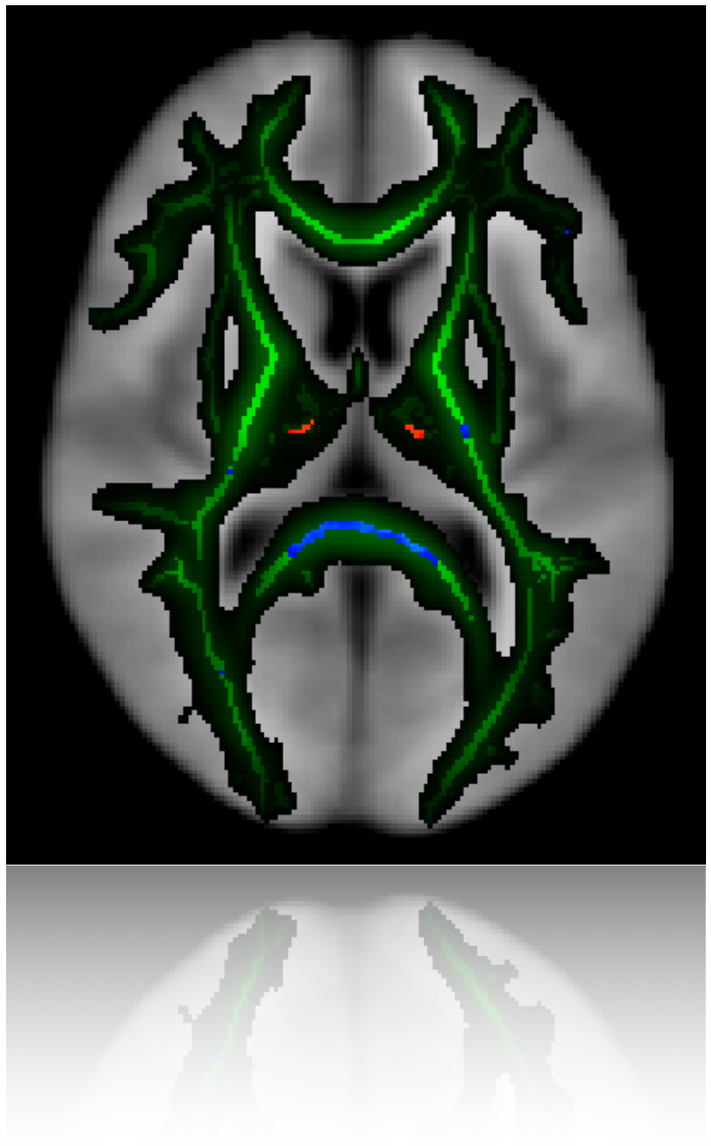
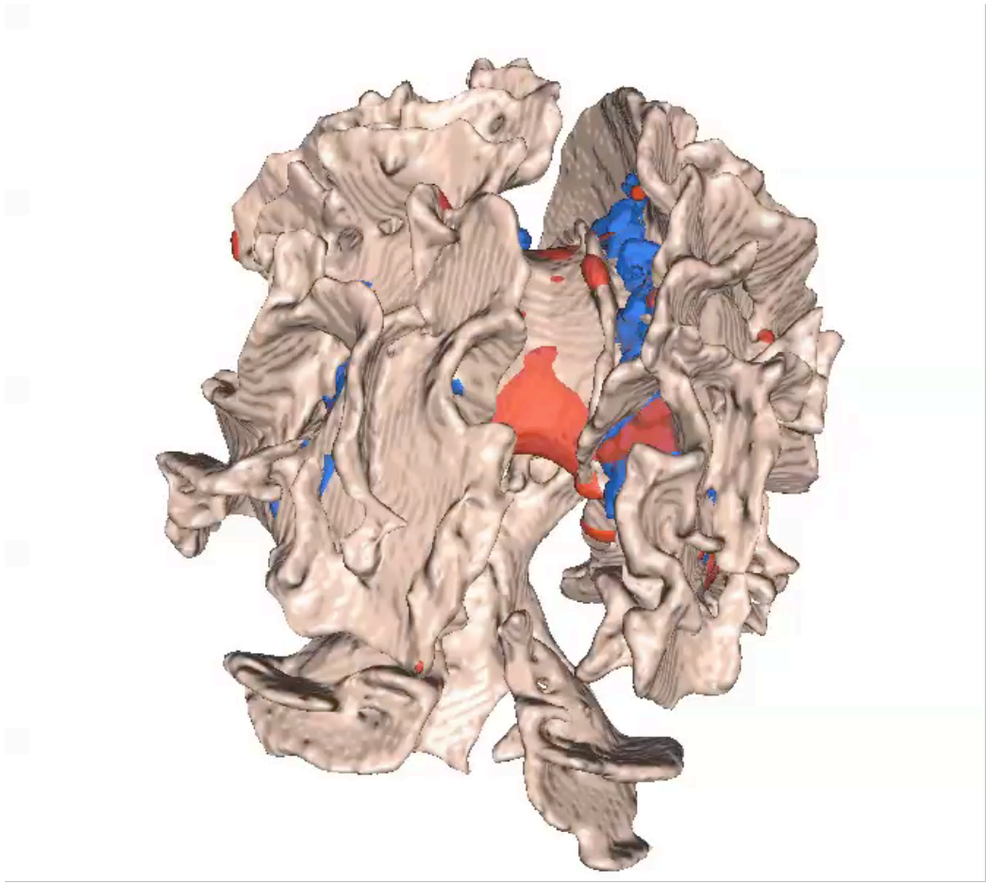
TBSS : Tract-Based Spatial Statistics

Robust "voxelwise" cross-subject stats on diffusion-derived measures

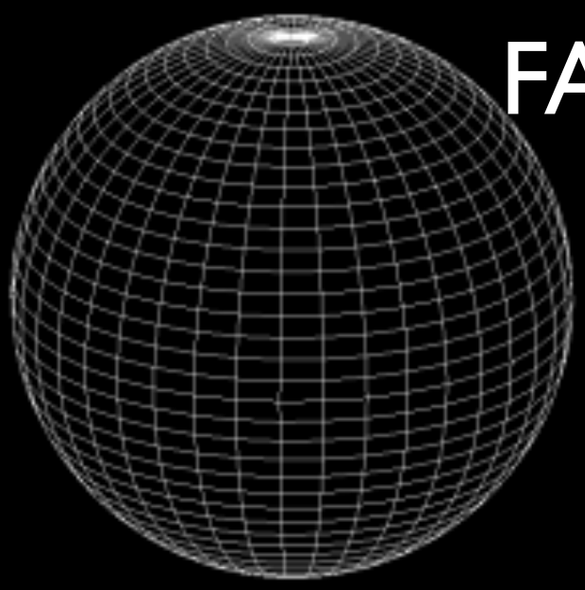




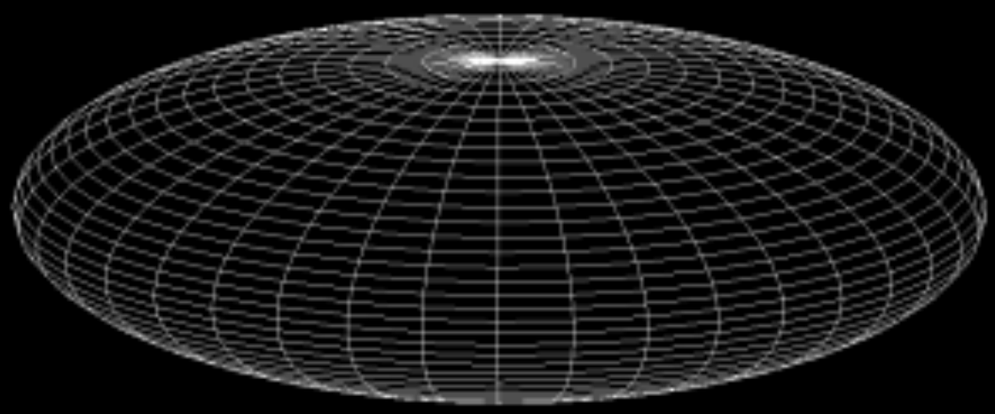
Tensor-derived parameters: Fractional Anisotropy

- 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.

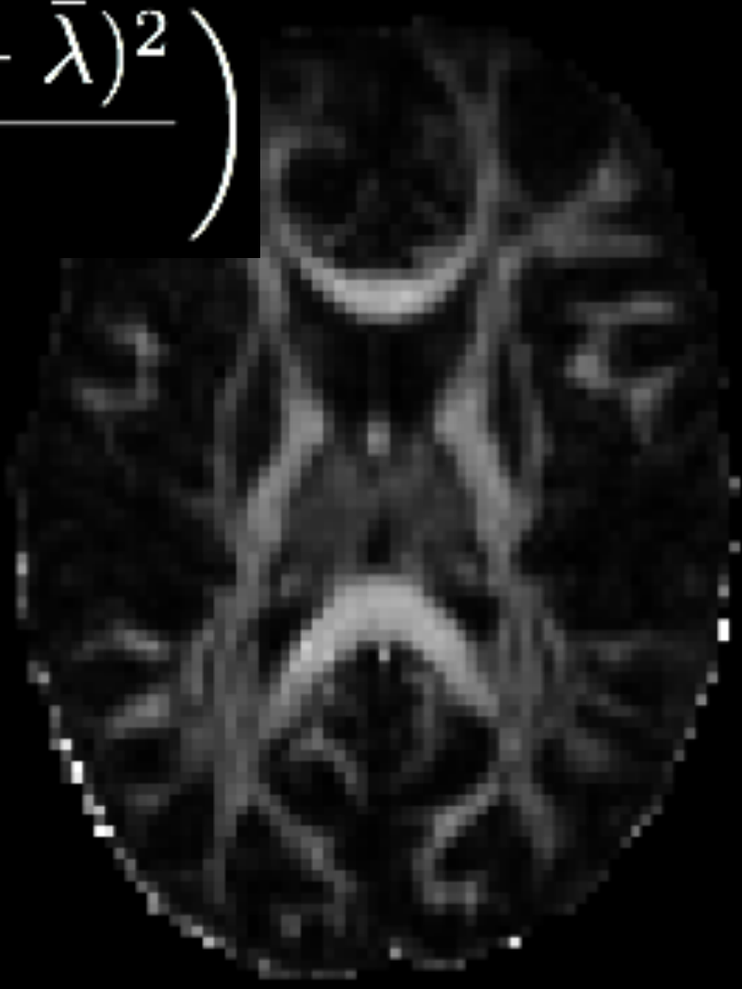
$$\mathrm{FA} = \sqrt{\frac{3}{2}\left(\frac{(\lambda_1 - \bar{\lambda})^2 + (\lambda_2 - \bar{\lambda})^2 + (\lambda_3 - \bar{\lambda})^2}{\lambda_1^2 + \lambda_2^2 + \lambda_3^2}\right)}$$



FA=0



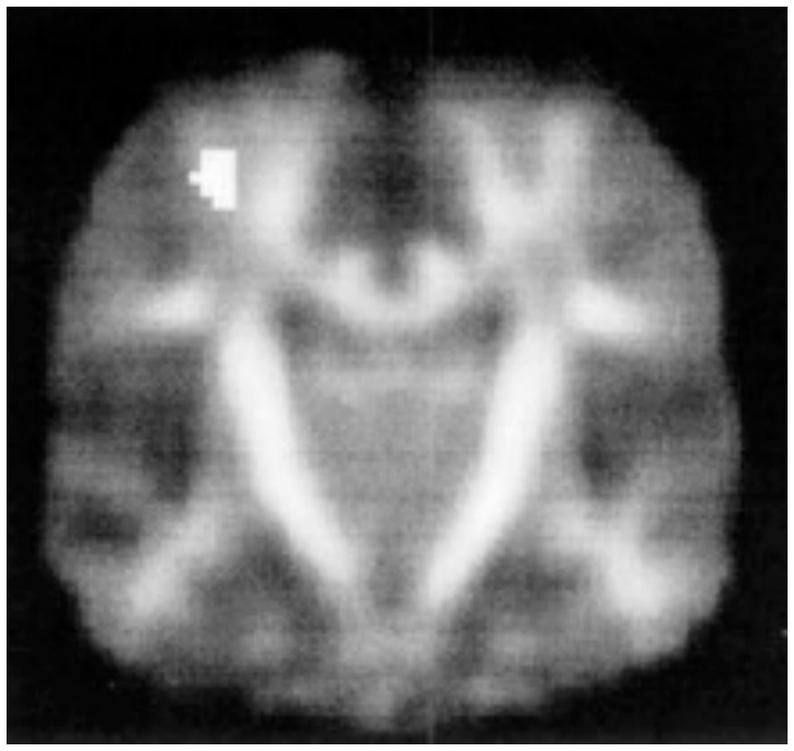
FA=0.8



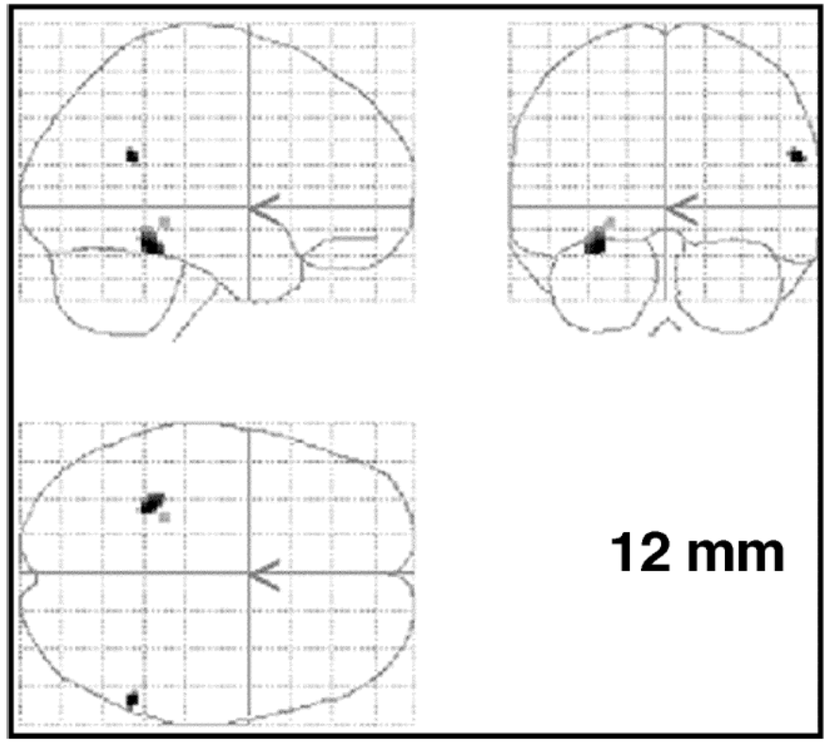
VBM-style Analysis of FA

- 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



Büchel 2004

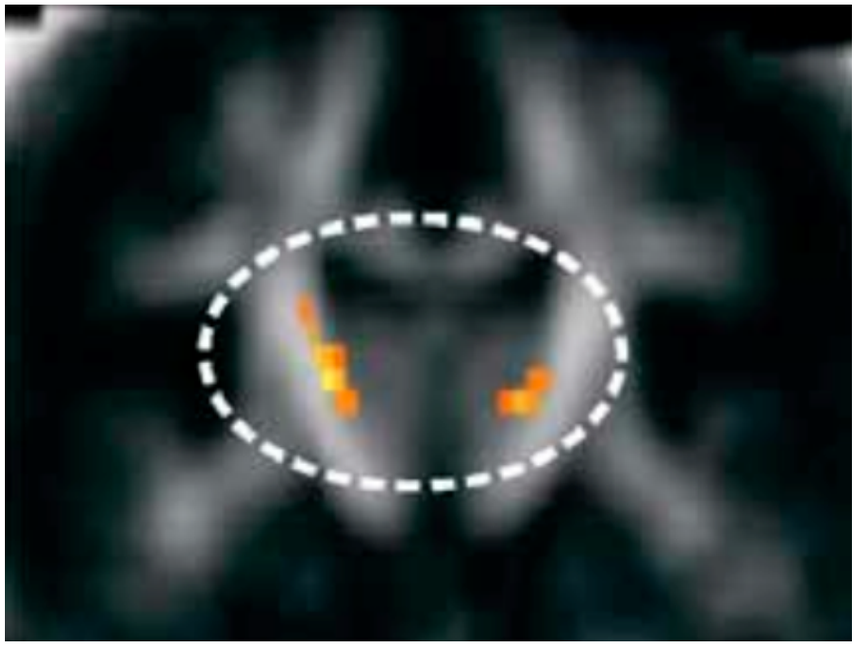
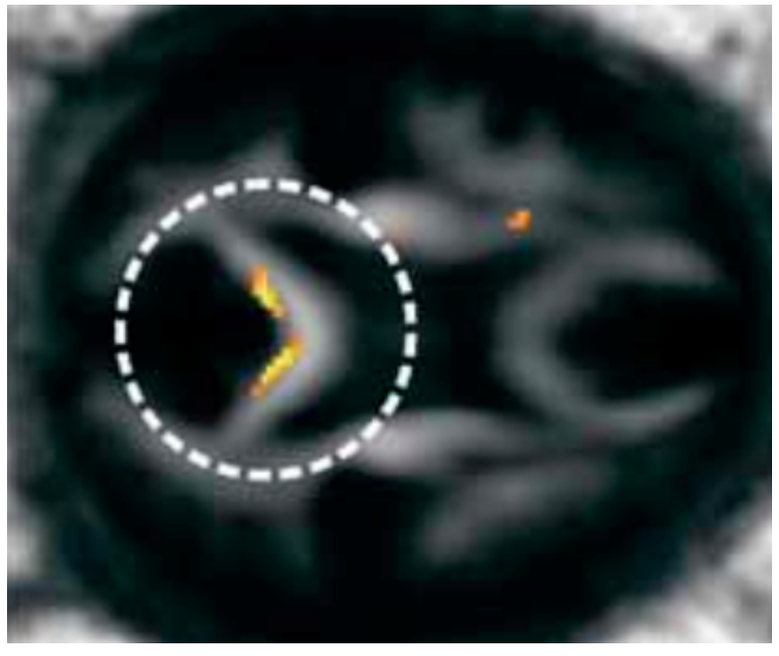
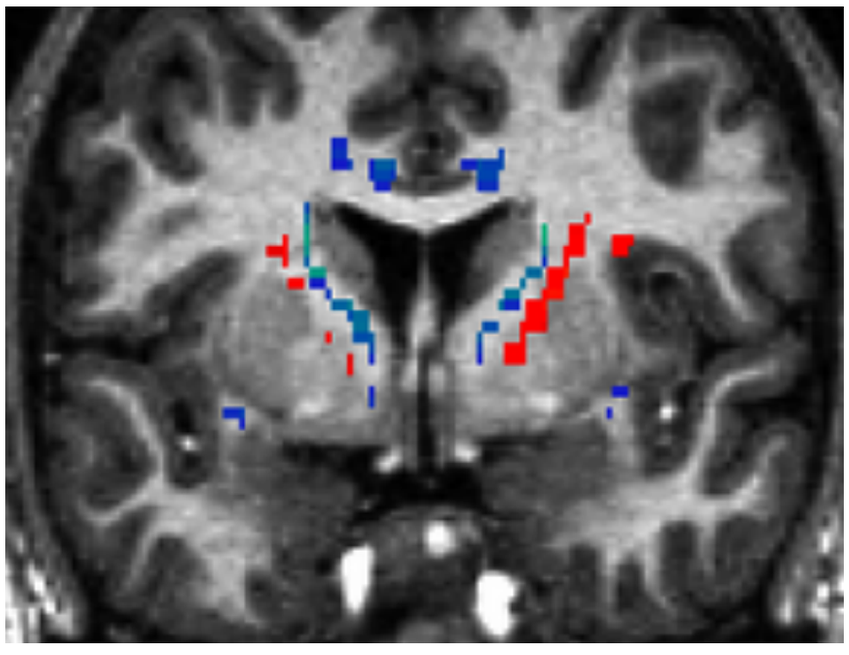


Jones 2005

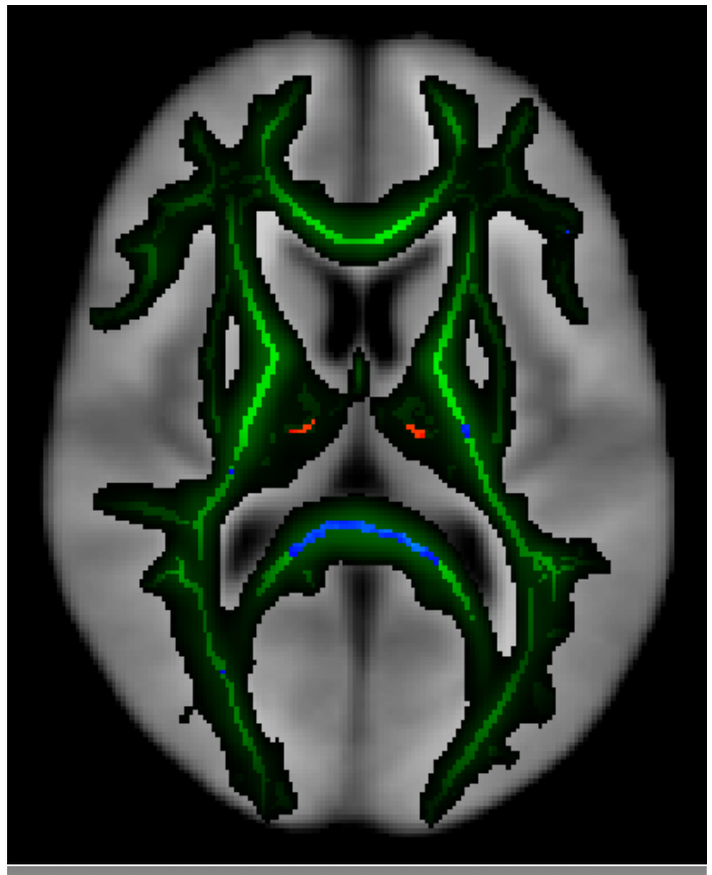
VBM-style Analysis of FA

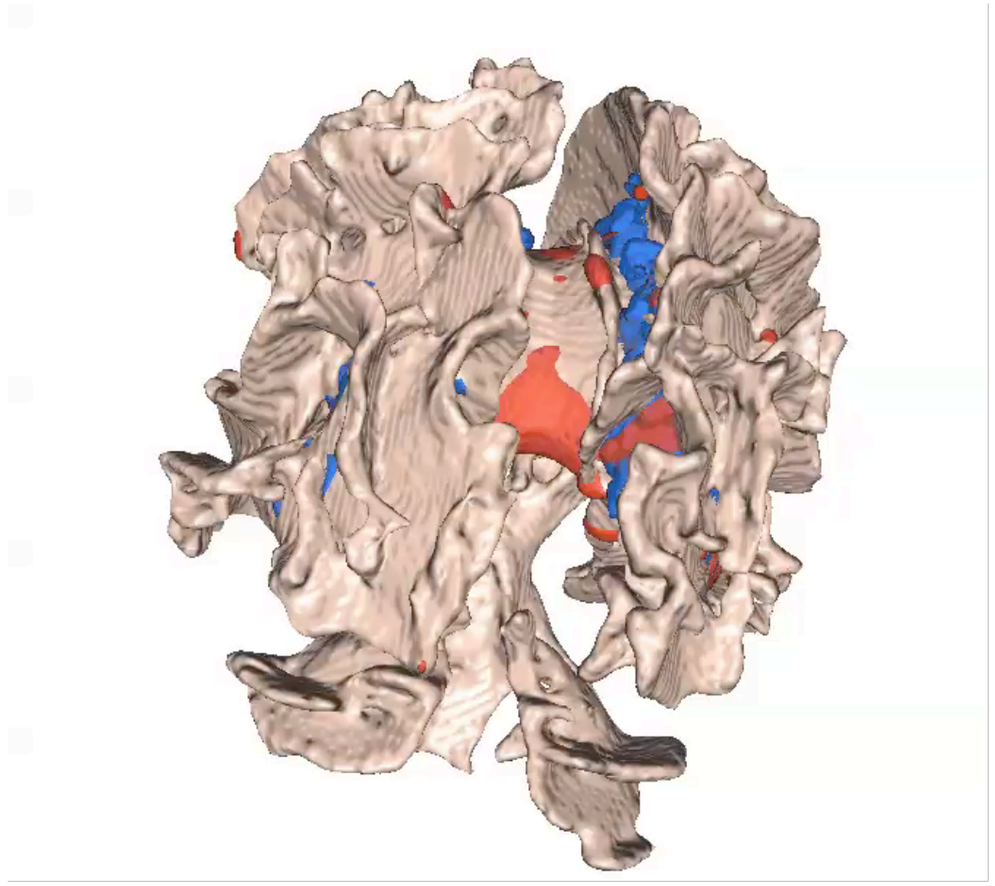
- Strengths
  - Fully automated & quick
  - Investigates whole brain

- 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

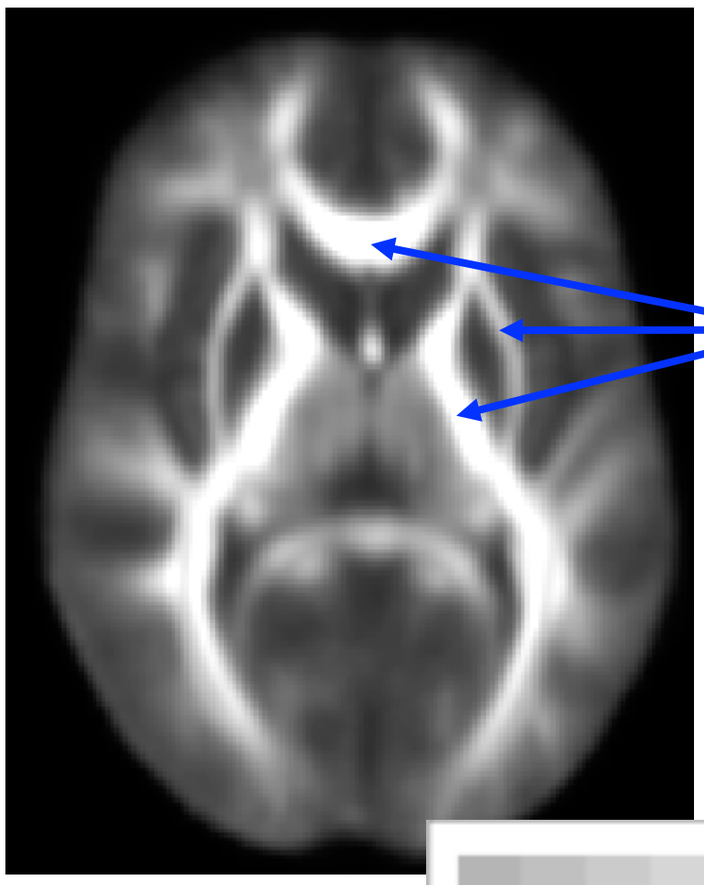
TBSS : Tract-Based Spatial Statistics

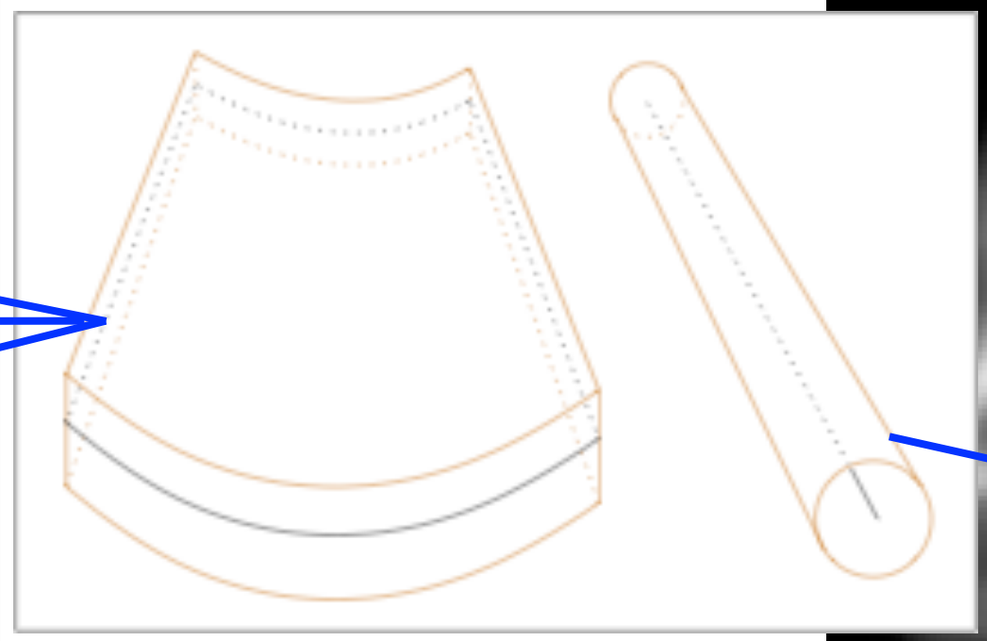


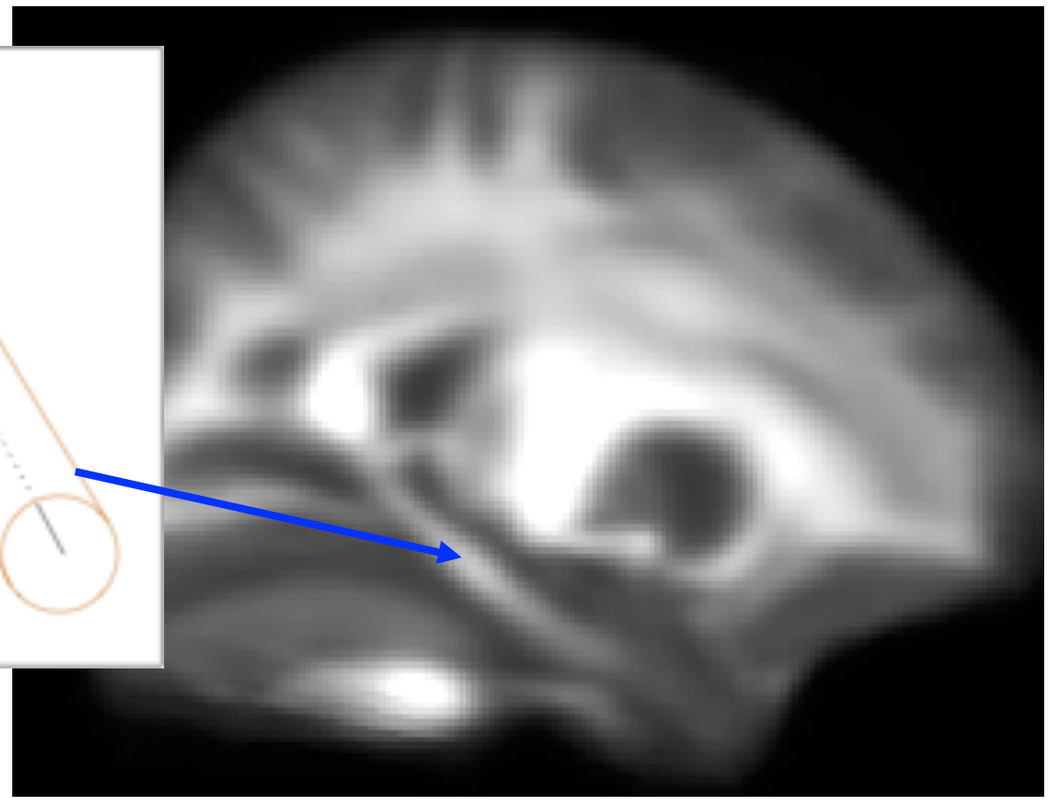


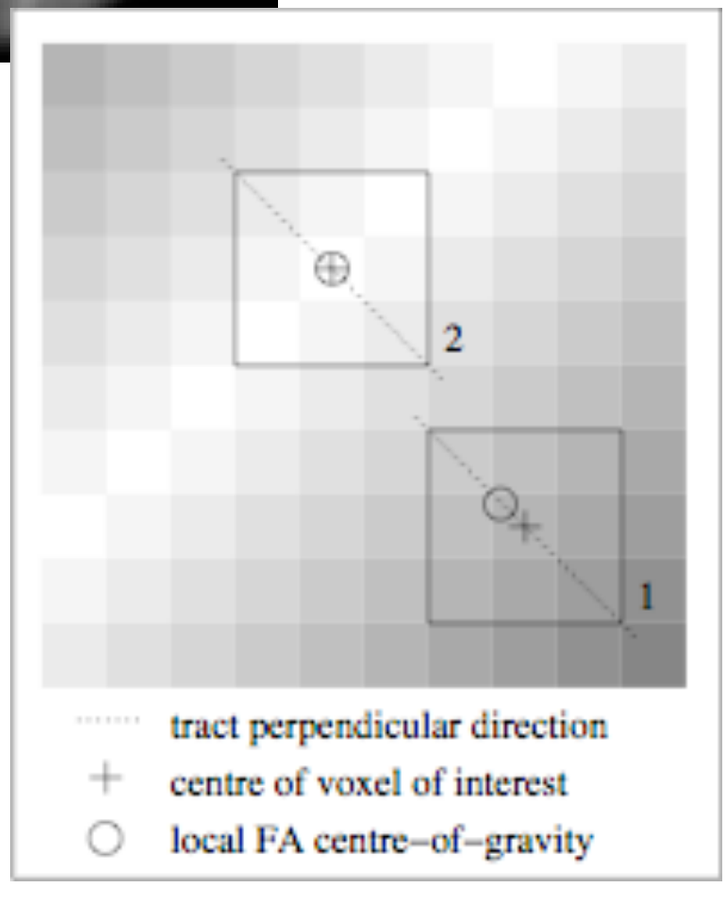
- Need: robust "voxelwise" cross-subject stats on DTI
- Problem: alignment issues confound valid local stats
- TBSS: solve alignment using alignment-invariant features:
- Compare FA taken from tract centres (via skeletonisation)

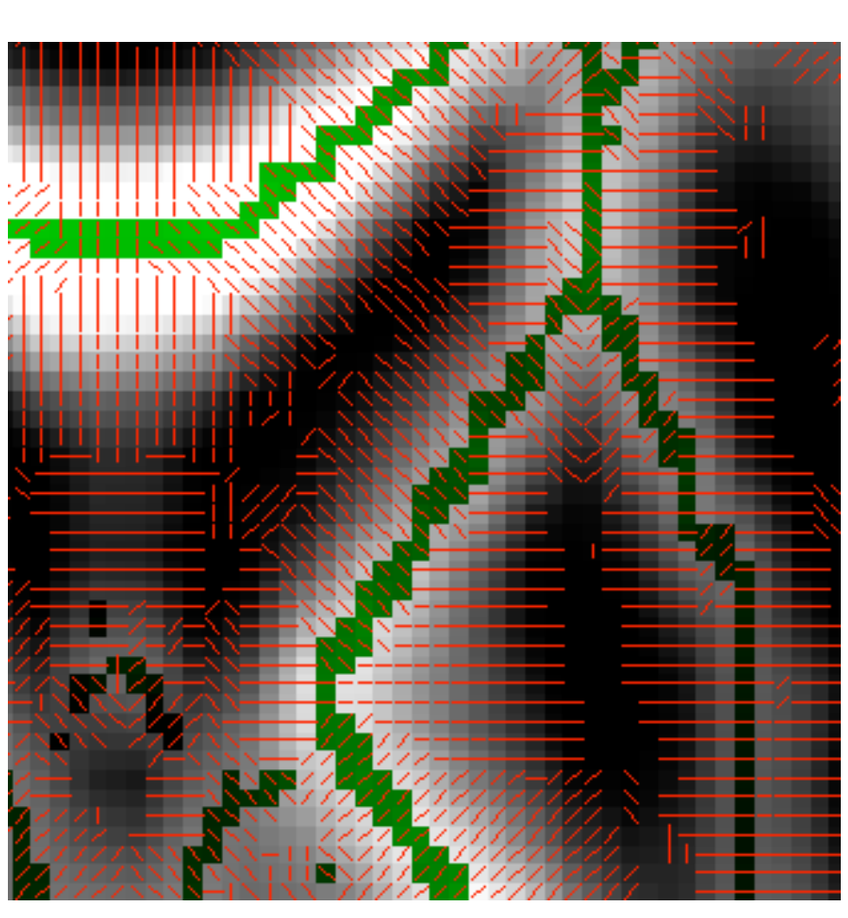
2. “Skeletonise” Mean FA





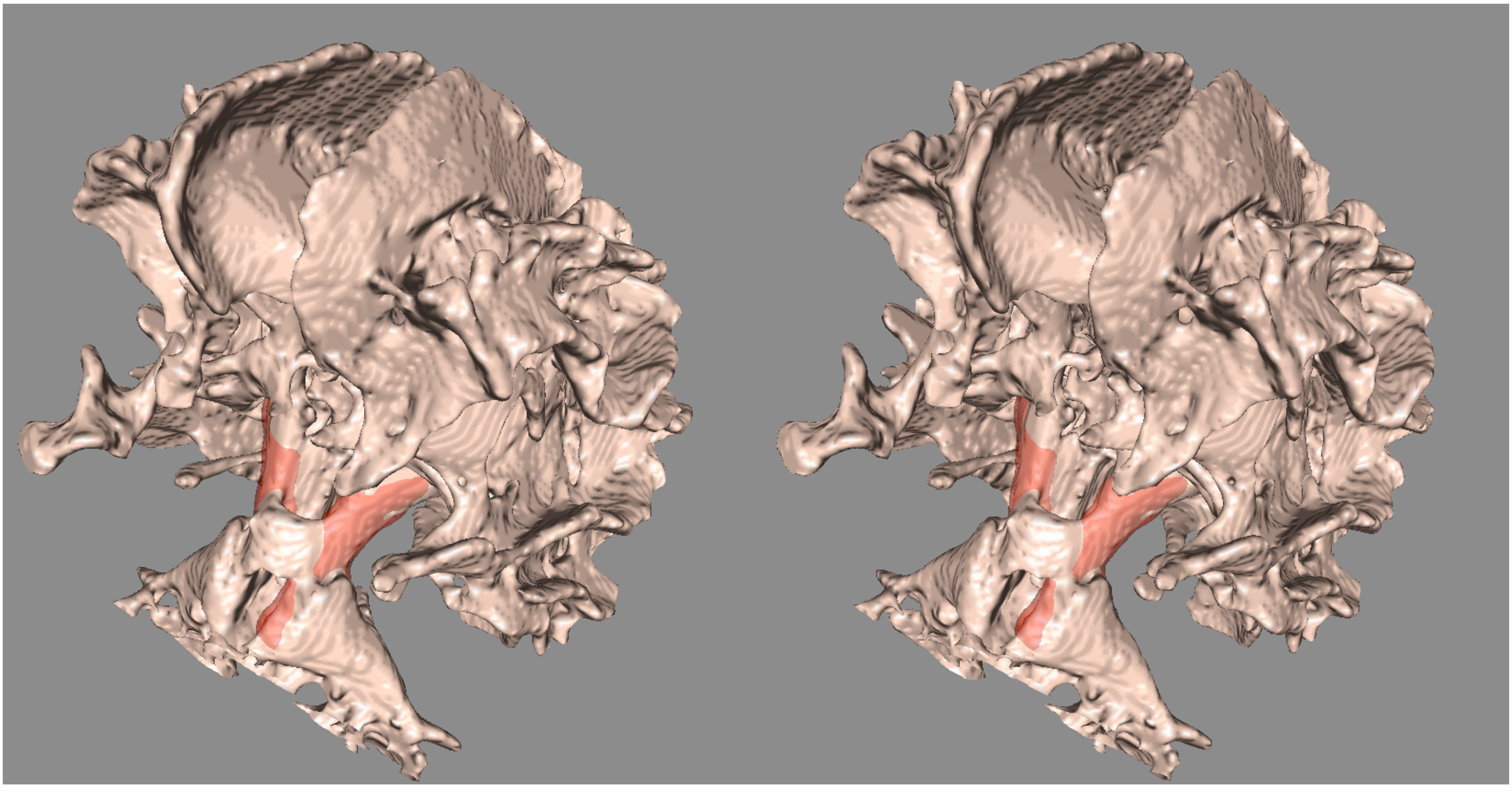






3. Threshold Mean FA Skeleton

giving "objective" tract map



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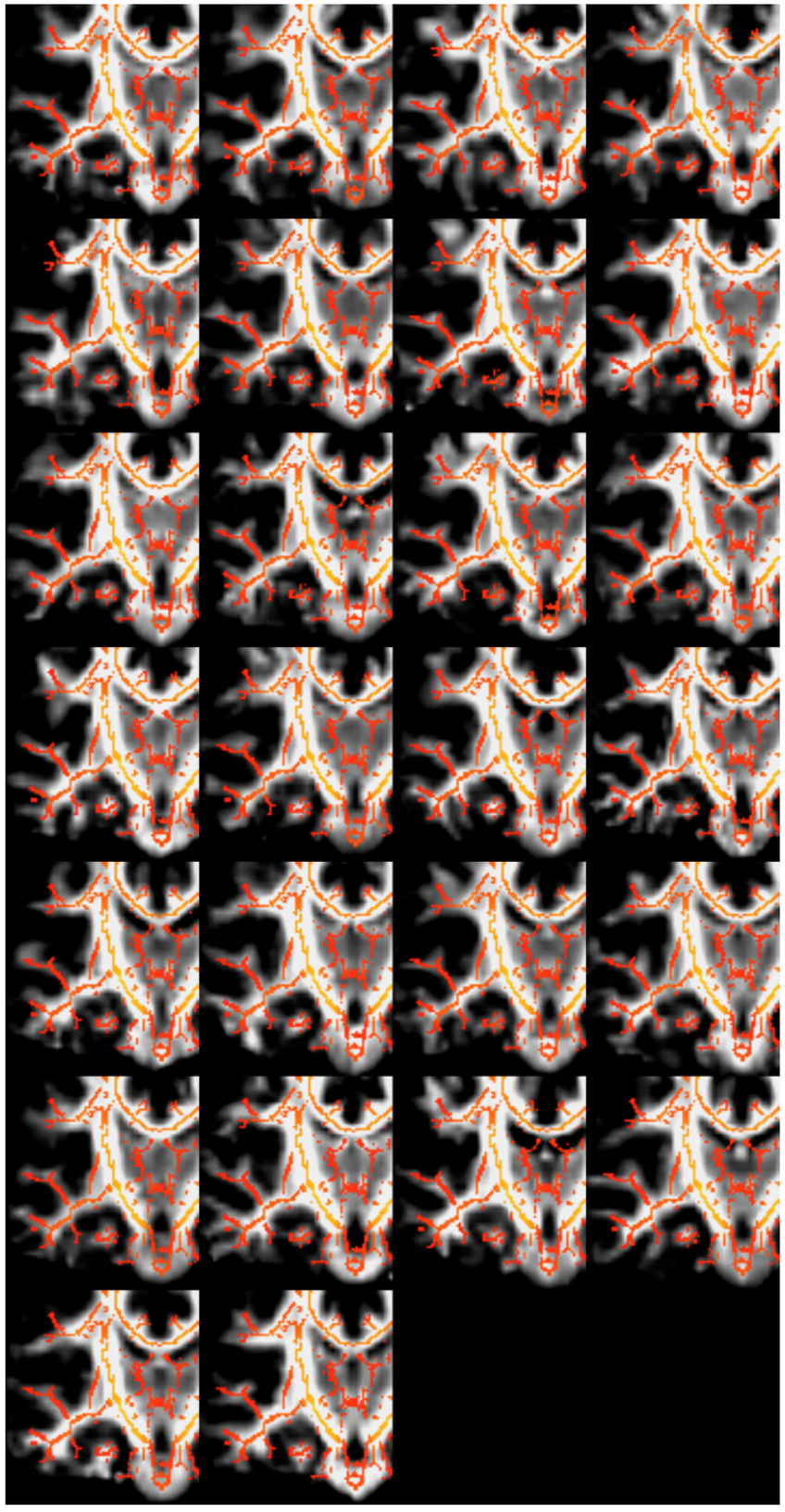
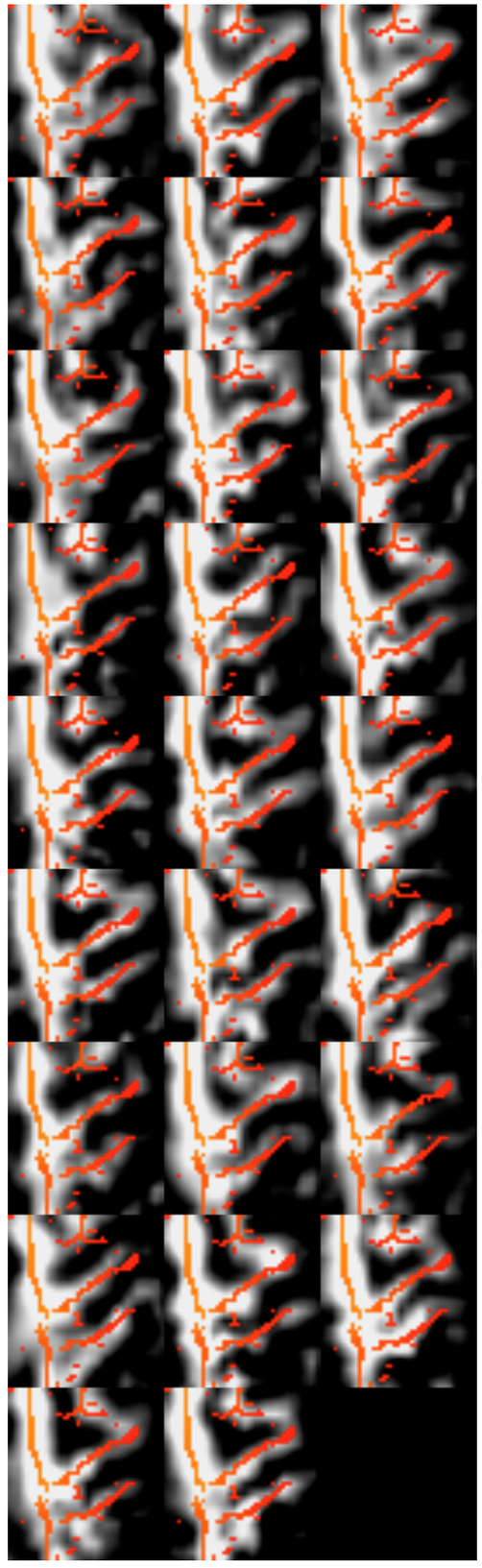
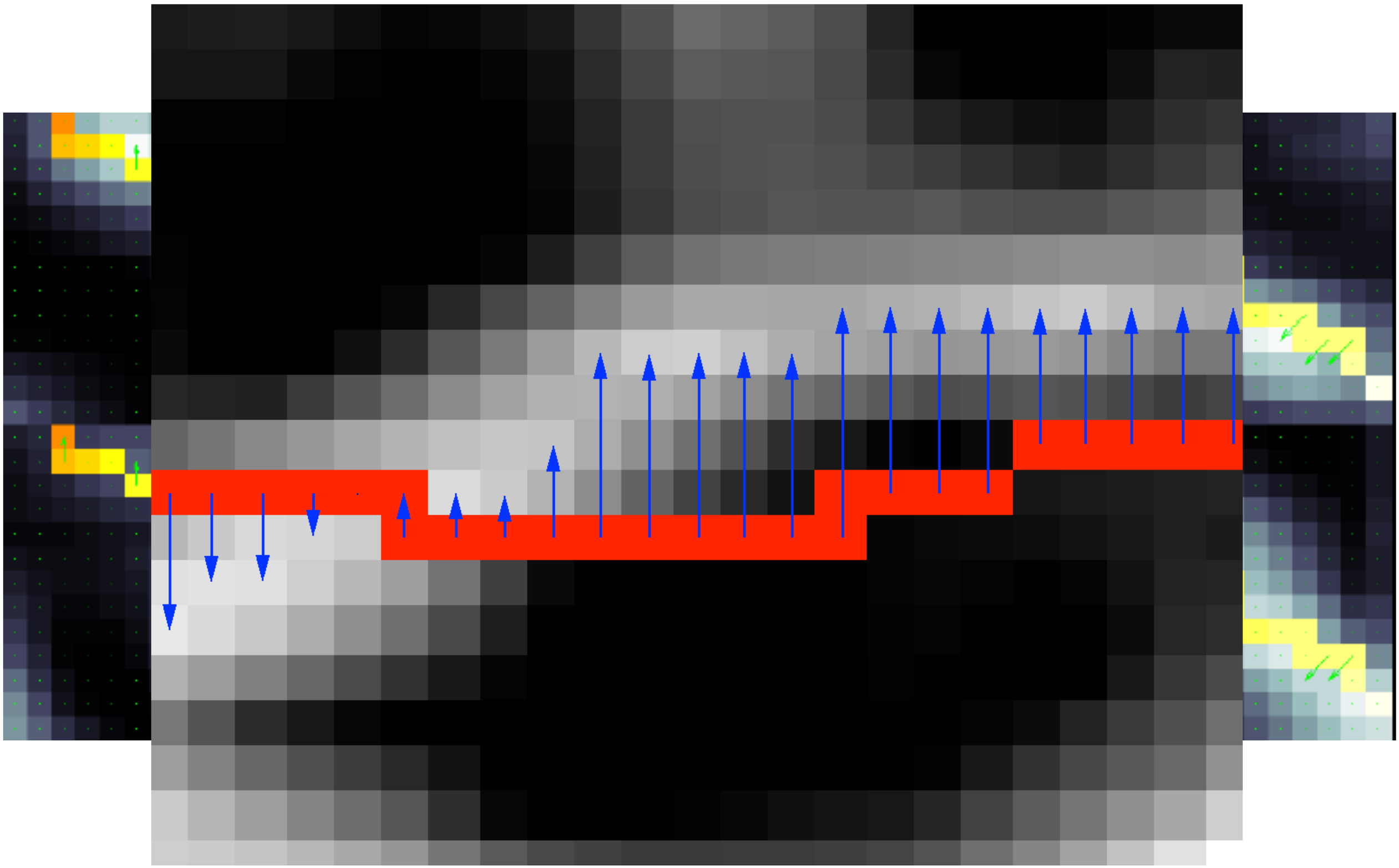
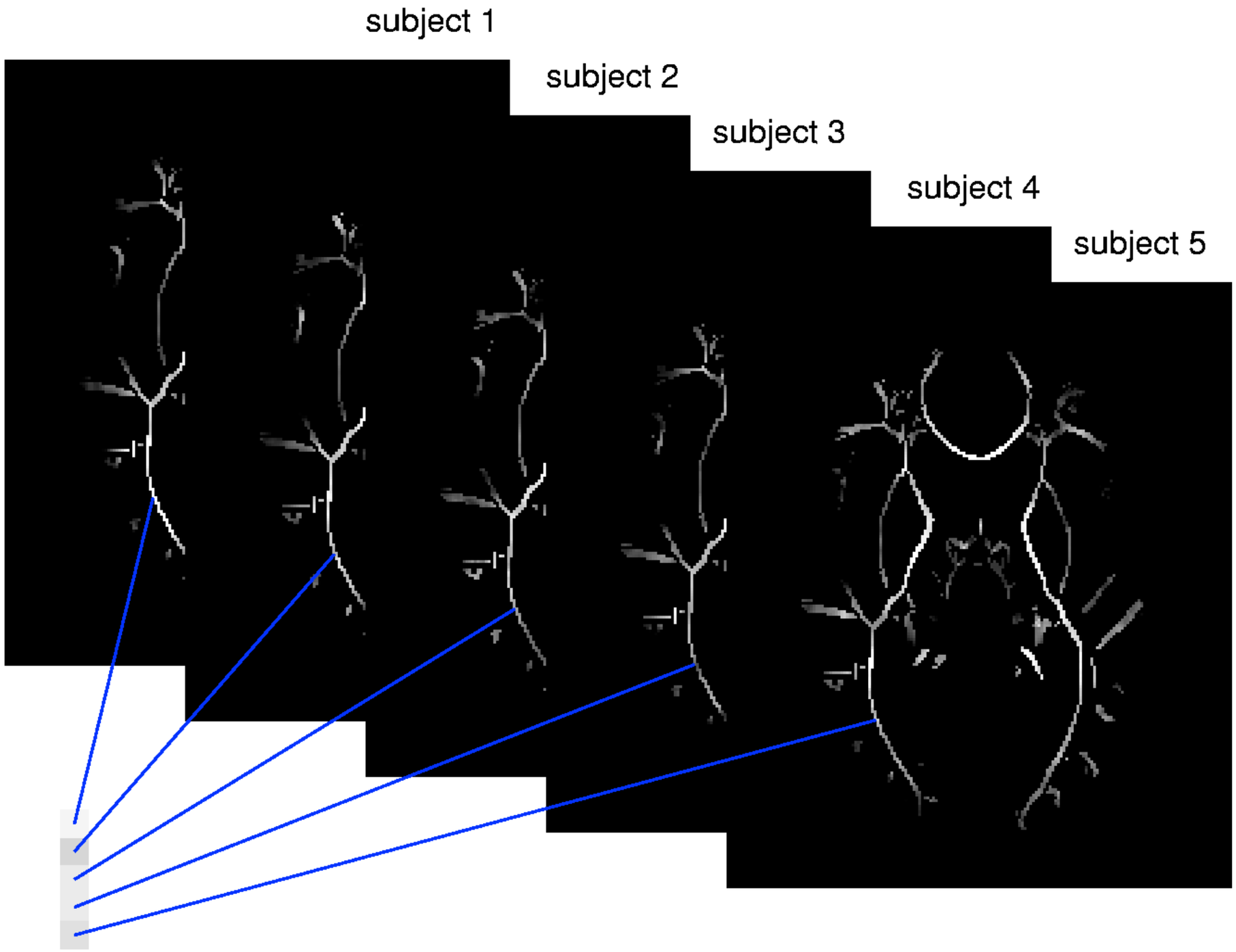




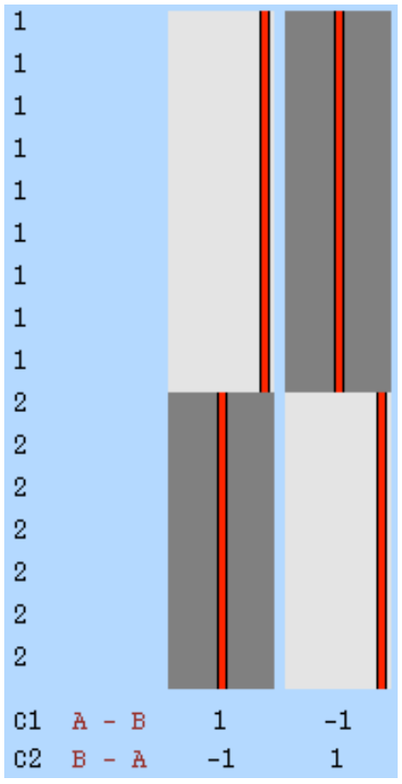
4. For each subject's warped FA, fill each point on the mean-space skeleton with nearest maximum FA value (i.e., from the centre of the subject's nearby tract)

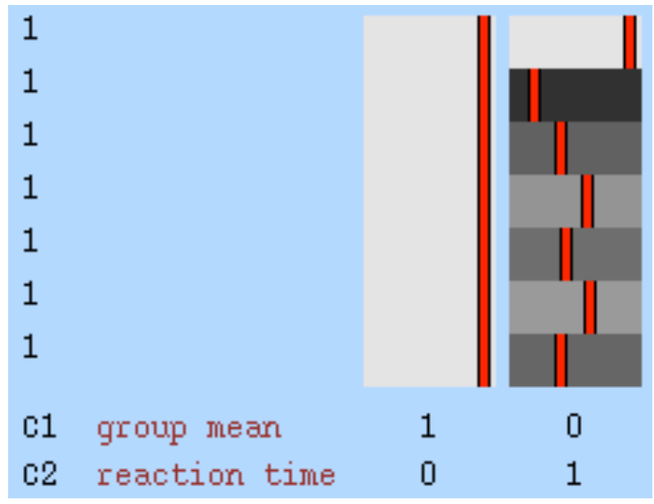


5. Do cross-subject voxelwise stats on skeleton-projected FA and Threshold, (e.g., permutation testing, including multiple comparison correction)



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

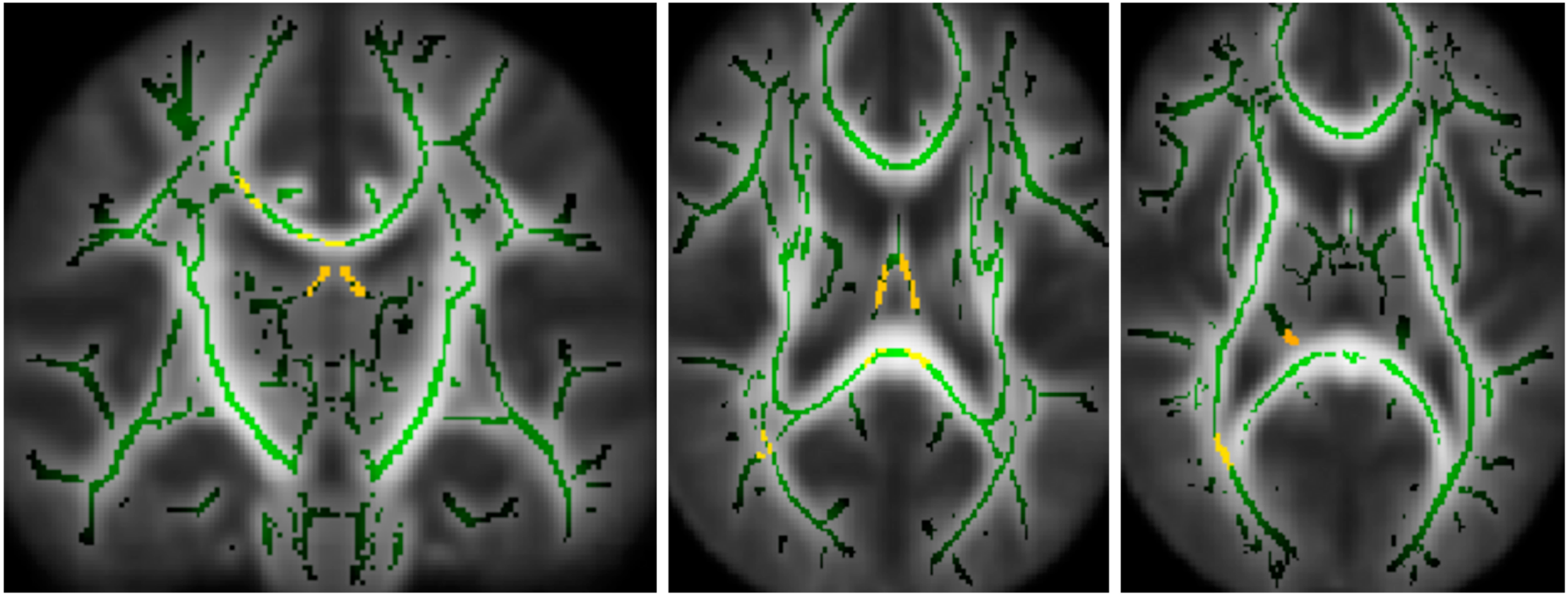




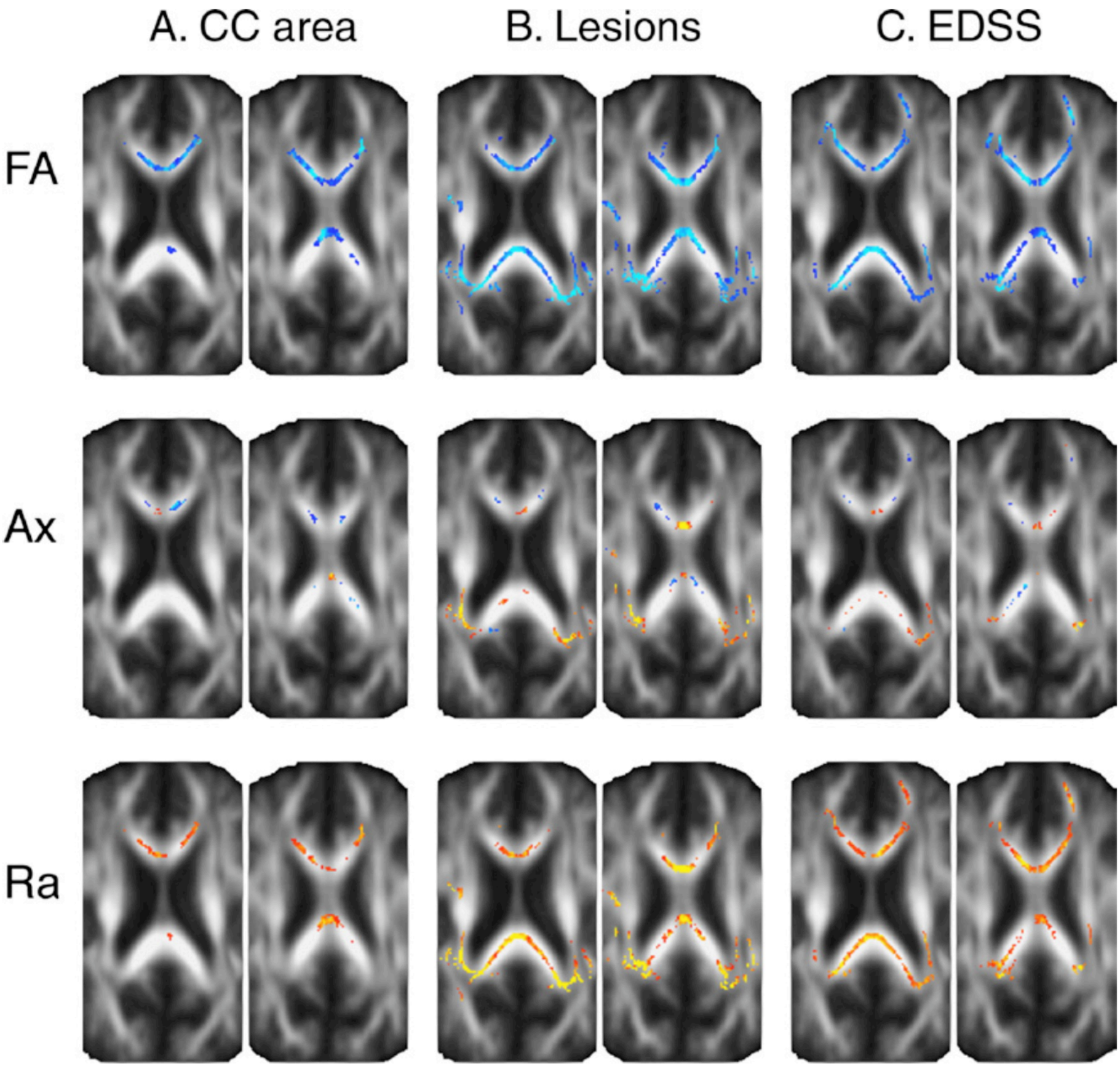
Schizophrenia (Mackay)

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.)



Multiple Sclerosis (Cader, Johansen-Berg & Matthews)



TBSS - Conclusions

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