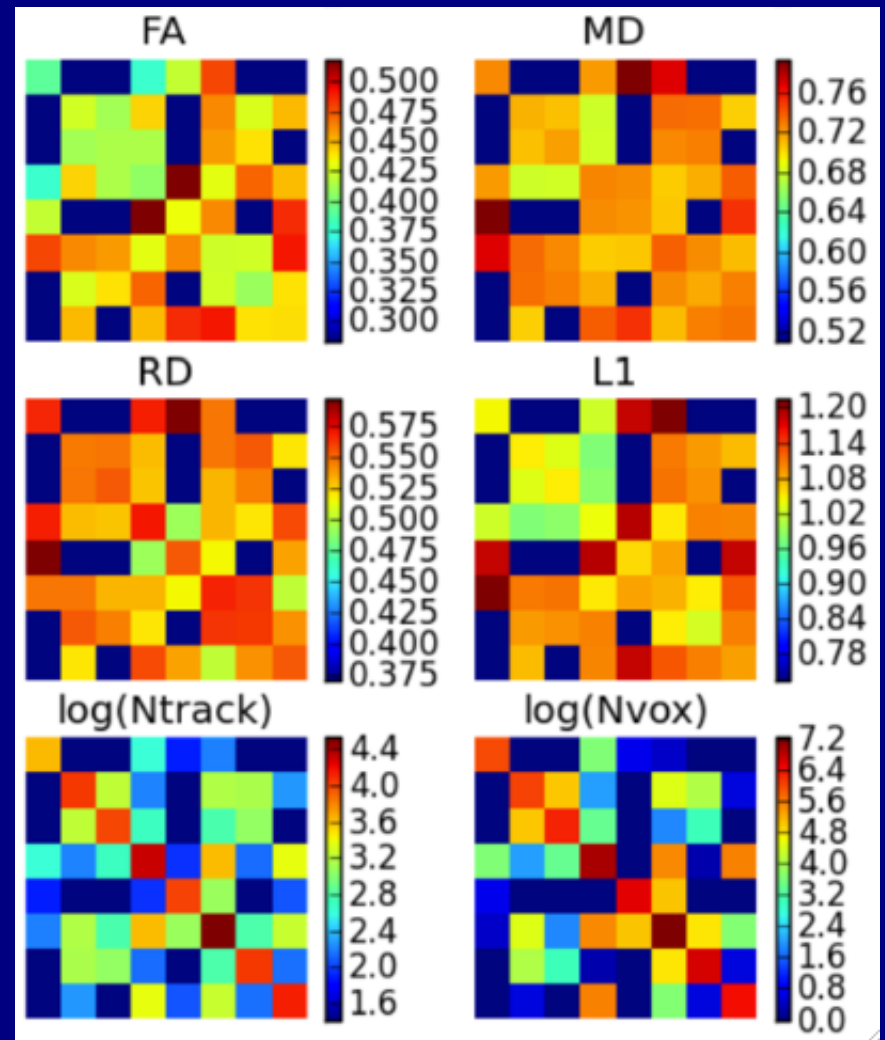


WM (ROI) Quantities

For connected pairs of GM ROIs in a network, have an average WM property (or can map to T1, PD...) →

Have produced sets of localized structural/anatomical quantities for comparison with functional values or behavioral scores, genetics, etc.

Can use for group or individual comparisons/regressions.



WM (ROI) Quantities

For connected pairs of GM ROIs in a network, have an average WM property (or can map to T1, PD...) →

Have produced sets of localized structural/anatomical quantities for comparison with functional values or behavioral scores, genetics, etc.

Can use for group or individual comparisons/regressions.

3dNetCorr: correlation matrices
Of average time series in ROIs
(e.g., uninflated GM ROIs from 3dROIMaker)

