ANALYSIS OF DTI DATA

Part 2

DO TROMP - 2015

DTI ANALYSIS STEPS (Tutorial 1):

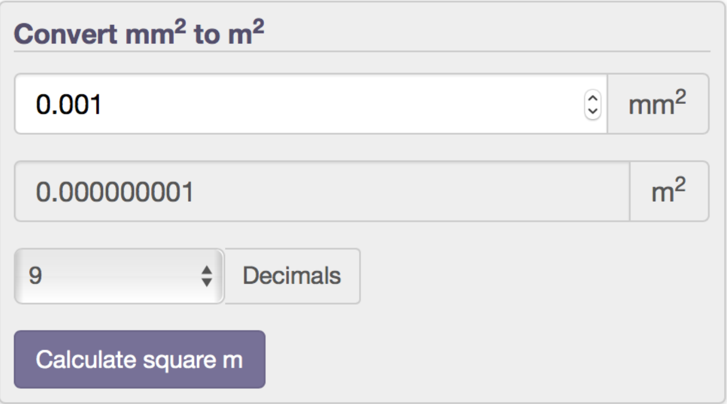
1. From scanner format to a usable format
2. Correct distortions common to diffusion images (EPI and eddy currents)
3. Remove any non-brain tissues
4. Make the gradient direction file
5. Fit the tensors
6. Check the fit of the tensors

DTI ANALYSIS STEPS (Tutorial 2):

1. Standardize tensor images for normalization
2. Make population template by normalizing images
3. Register population template to MNI space
4. Produce scalar images (FA, MD, AD, RD) and check quality
5. Run whole brain voxel-wise statistics

1. Standardize tensor images for normalization

- Use correct diffusivity unit for DTI-TK:
  - DTI-TK uses: 0.001 mm^2/s
  - Our unit is: 1 m^2/s
  - Thus multiply our tensor image with factor: 10^9



- Remove extreme outliers

- Make sure all tensors are symmetric and positive

2. Normalization, Why?

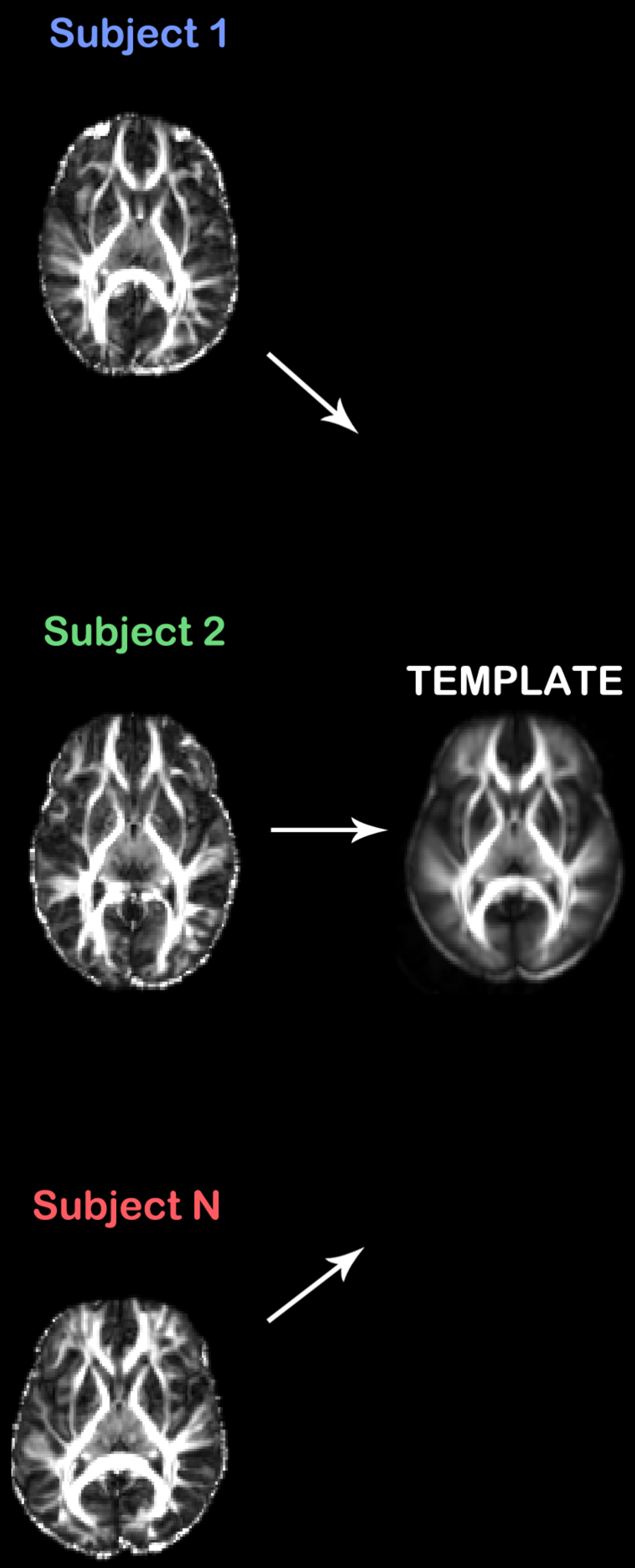
- Establishes a one-to-one correspondence between the brains of different individuals; by minimizing the sum of squared differences between each subject and the template

- Allows for:
    - Identification of commonalities and differences between groups (e.g. patients vs. healthy individuals)

- Advantages:
    - Significant clusters can be reported according to their Euclidian coordinates within a standard space (e.g. MNI or Tailarach)

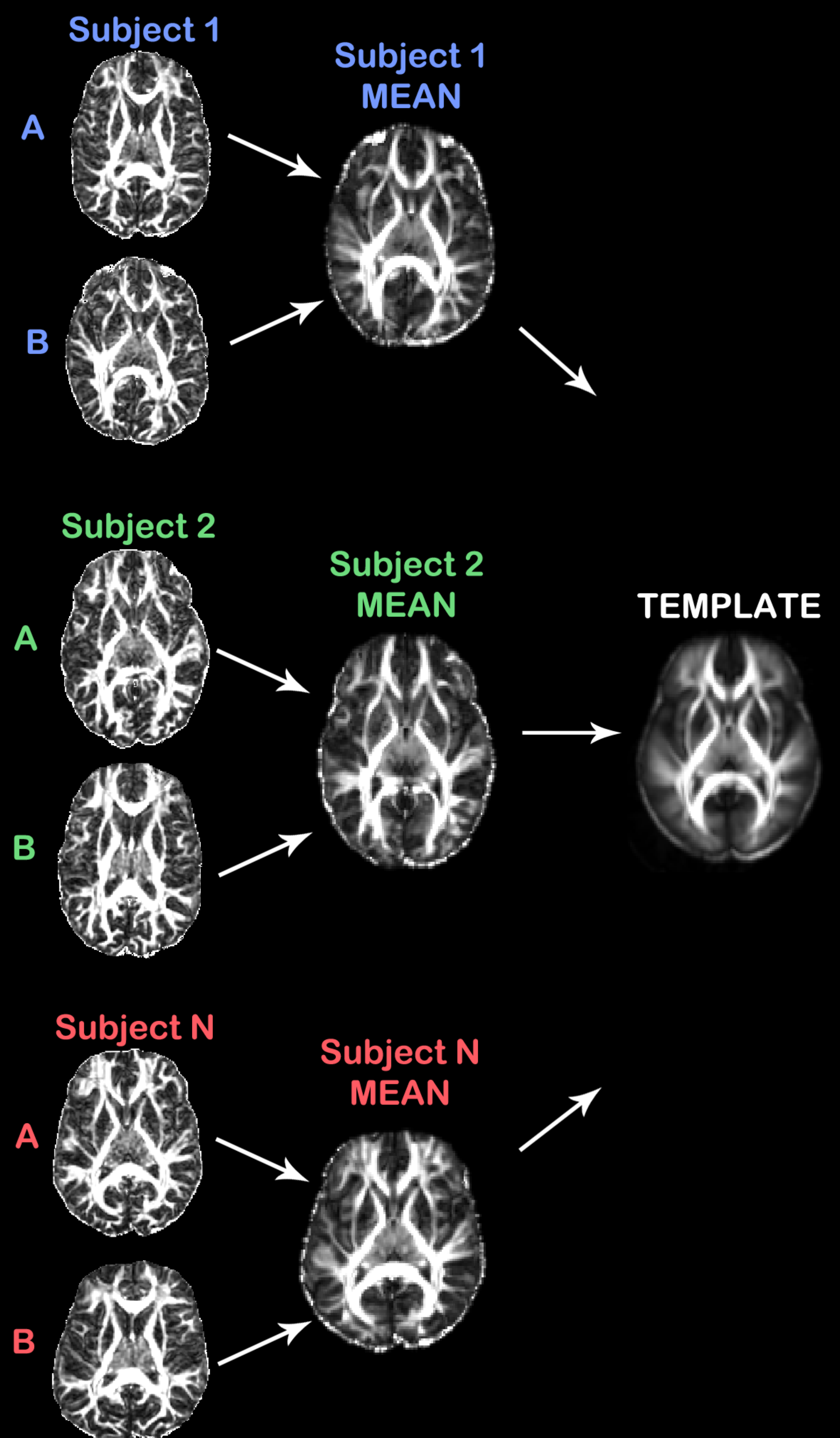
Source: Wellcome Trust Centre

normalization



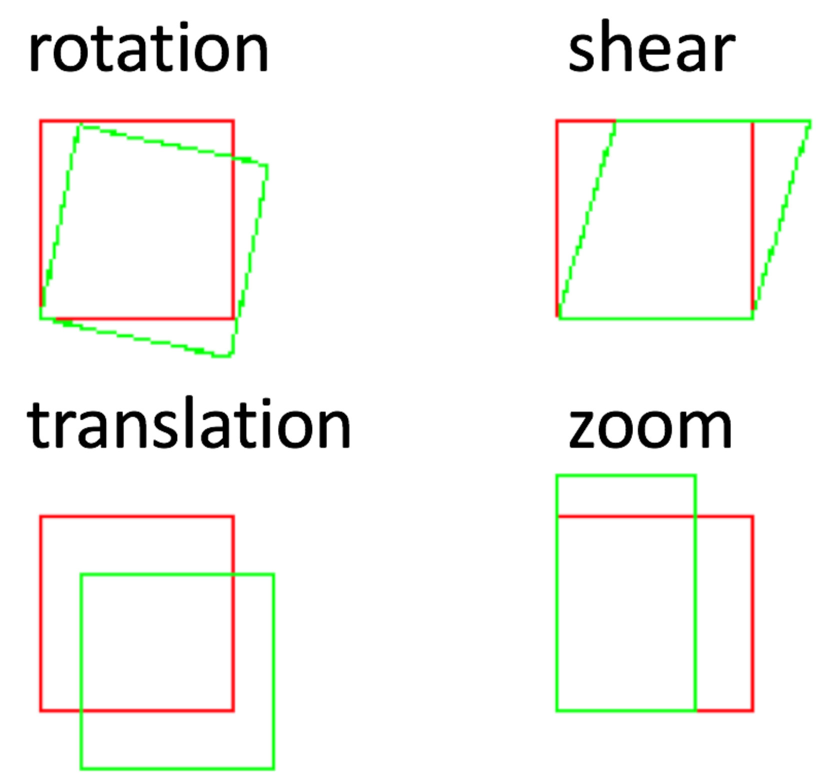
Two-step normalization

(e.g. longitudinal or twin study)

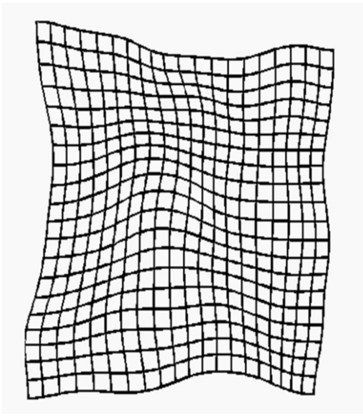


2. Normalization, How?

- **Linear Registration:**
  - Rigid transformation (rotation & translation in x, y, z)
  - Affine transformation (rotation, translation, shear, zoom in x, y, z)

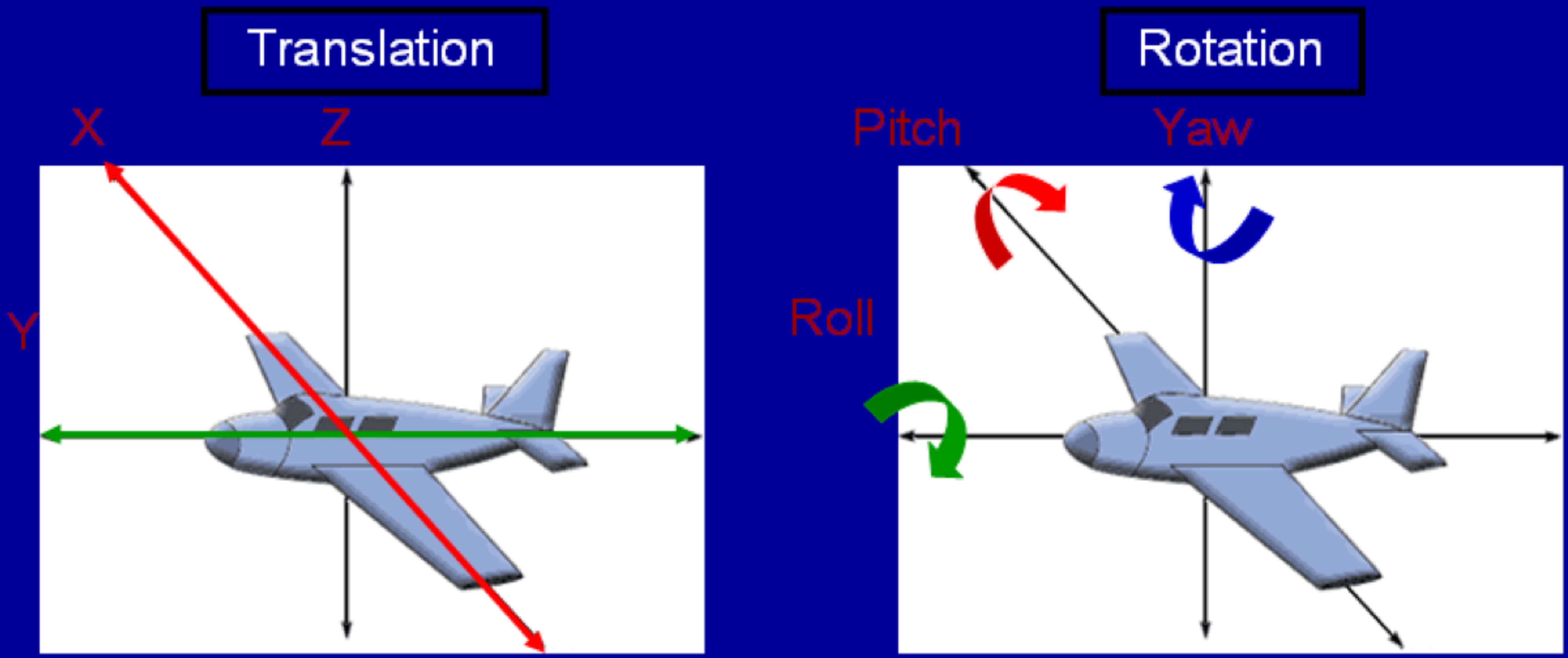


- **Non-linear Registration:**
  - Diffeomorphic transformation (warp)



2. Normalization, How?

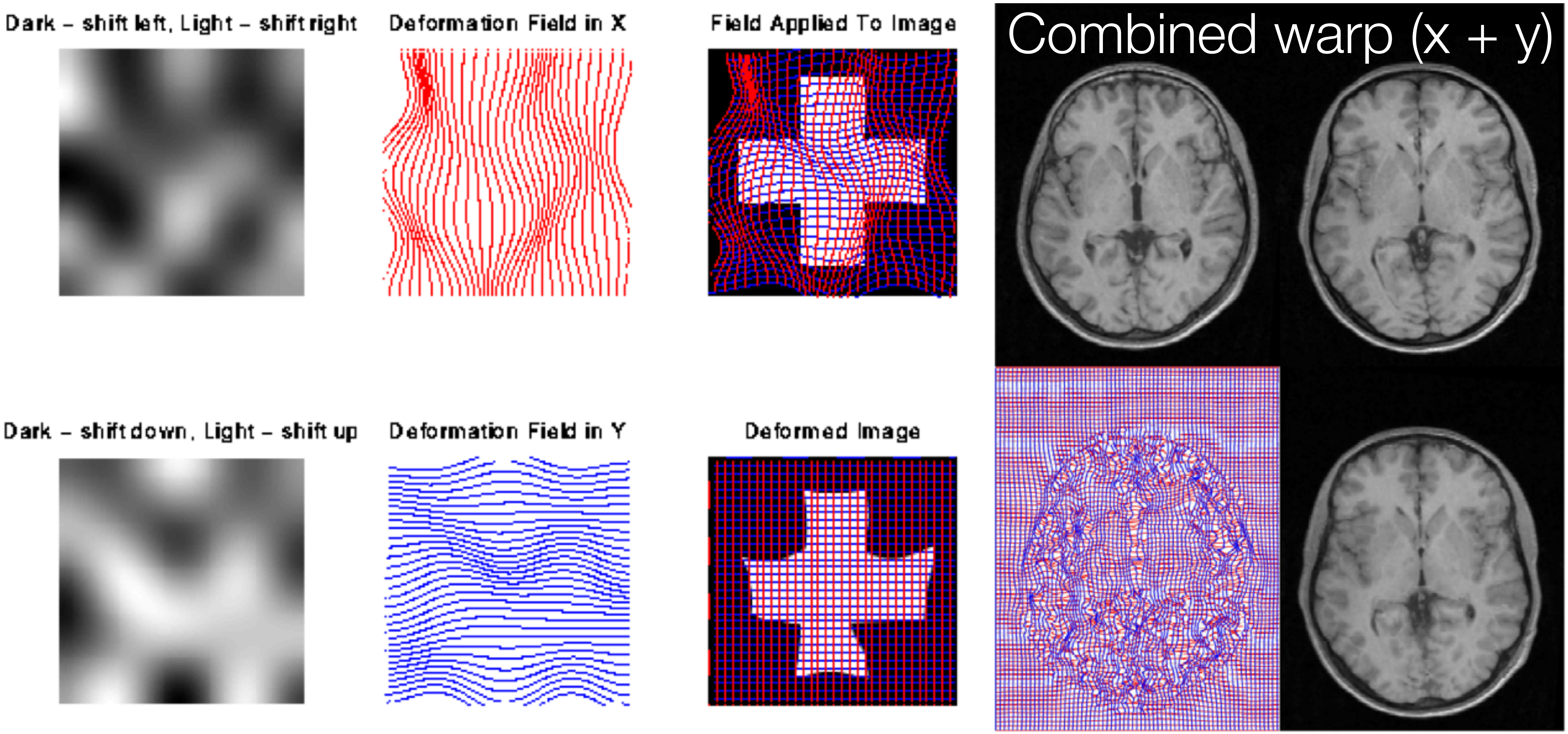
Rigid transformations in 3 dimensions:



Source: Wellcome Trust Centre

2. Normalization, How?

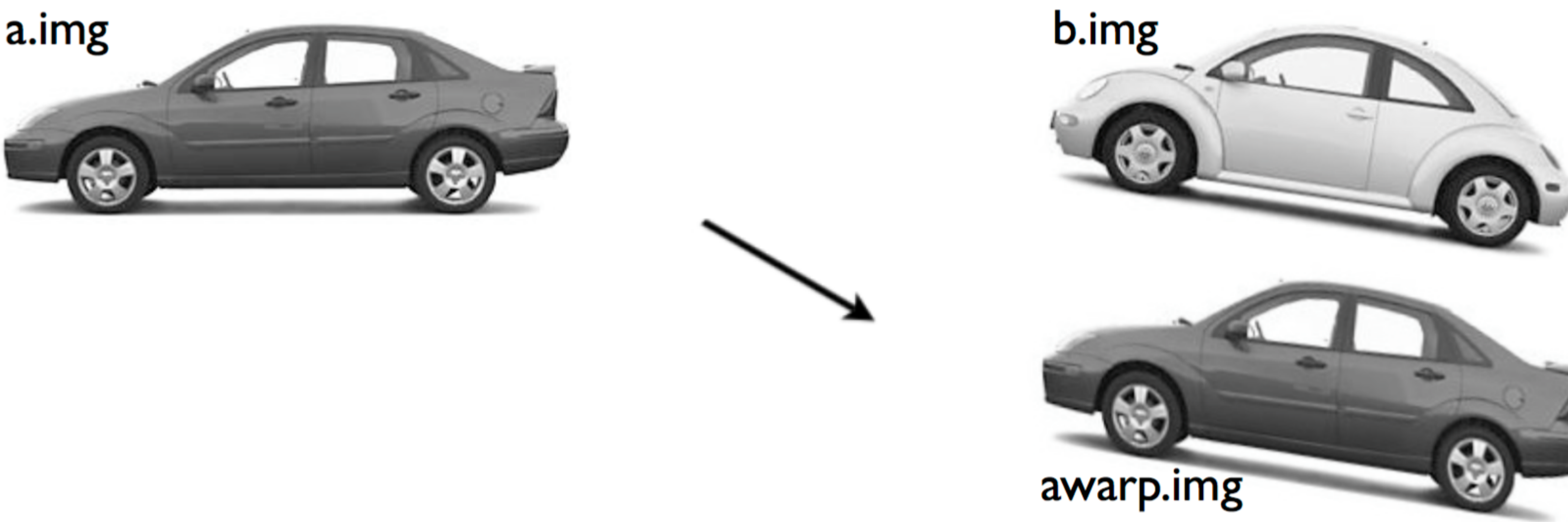
Diffeomorphic transformation in 3 dimensions (2 shown):



Source: [Wellcome Trust Centre]

2. Normalization, How?

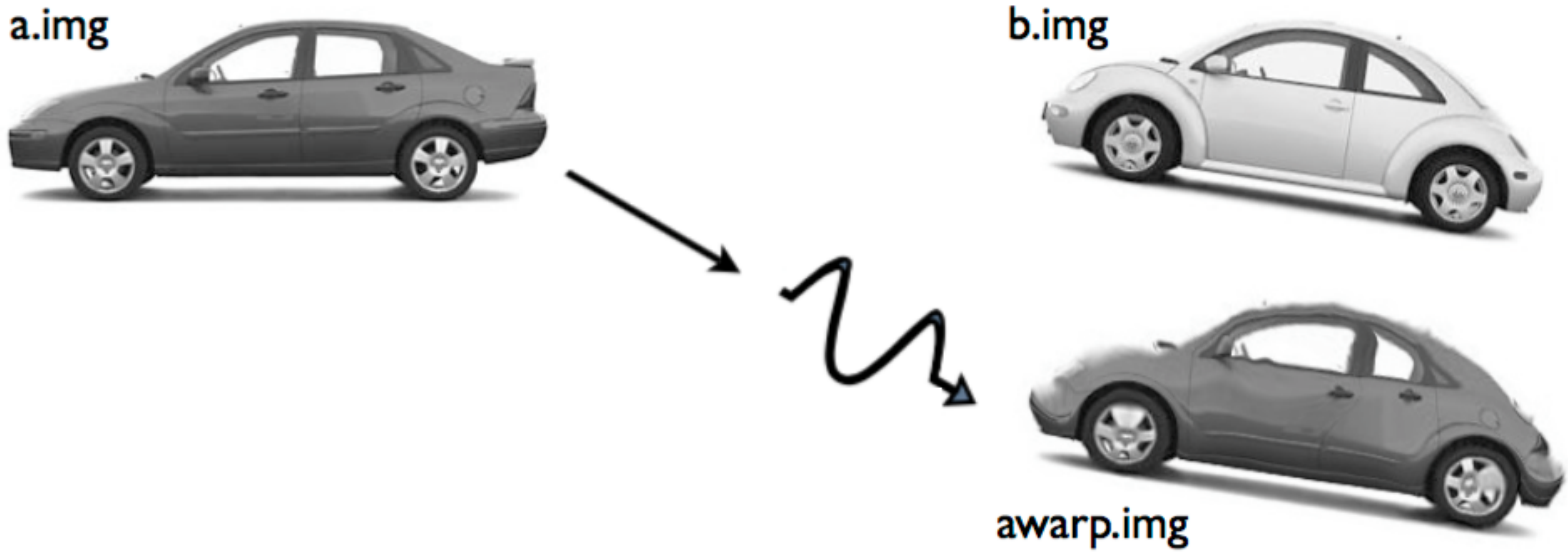
Linear
Transform



Adapted from: ANTS Manual

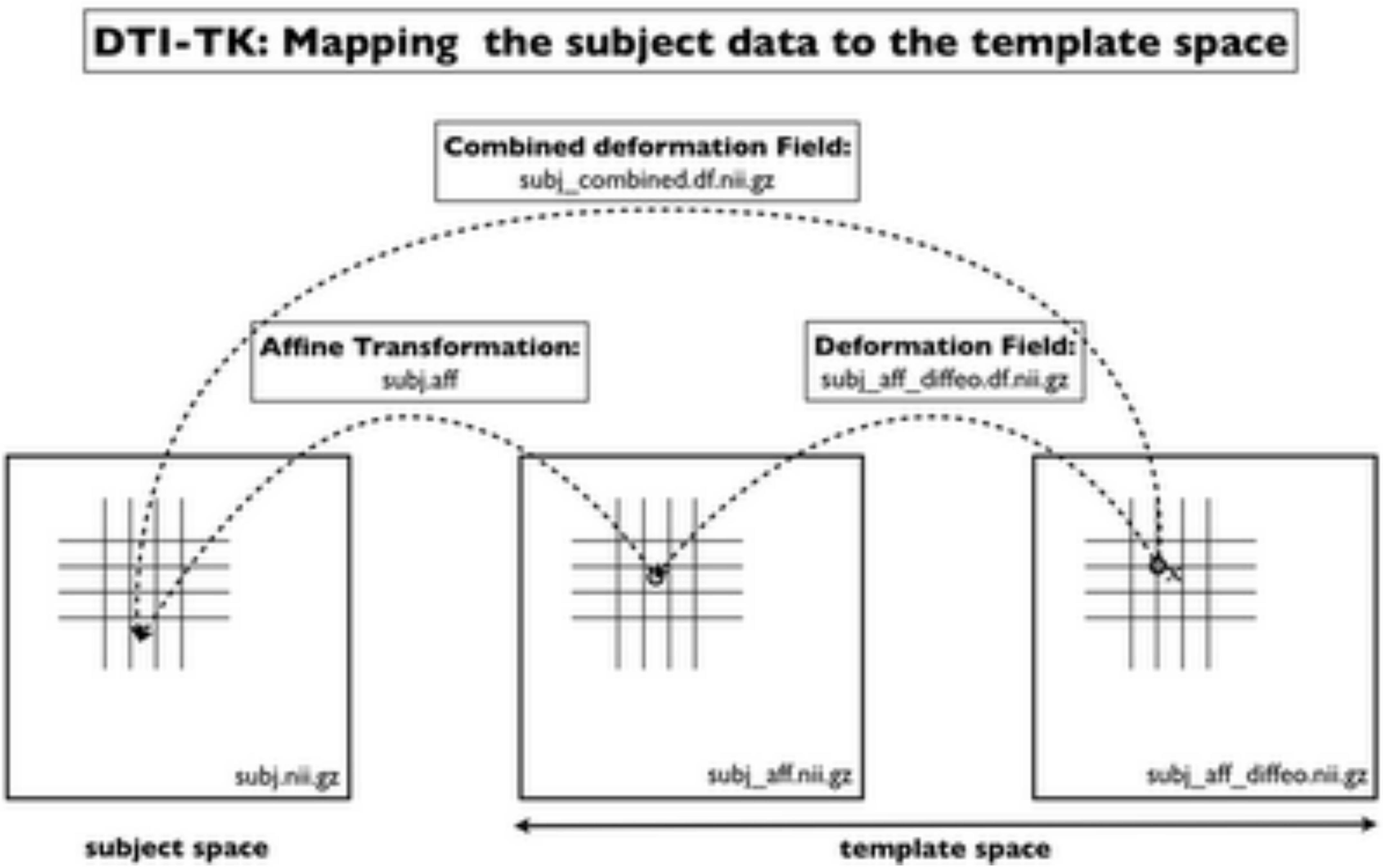
2. Normalization, How?

Linear + Non-Linear
Transform



Adapted from: ANTS Manual

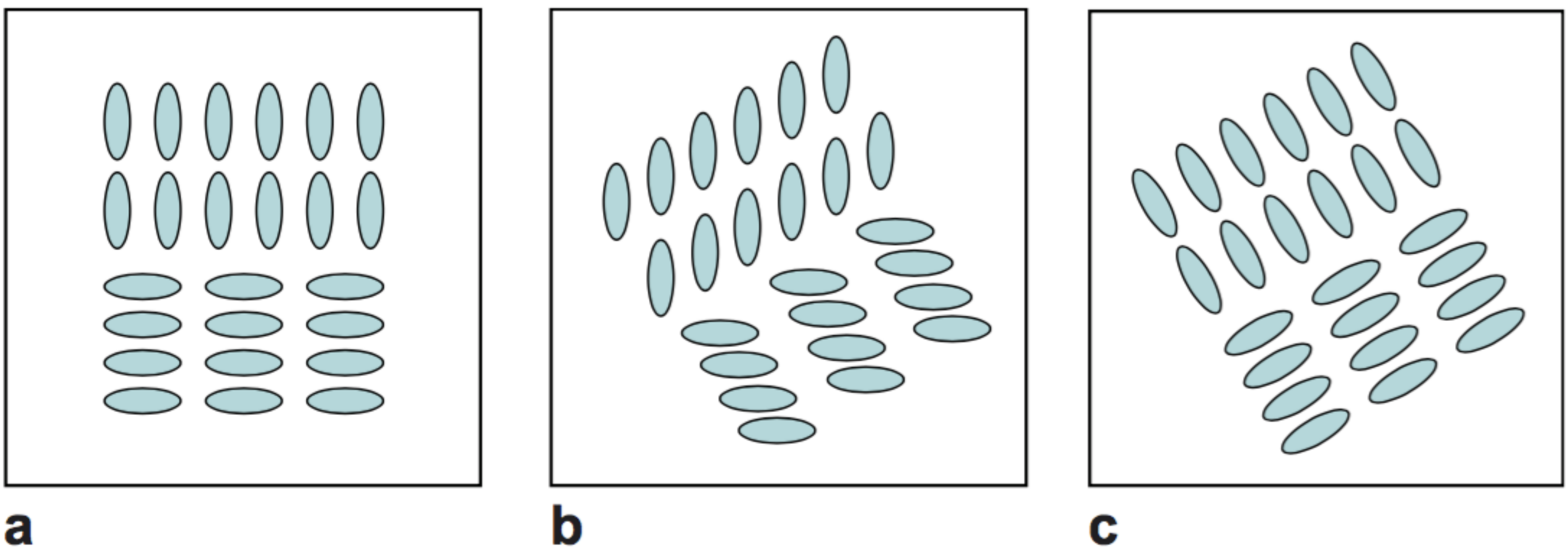
2. Normalization, How?



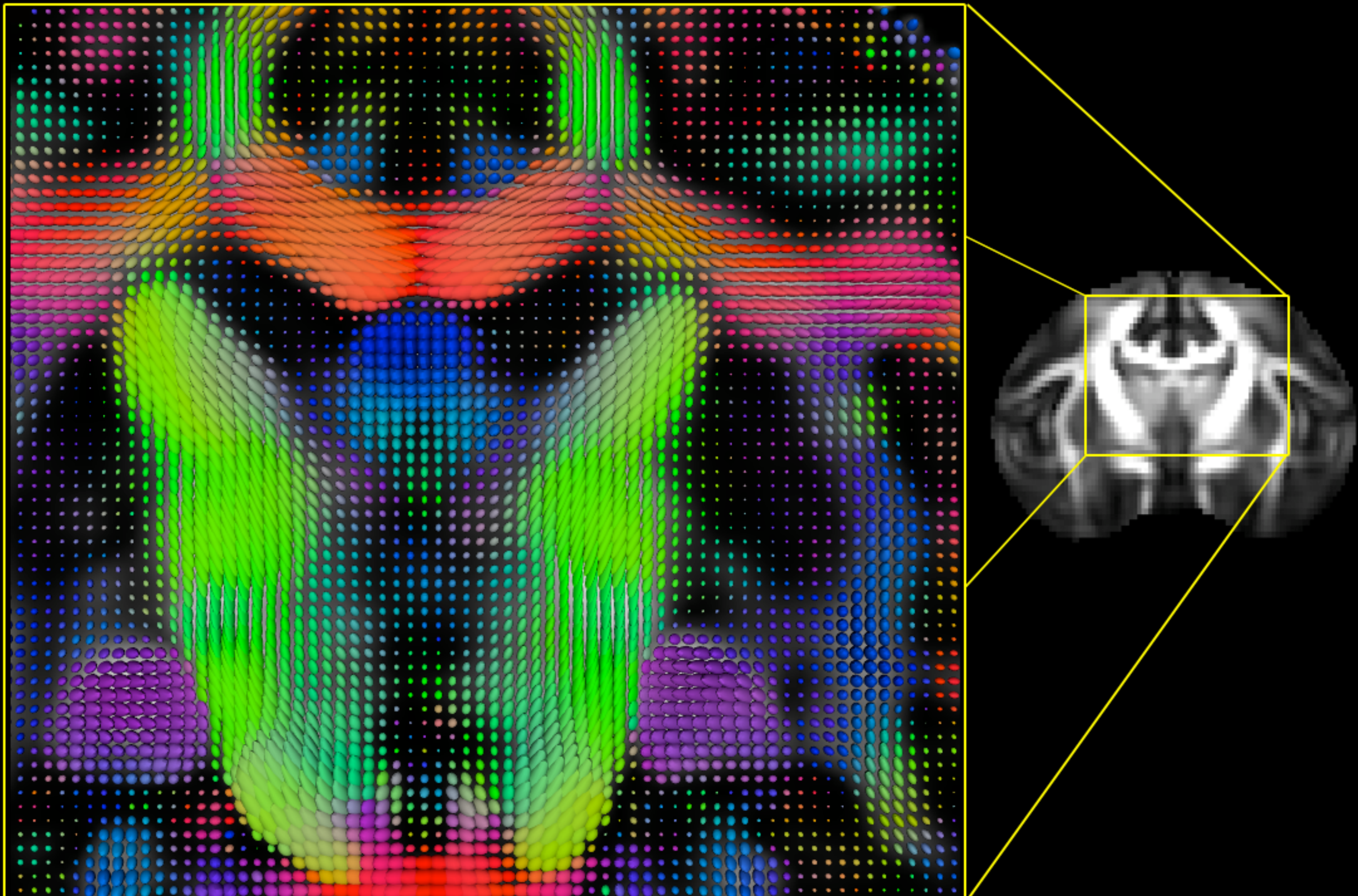
Source: DTI-TK

2. Normalization, Tensors?

Original | Volume rotation | Volume rotation with adjusted tensor orientation



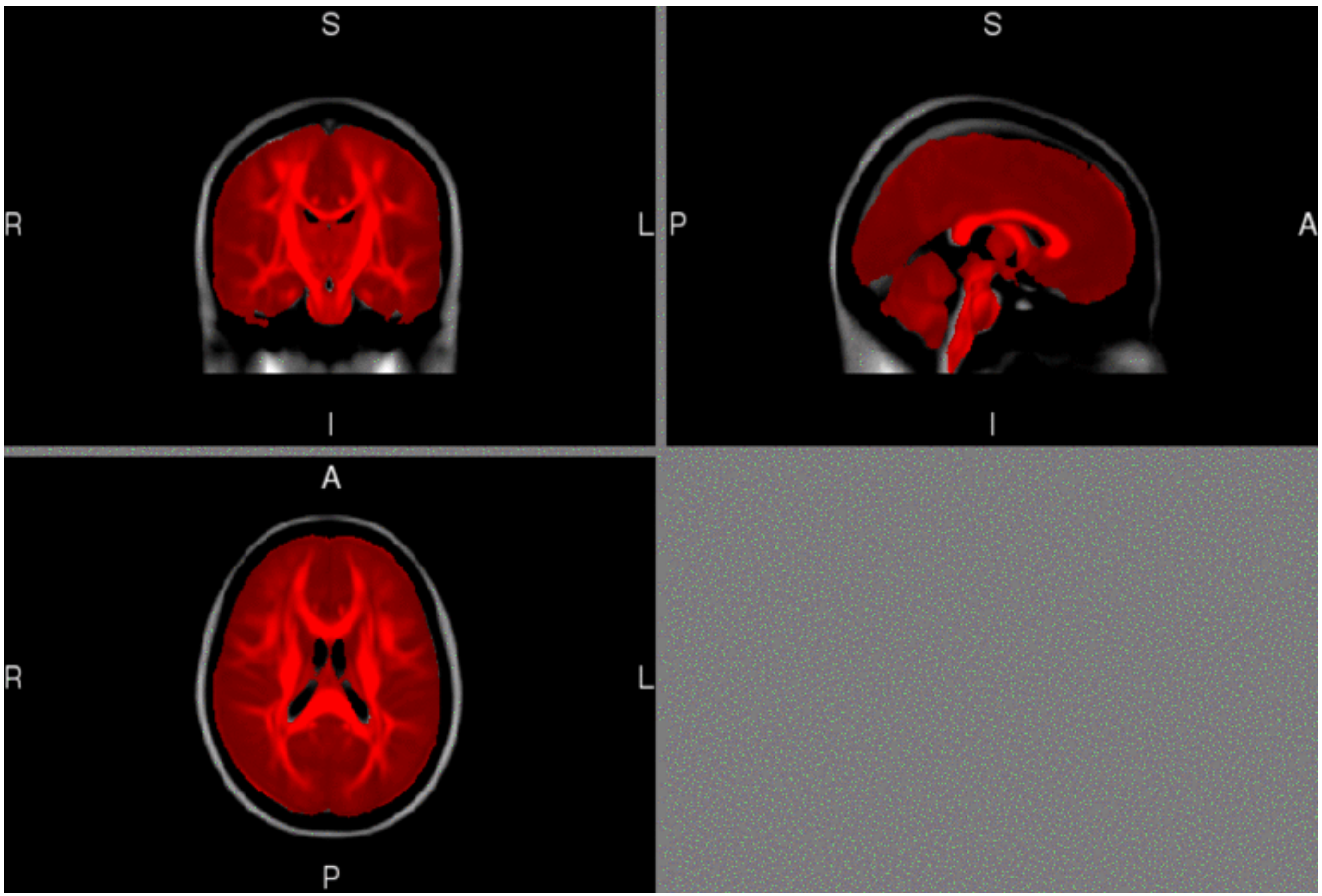
Zhang et al. (2006)



Tensor normalization is most reliable in regions with high anisotropy

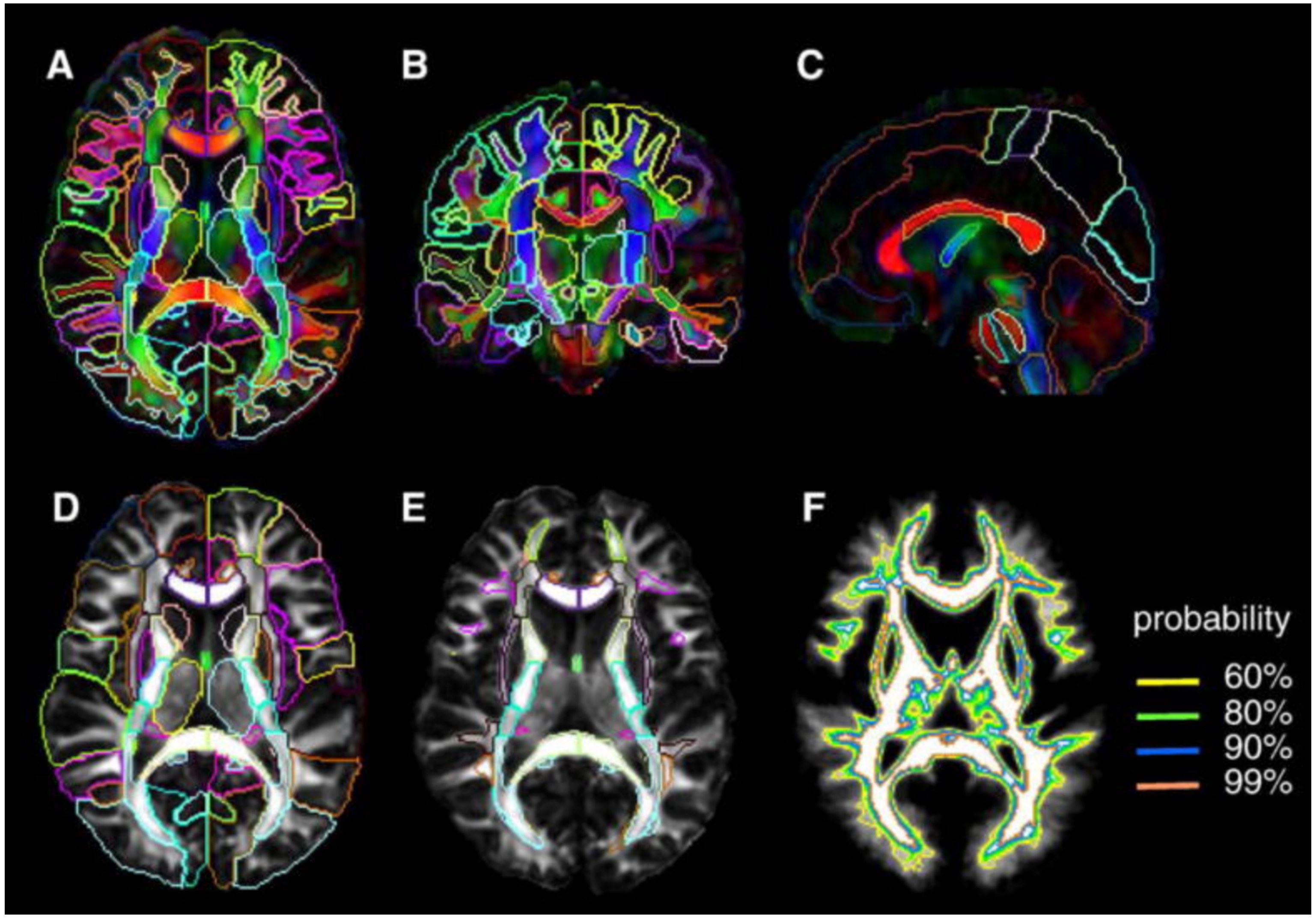
3. Register population template to MNI space

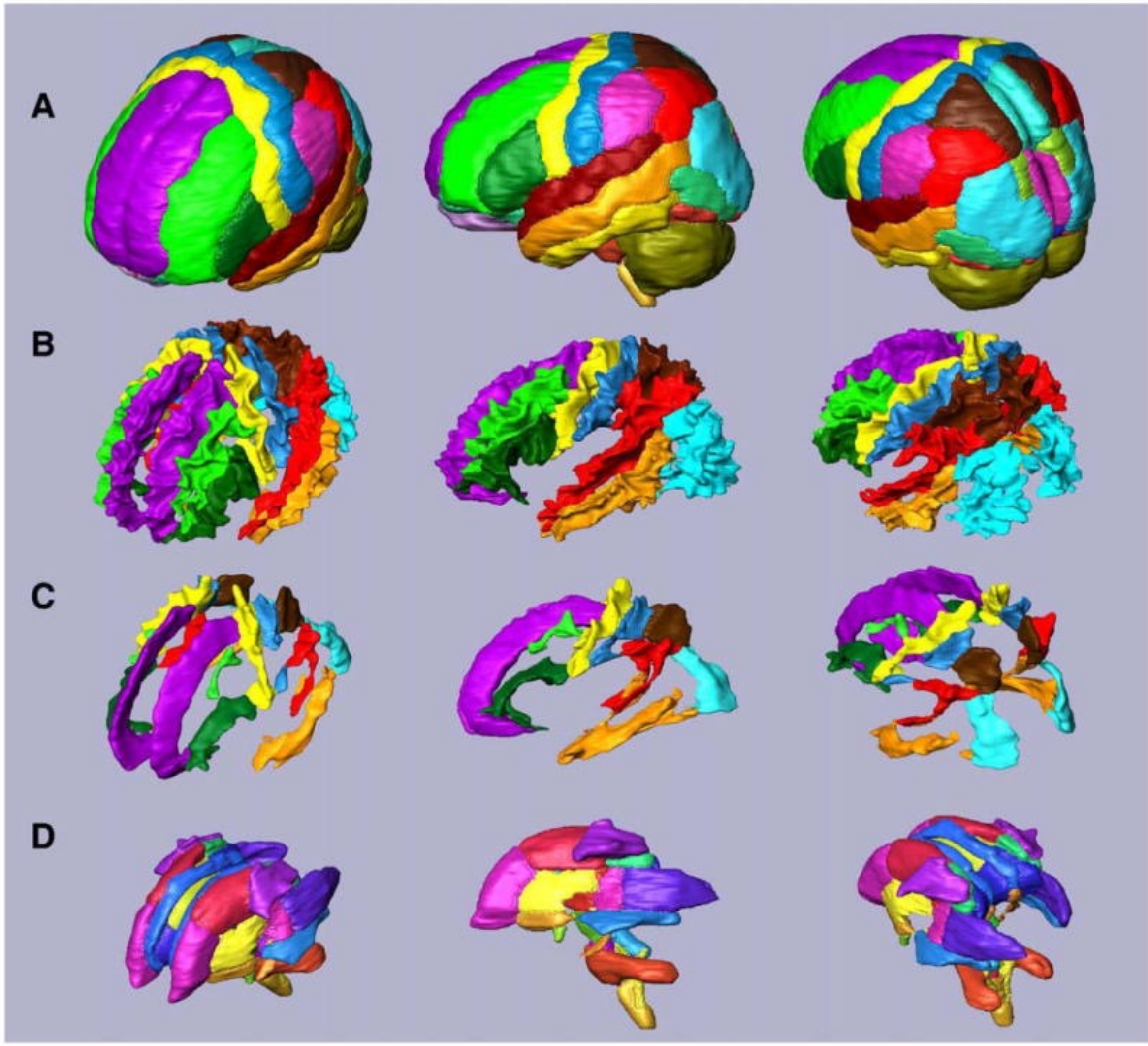
- Cross modality registration: Population FA -> MNI T1



3. Register population template to MNI space

JHU white matter atlas in MNI space





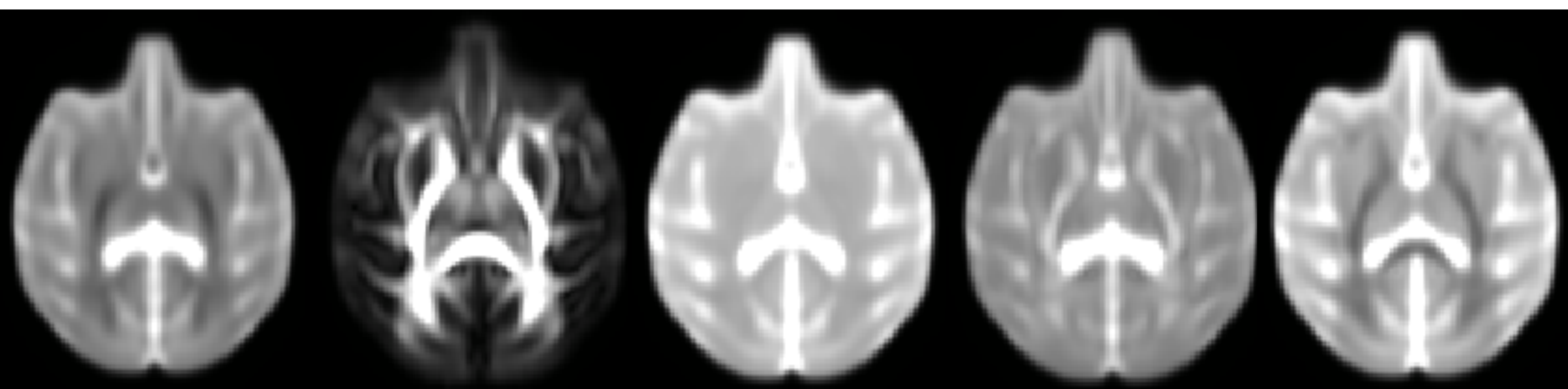
Oishi et al. (2009)

http://www.dtiatlas.org

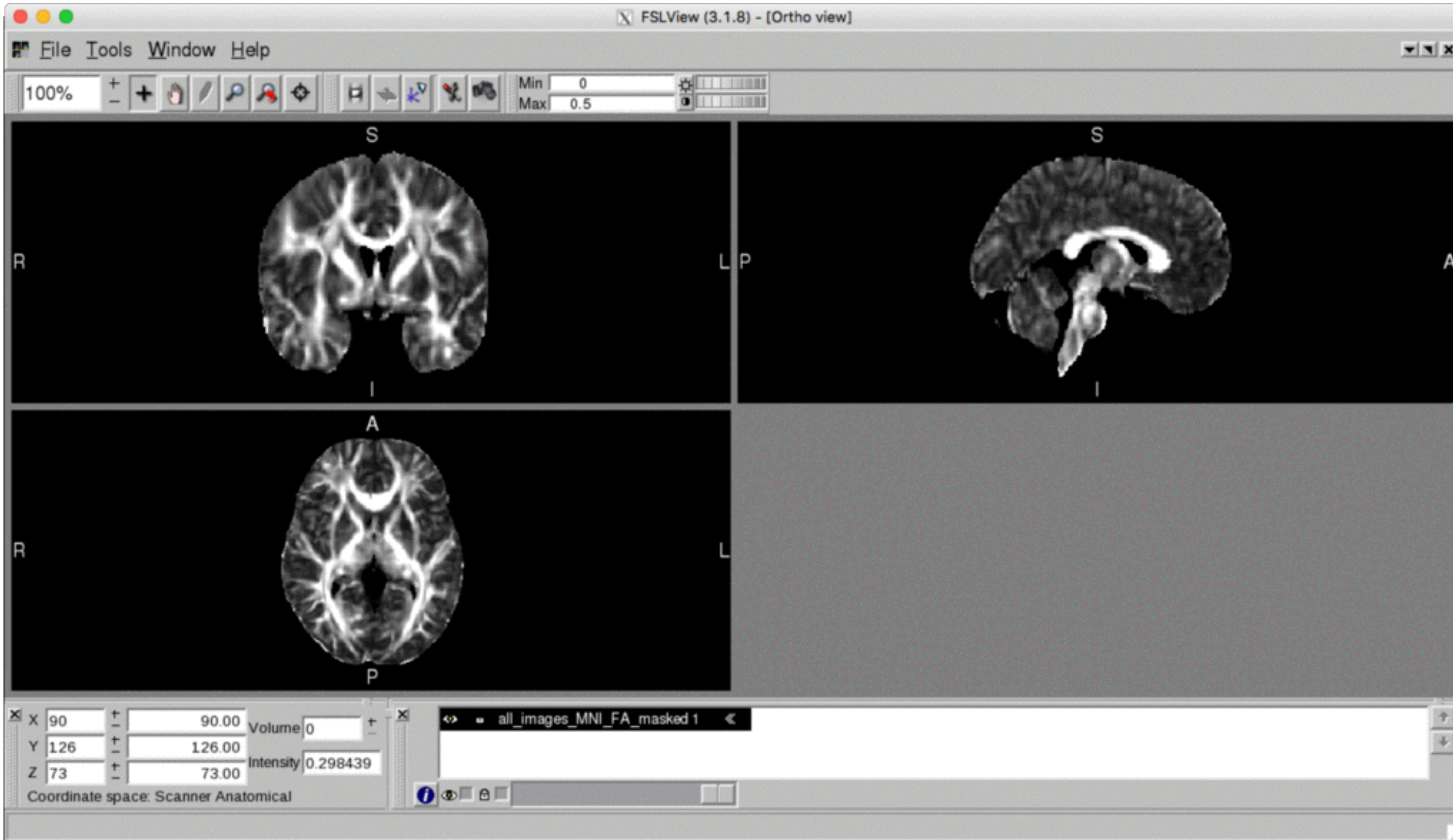
4. Produce scalar images (FA, MD, AD, RD)

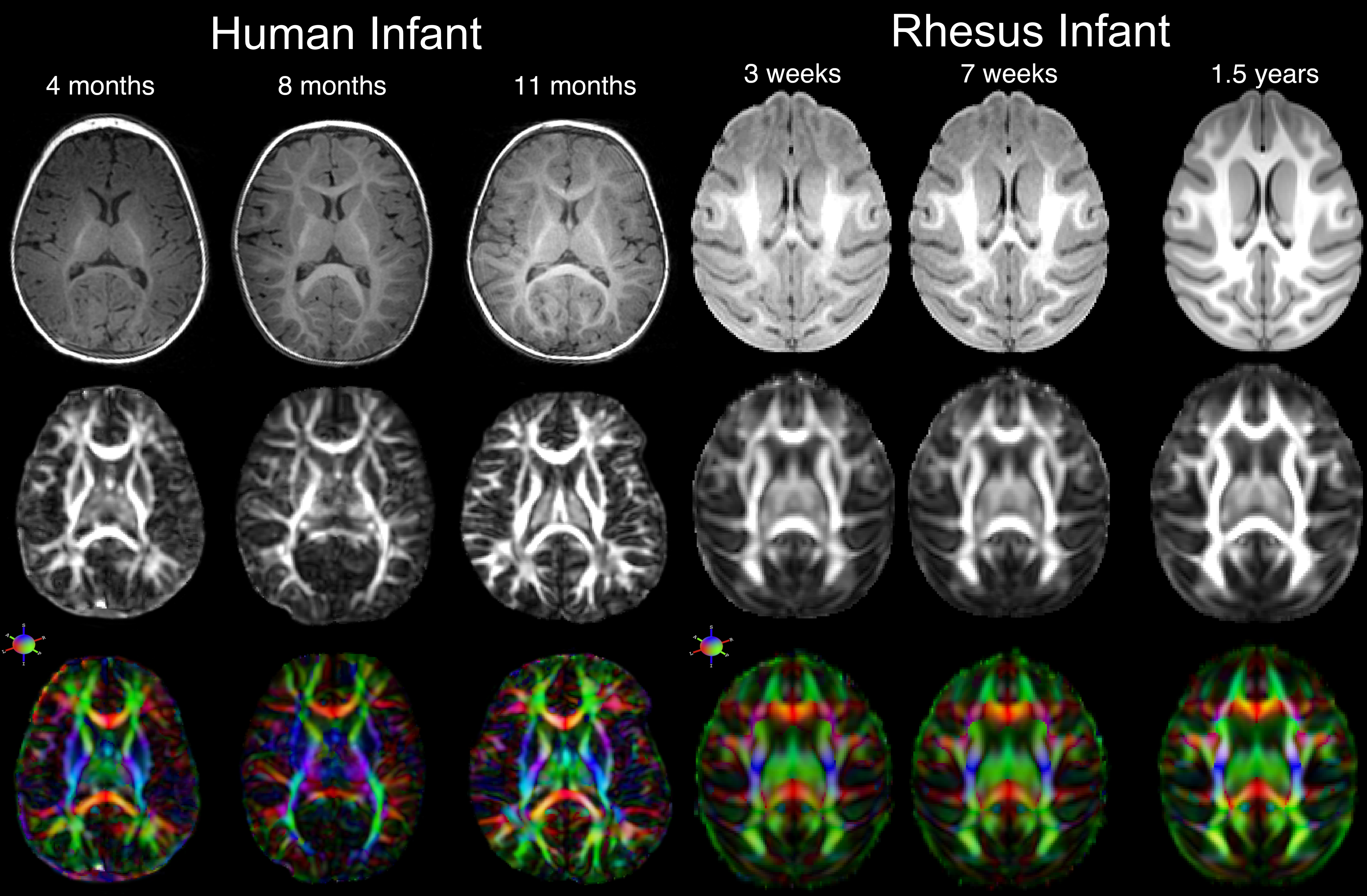
```
TVtool -in tensor.nii.gz -fa -out tensor_fa.nii.gz
TVtool -in tensor.nii.gz -tr -out tensor_tr.nii.gz
TVtool -in tensor.nii.gz -ad -out tensor_ad.nii.gz
TVtool -in tensor.nii.gz -rd -out tensor_rd.nii.gz
```

TENSOR FA MD AD RD



4. Produce scalar images (FA, MD, AD, RD)

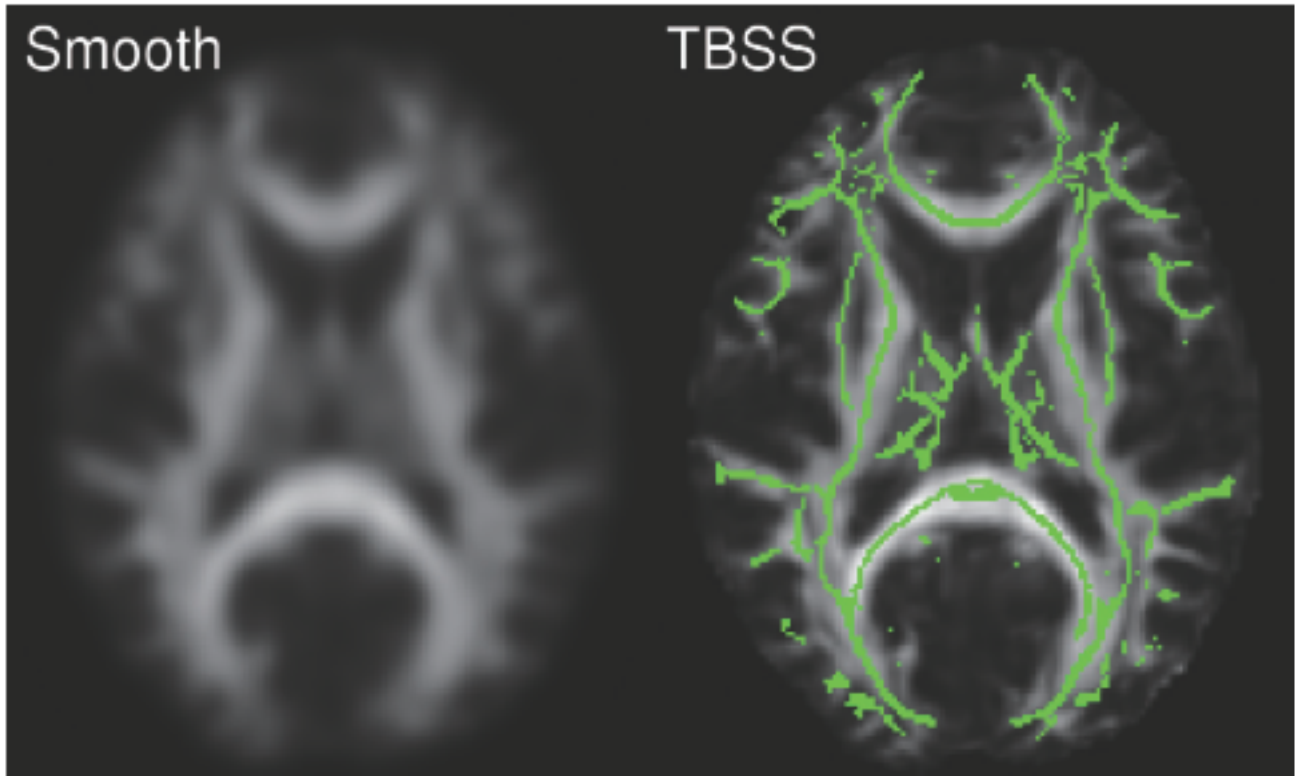



Human Infant
Rhesus Infant
4 months
8 months
11 months
3 weeks
7 weeks
1.5 years

5. Run whole brain voxel-wise statistics

- Statistical analyses of DTI scalar images in MNI space are identical to analyses of other modalities (e.g. fMRI/T1/PET)

- Tract-based spatial statistics (TBSS) commonly used method due to its implementation in FSL, its issues:
    - Improved normalization tools reduce efficacy of TBSS
    - Easy to miss effects in smaller tracts



5. Run whole brain voxel-wise statistics

- Instead use:
  - Statistical parametric mapping (SPM; MatLab based)
  - Randomise (FSL; will run non-parametric tests)
  - More background on this with Jeanette Mumford

5. Run whole brain voxel-wise statistics

eTable 1. Group Differences in Whole-Brain, Voxelwise FA Values

	Region	**Peak Coordinates (x,y,z)**	**Size (mm^3)**
Full Sample	R uncinate fasciculus*	27, 42, -3	78
	L uncinate fasciculus**	-24, 27, 2	110
	R arcuate fasciculus	41, -41, 17	135
	L inferior frontal gyrus	-42, 21, -8	1736

Tromp et al. (2012)

6. Share your data

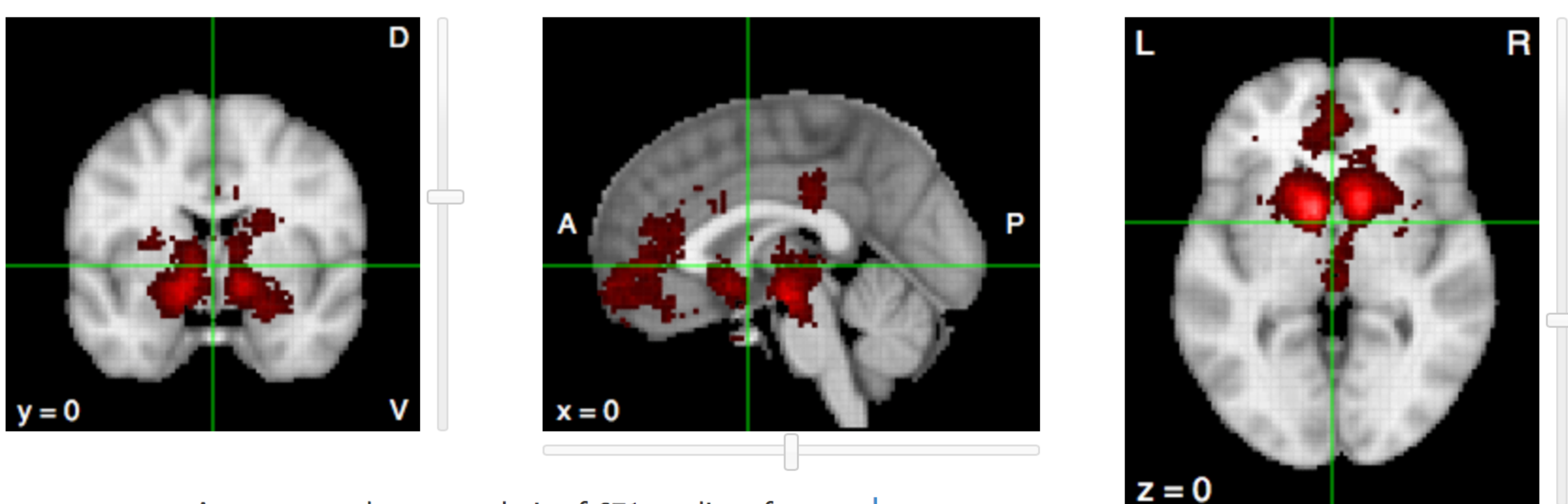
neurosynth.org

Neurosynth.org (beta) Home Meta-analyses Studies Locations Decoder Code FAQs Sign in

neurosynth.org

Neurosynth is a platform for large-scale, automated synthesis of functional magnetic resonance imaging (fMRI) data.

It takes thousands of published articles reporting the results of fMRI studies, chews on them for a bit, and then spits out images that look like this:



An automated meta-analysis of 671 studies of reward


Questions?