

Imaging connectivity: Statistical modelling and the wiring of the brain

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Overview

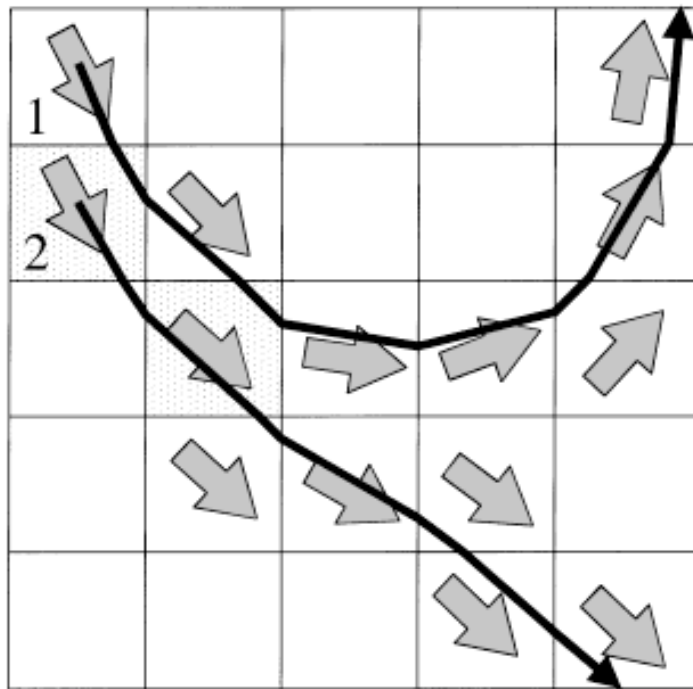
- Diffusion MRI and white matter
- Difficulties with fibre tracking in groups
- A model-based streamline matching approach
- Applications of this model
- The relationships between tracts
- Conclusions

Introduction

- **Diffusing** water molecules probe the microstructure of living tissue, and **MRI** can be sensitised to this process
- Some tissues have linear structure with clear orientation (e.g. neural white matter, muscle), and diffusion profiles reflect this
- Diffusion MRI and **tractography** can be used to reconstruct trajectories of linear structures using **streamlines**
- But robust and consistent **segmentation** for group analysis is not straightforward
- Intrinsic differences between subjects should be retained; processing inconsistencies should not

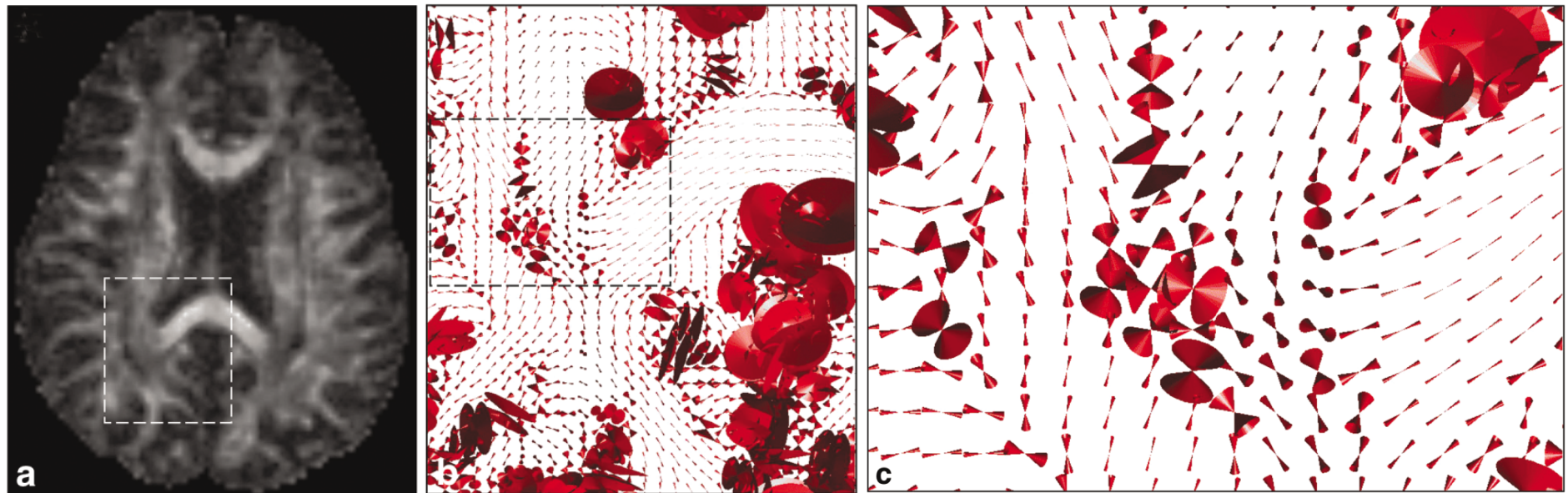
Fibre tracking

- Tract reconstruction from a **seed point** based on local information
- Can be very sensitive to seed location



Xue et al., *Magn Reson Med*, 1999

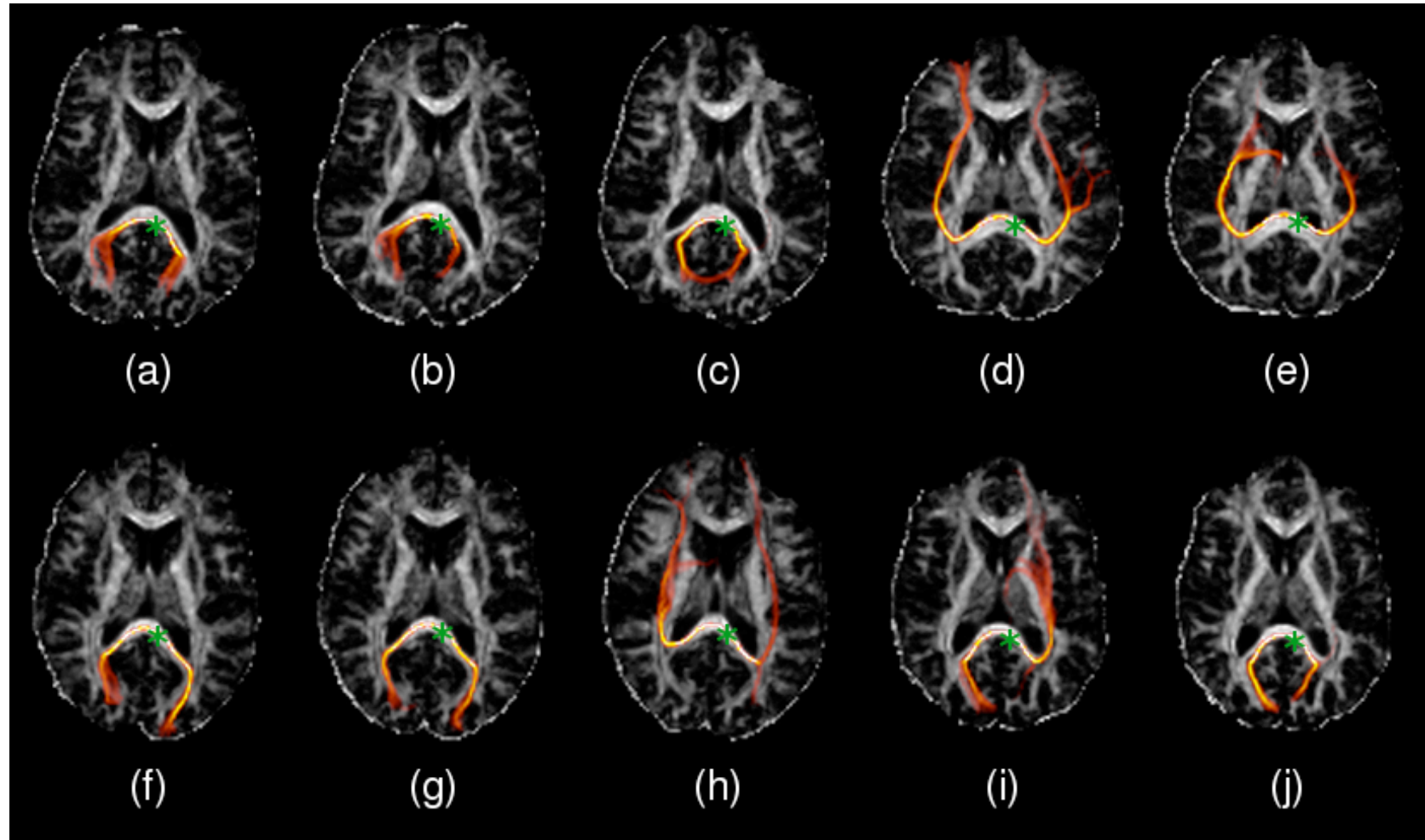
Noise and uncertainty



Jones, *Magn Reson Med*, 2003

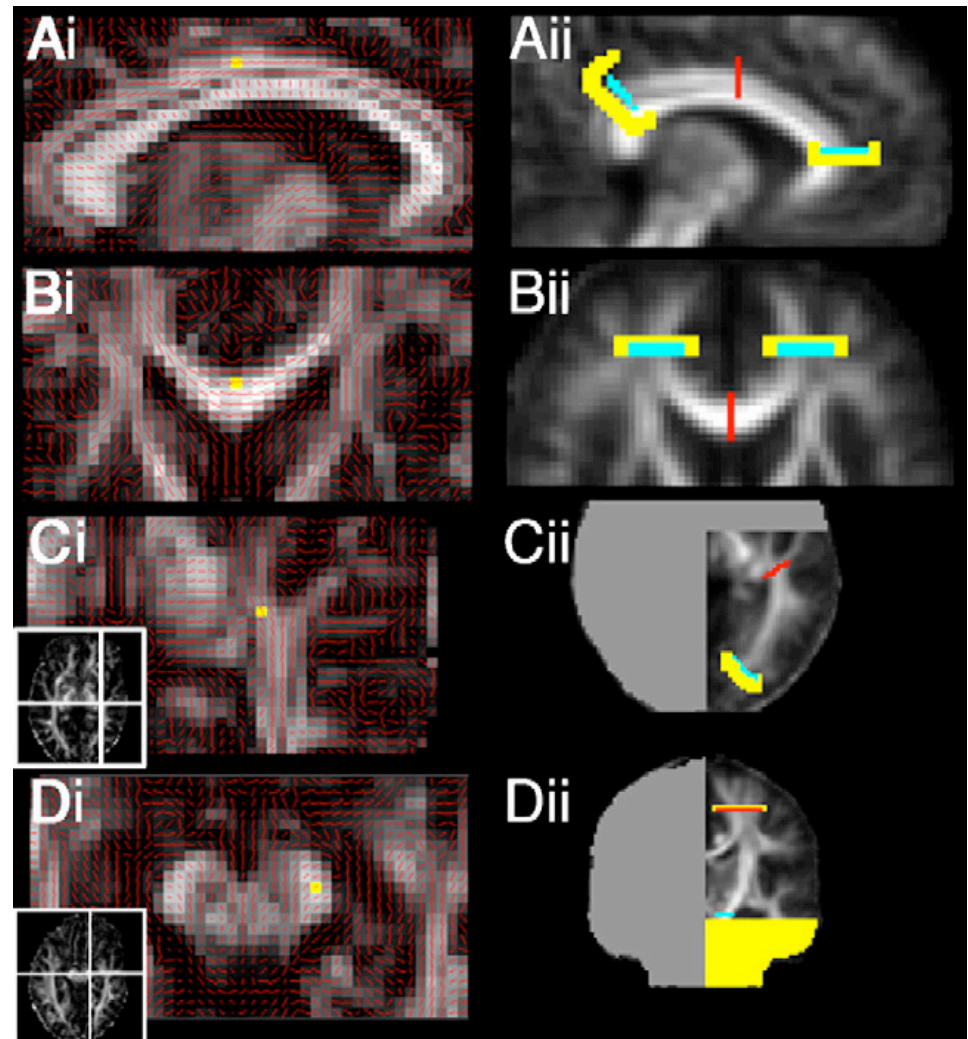
- Tracking process accumulates local errors
- Trajectory can jump from one fasciculus to another
- **Probabilistic** tractography gives a sense of these effects

Unconstrained tractography



Use of ROIs

- Standard practice in applications
- Deterministic or probabilistic tractography
- Overseeding (nonspecific initialisation), plus constraints
- Several ROI types may be needed for consistent results
- Transferrability between subjects and/or populations?



Streamline matching

- Streamlines typically have small diameter (notionally none)
- Entire physical structure needs several streamlines to represent it
- Given a streamline, does it represent **the same** structure as another?
- Is it part of a **particular** anatomical structure?
- What is its **homologue** in another subject?

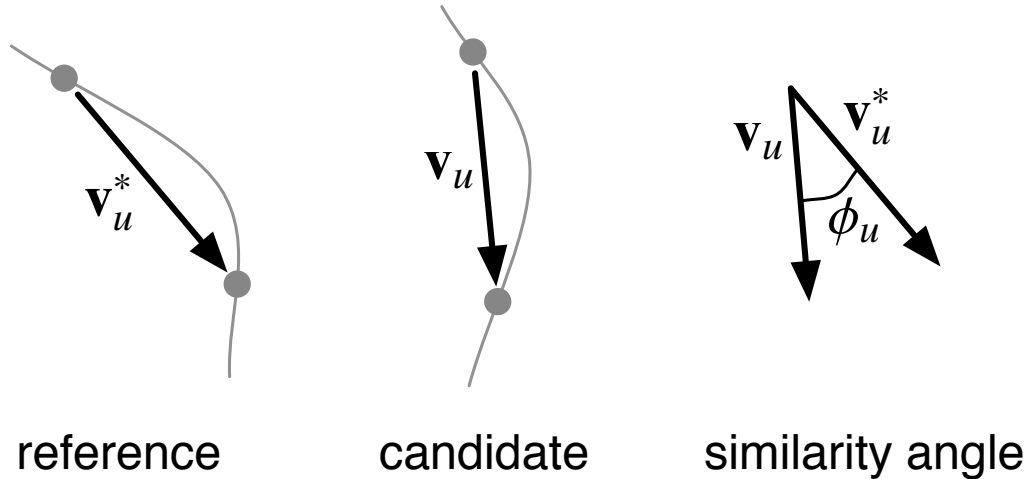
- Could a matching approach be used to segment known tracts?

Neighbourhood tractography

- Assumption: comparable tracts have similar shape and length
- Choose or create a **reference tract**
- Generate a number of **candidate tracts** using different seed points (forming a neighbourhood in space)
- Assess the **plausibility** of each candidate as a match to the reference, using a statistical model
- Choose one or more plausible trajectories

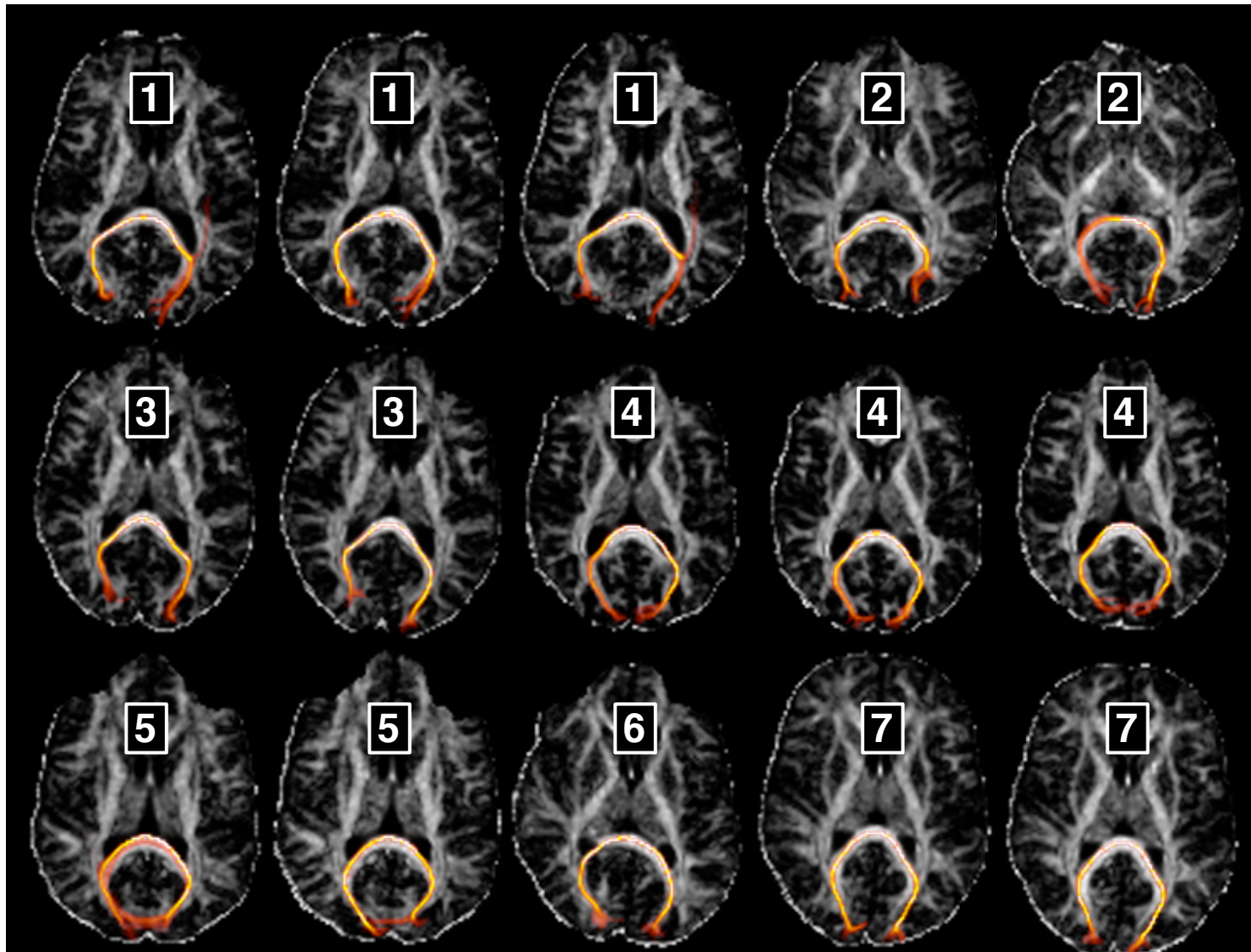
- Mimics process of a human operator, without the use of ROIs
- Reliance on **registration** is minimal

Comparing tracts

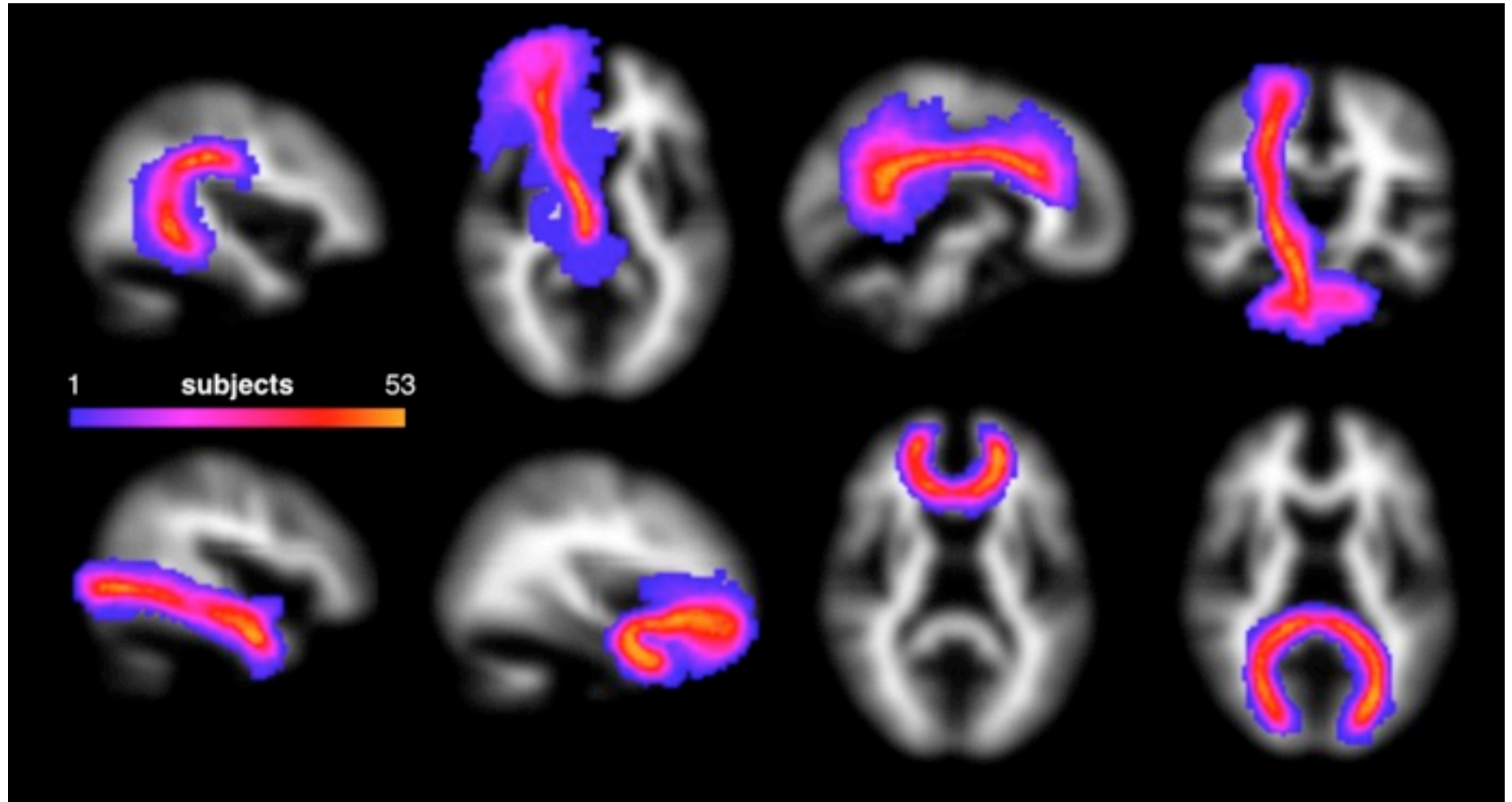


- Greater deviation from reference assumed to be less likely
- Expected variability is *learned* from **training tracts**, and can vary along tract
- Thereby assess plausibility of any novel candidate

Consistency across scans



Tract group maps (53 children)



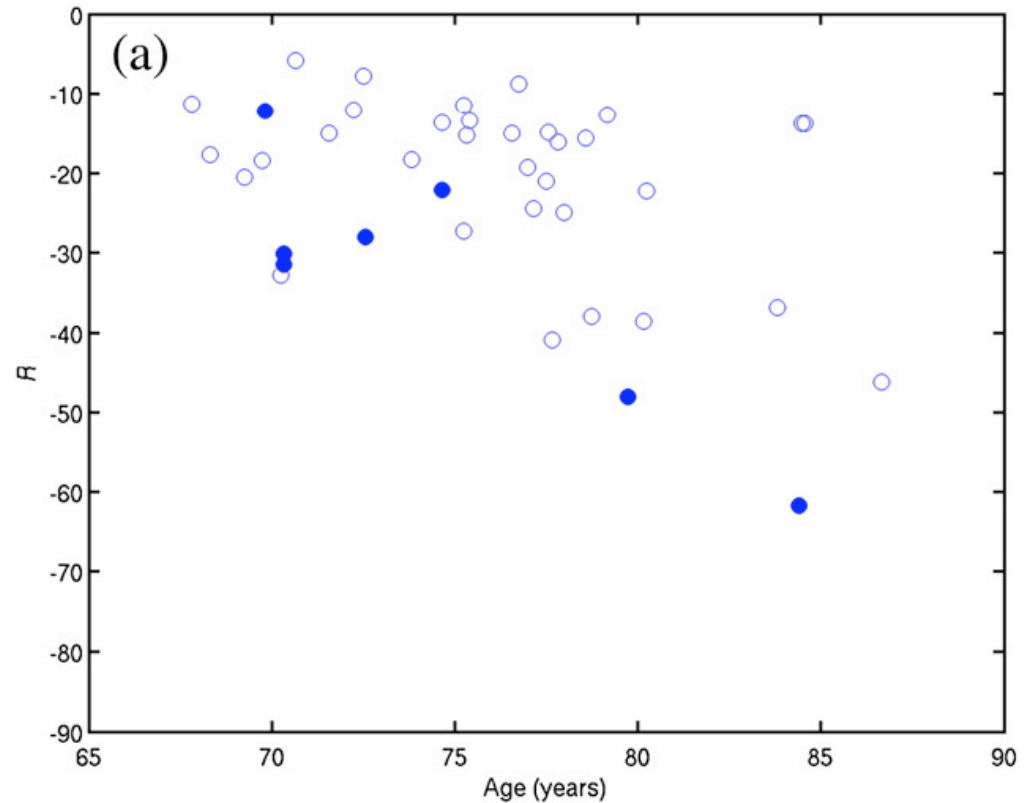
Why model?

- Probabilistic matching to reference tract
- Structured description of tract shape variability across population
- Can use tract likelihoods under the model as a **goodness of fit** measure

- But forced to make a number of assumptions

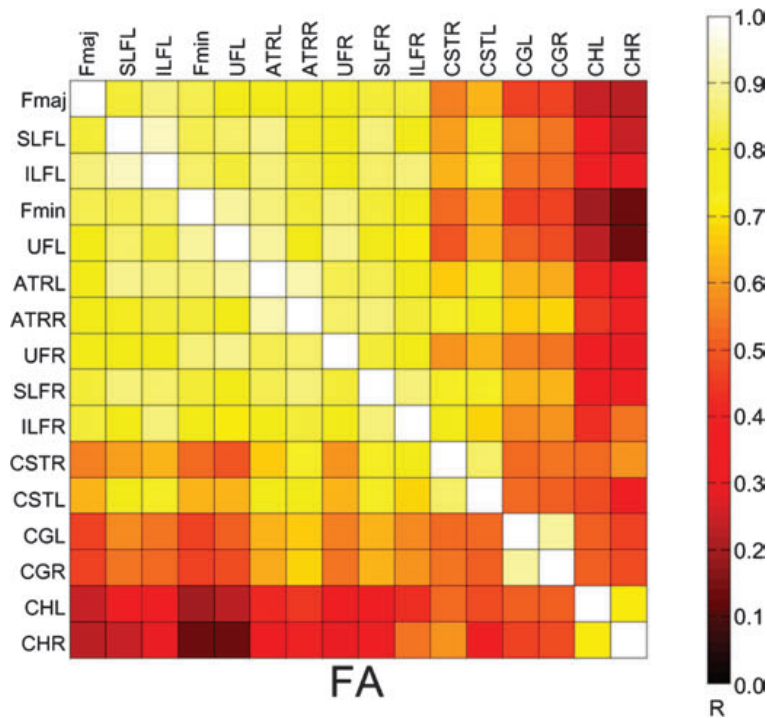
Gradual shape change

- Goodness of fit shows up gradual changes in morphology
- GoF for genu (forceps anterior) declines with age across c. 65–85 year old population
- Ventricular enlargement a significant factor

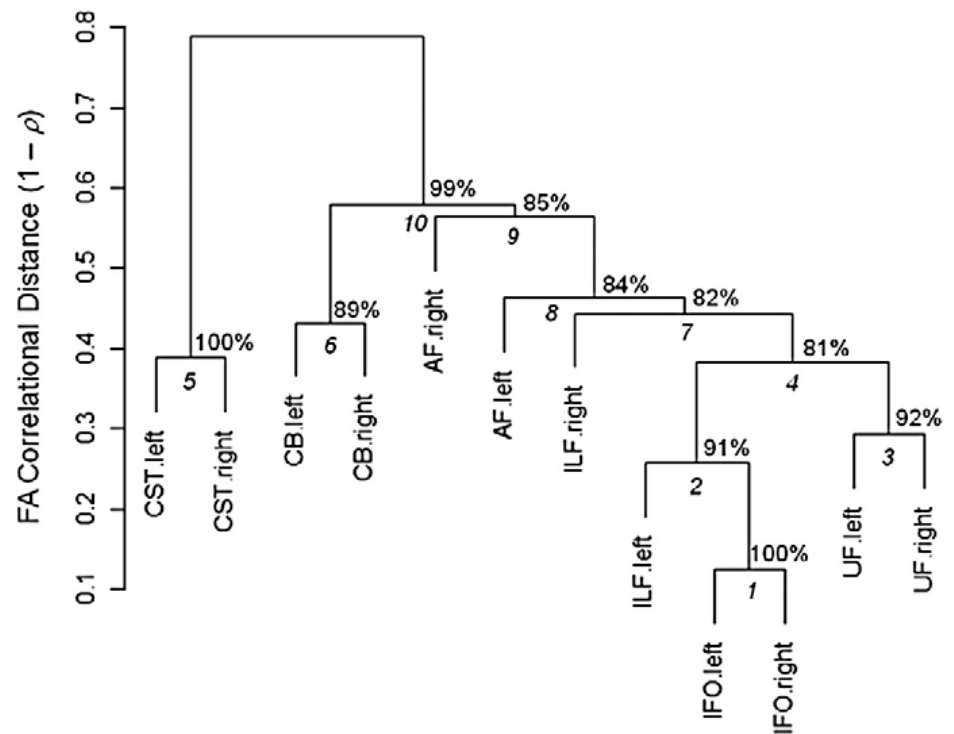


Bastin et al., *NeuroImage*, 2008

Different tracts' properties are correlated



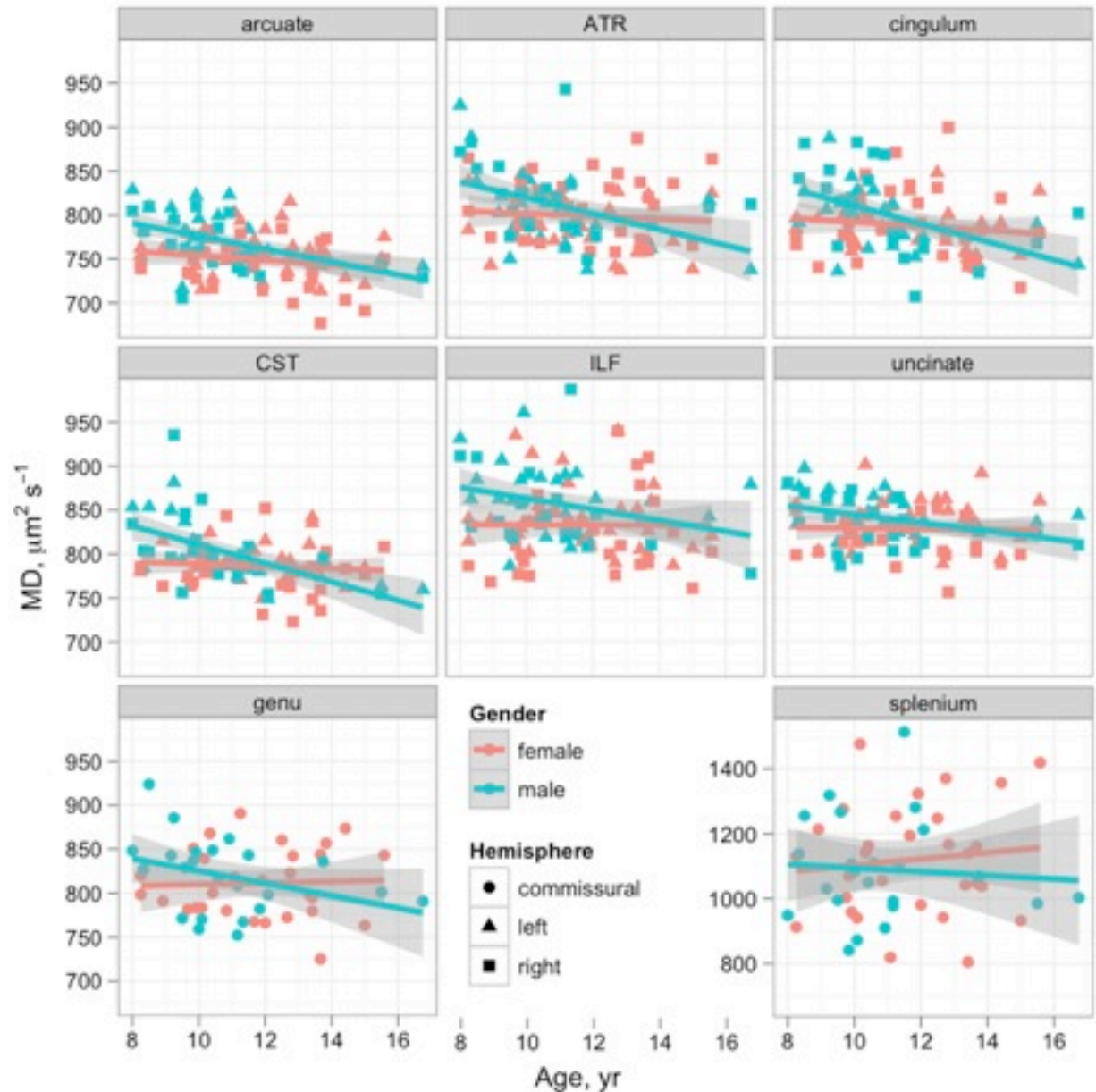
Westlye et al., *Cereb Cortex*, 2010



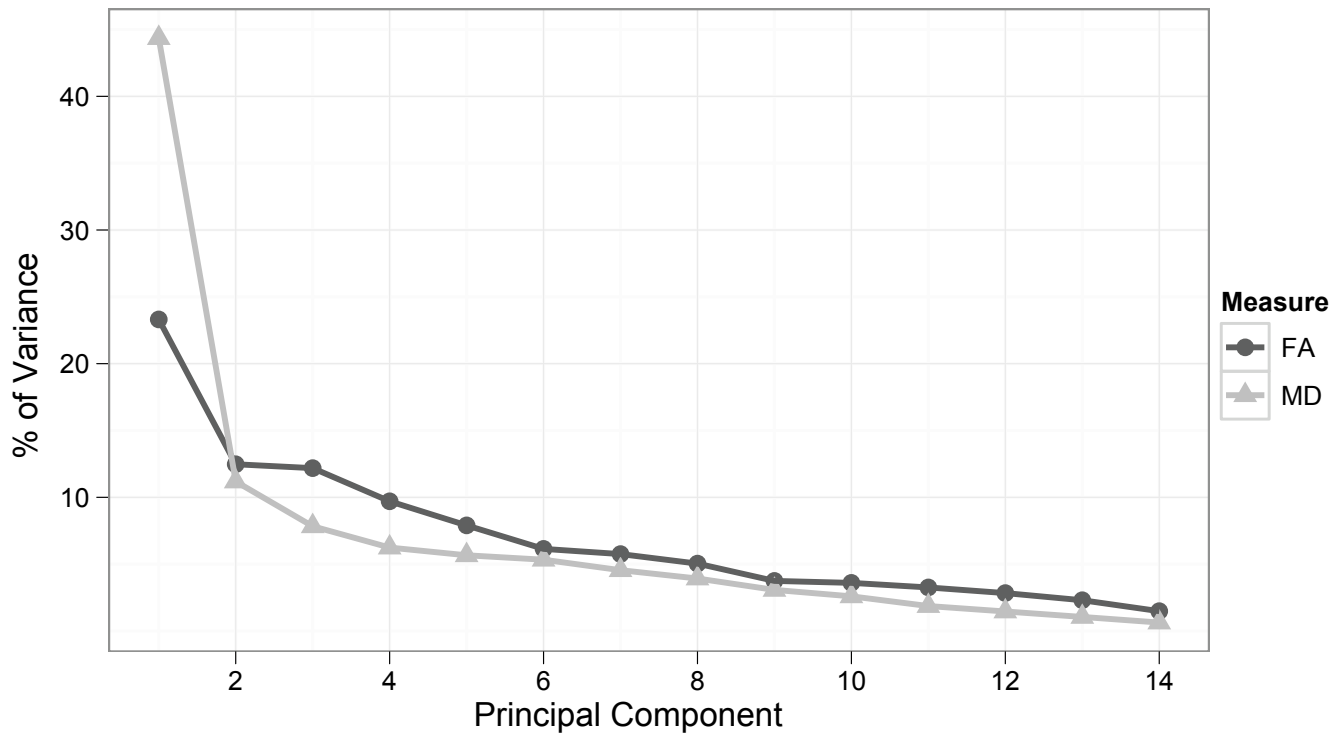
Wahl et al., *NeuroImage*, 2010

MD vs age

- Consistent downwards trend (except splenium) over age range 8–17 yr
- Values in males higher at lower ages; later more similar to girls



Tract segmentation + PCA



- Substantial shared variance in both diffusion tensor measures
- Can relate scores to cognitive and/or demographic factors

Conclusions

- Streamline matching approach is useful for consistent tract segmentation in groups
- Little human interaction need be required
- Prior information (reference tracts) can be reused between heterogeneous groups
- Different tracts are linked, and principal components analysis can be used to identify common factors

Thanks

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- Amos Storkey
- Faraneh Vargha-Khadem

Resources

- TractoR software package: <https://github.com/jonclayden/tractor>
- Research home page (including publications): <http://www.homepages.ucl.ac.uk/~sejjd2/research>
- E-mail: j.clayden@ucl.ac.uk

The logo for TractoR, with 'Tracto' in brown, 'R' in blue, and a stylized yellow and orange swoosh passing through the 'o' and 'R'. The 'o' is replaced by a circular pattern of small dots.