MRC Cognition and Brain Sciences Unit

UNIVERSITY OF CAMBRIDGE

# Diffusion MRI: Introduction to Tractography

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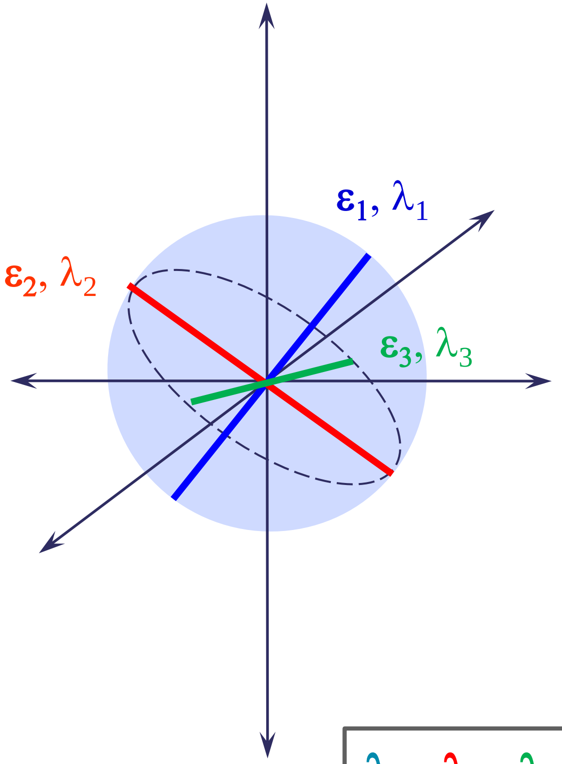
# Overview

- Introduction to Tractography
- Probabilistic Modelling
- Multiple-fibre models

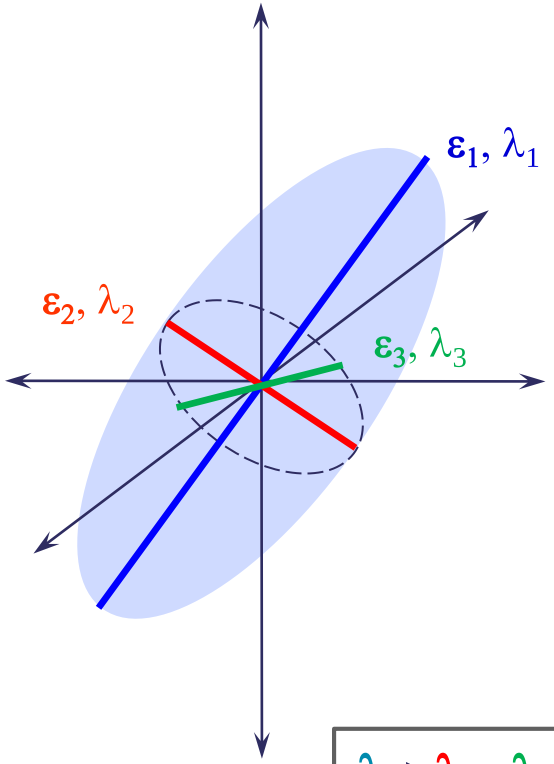
# Diffusion ellipsoid: Eigenvalues and eigenvectors

## Isotropic Diffusion




$\lambda_1=\lambda_2=\lambda_3$

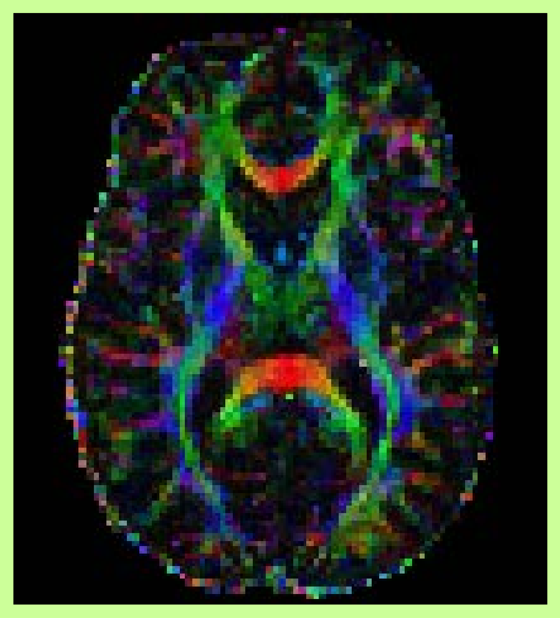
## Anisotropic Diffusion




$\lambda_1>\lambda_2\sim\lambda_3$

# Colour coded FA maps

- Let $\varepsilon_1$ designate the longest axis of the diffusion ellipsoid.
- $\varepsilon_1$ can be identified with the main direction of diffusion.
- This directional information can be added to the FA map using a colour code:



Red indicates directions in the *x* axis: right to left or left to right.

Green indicates directions in the *y* axis: front to back or back to front.

Blue indicates directions in the *z* axis: foot-to-head direction or vice versa.

**Colour coded FA map.**

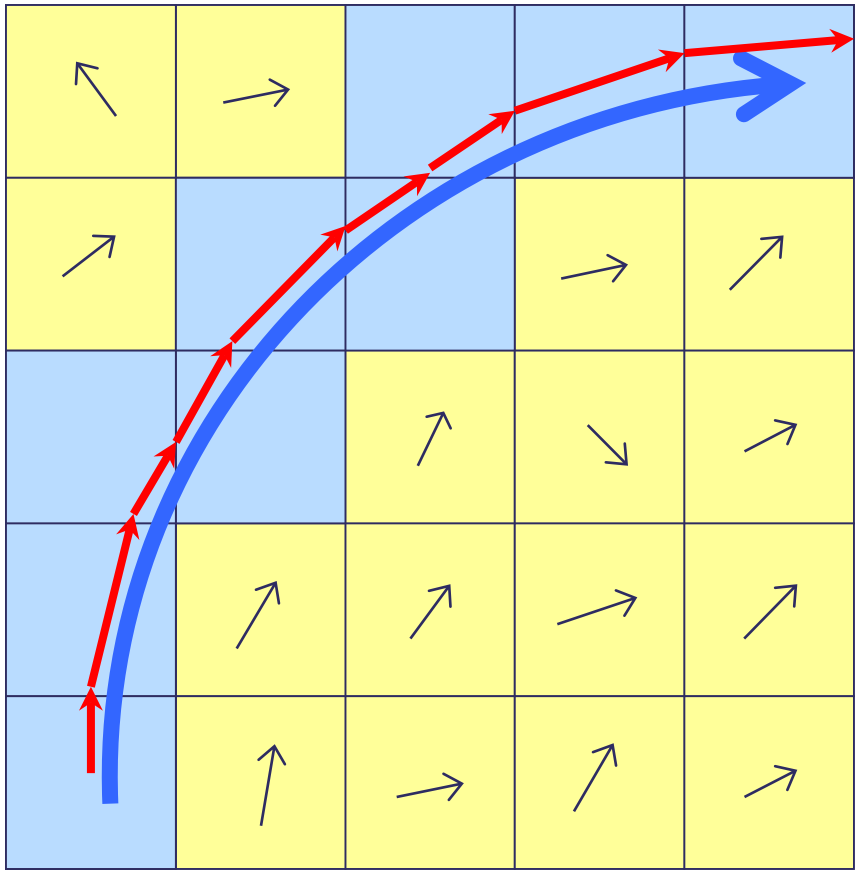
# Introduction to Tractography

# Tractography: basic principles

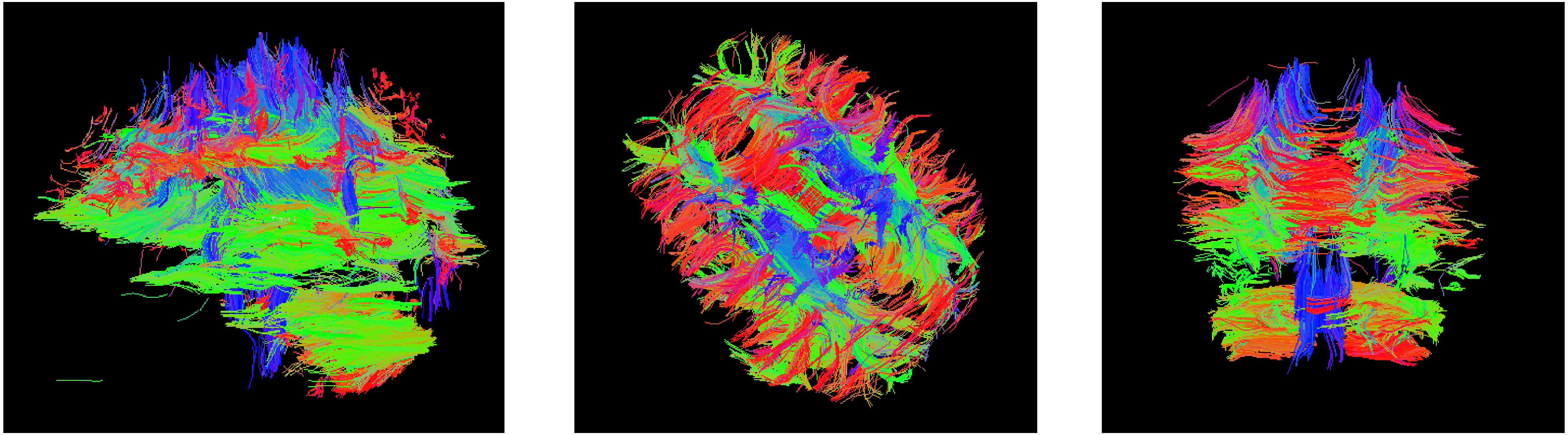
- After model fitting, the principal direction $\varepsilon_1$ can been calculated for all voxels.

- The trajectories of water molecules can be reconstructed using a method similar to the children's activity "connect the dots".

- We connect each voxel to the adjacent one toward which the fibre direction, $\varepsilon_1$, is pointing.



# Tractography in the Brain



Fibre tracks obtained for a dataset of a healthy volunteer using simple streamlining (FACT).

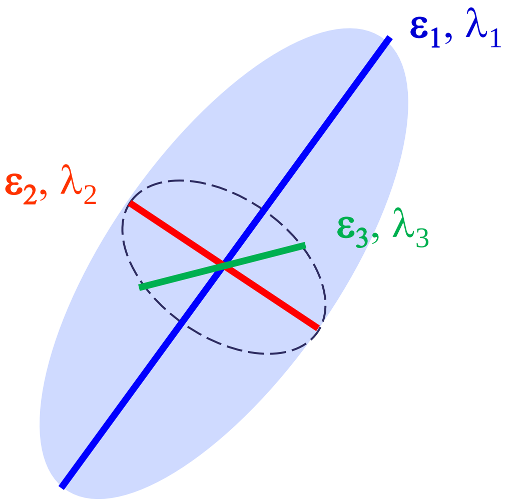
# Probabilistic Modeling of Diffusion MRI Signal

# Probabilistic Modelling

- The information provided by DTI can be very useful for the characterisation of brain white matter.
- However, the estimated tensor can be highly dependent on noise.
- Probabilistic modelling can be used to estimate a probability distribution function for the DTI model parameters.
- For the fibre orientation, this distribution is called orientation distribution function (ODF).

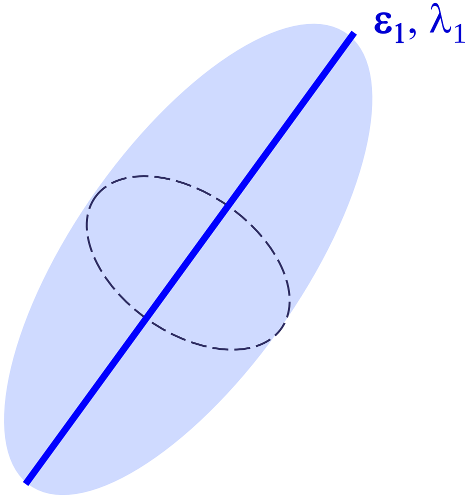
# Orientation Distribution Function (ODF)

**Anisotropic Diffusion**



# Orientation Distribution Function (ODF)

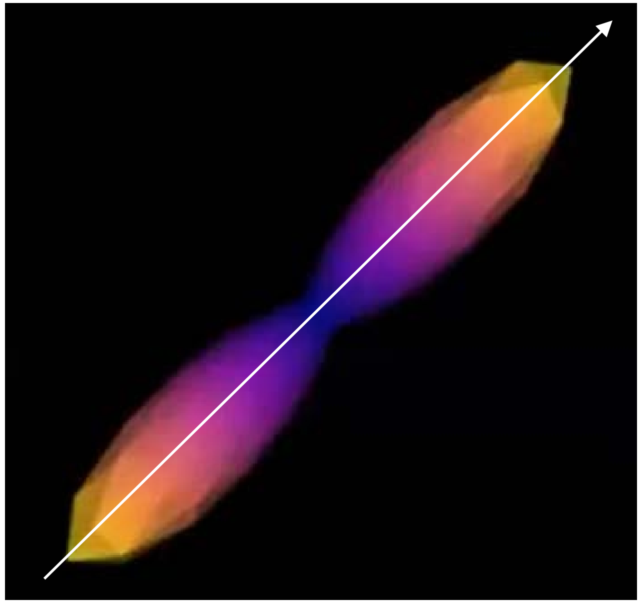
**Anisotropic Diffusion**




ODF calculated from the displacement probability distribution

For DTI:

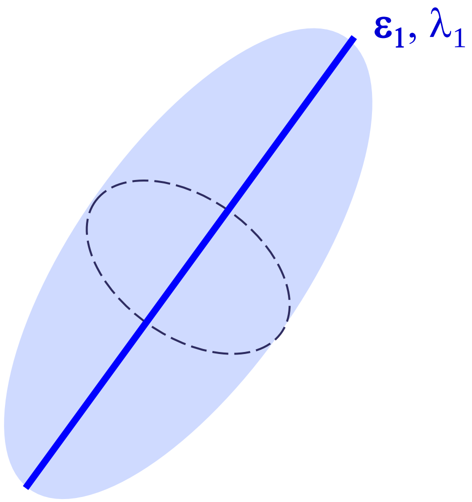
$$ODF(\boldsymbol{n}) = \frac{1}{4\pi\, |\boldsymbol{D}|^{1/2}} \left( \frac{1}{\boldsymbol{n}^T \boldsymbol{D}^{-1} \boldsymbol{n}} \right)^{3/2}$$



*Rafael Neto Henriques*
*Pybrain workshop 2020*

# Orientation Distribution Function (ODF)

**Anisotropic Diffusion**

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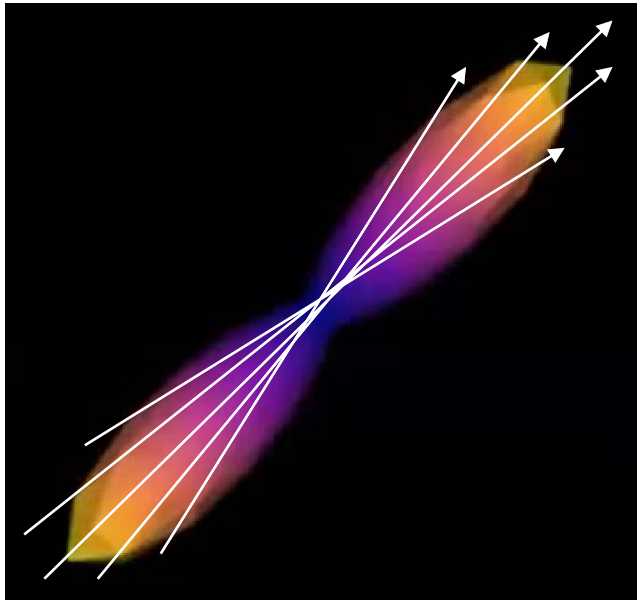
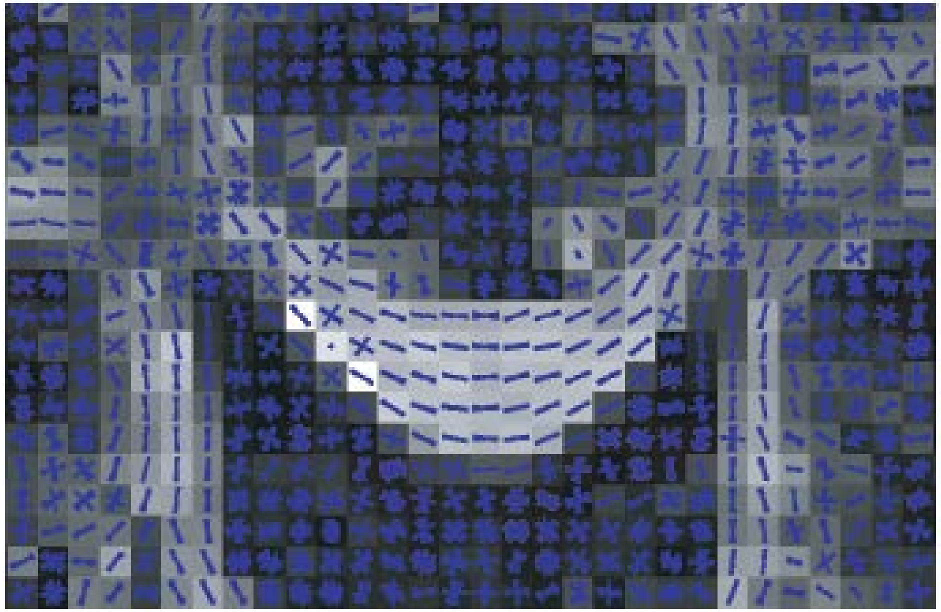


*Rafael Neto Henriques*
*Pybrain workshop 2020*

# Orientation Distribution Function (ODF)

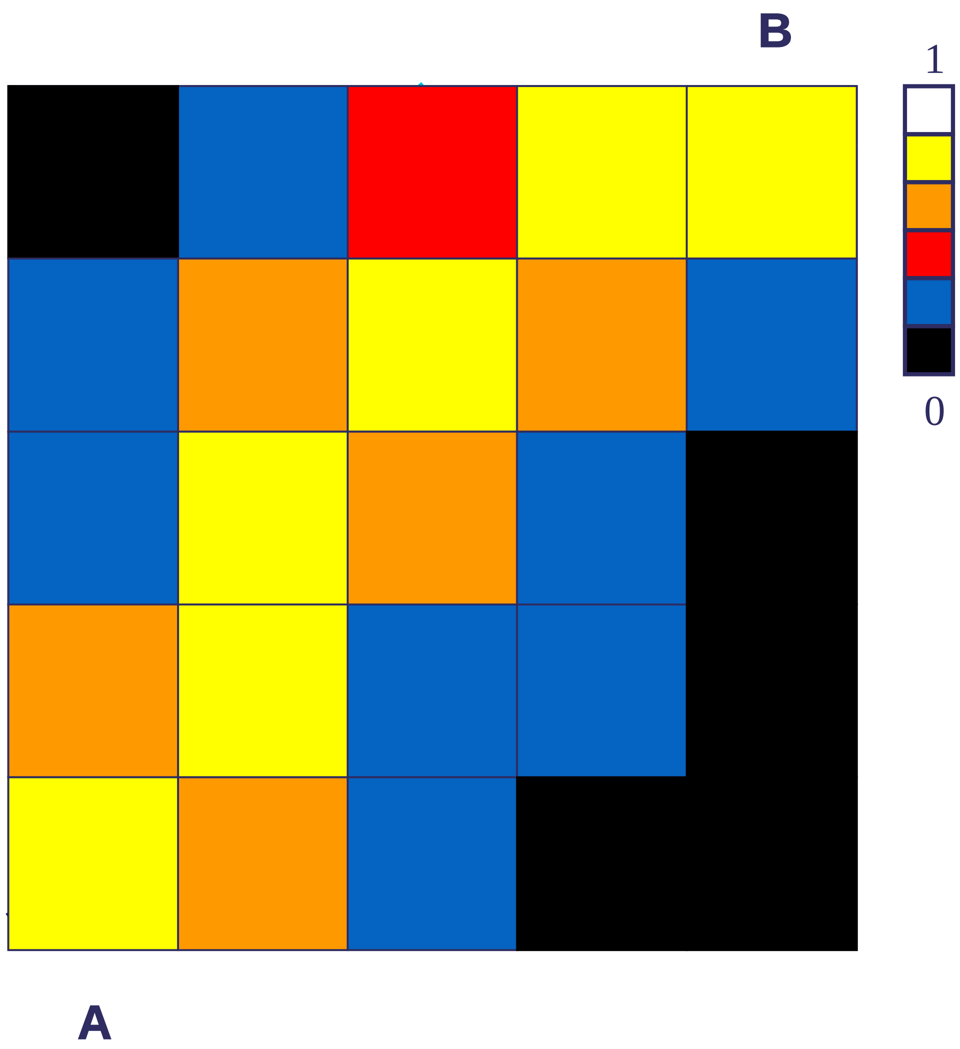
- Example: 10 samples extracted from the ODF of each voxel



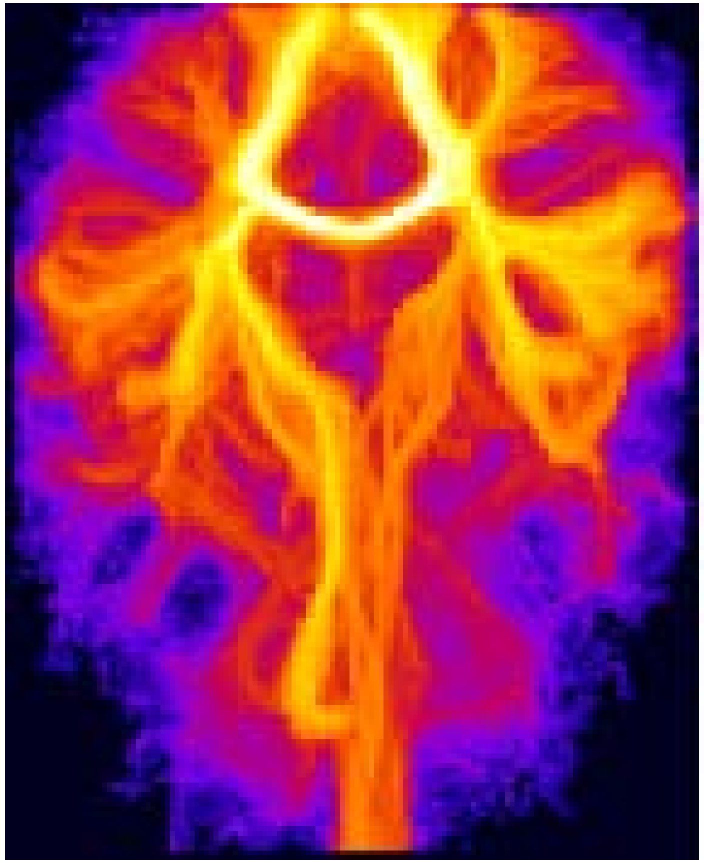
- Regions of one-fibre populations have very narrow distributions, while regions of crossing fibres show greater variability.

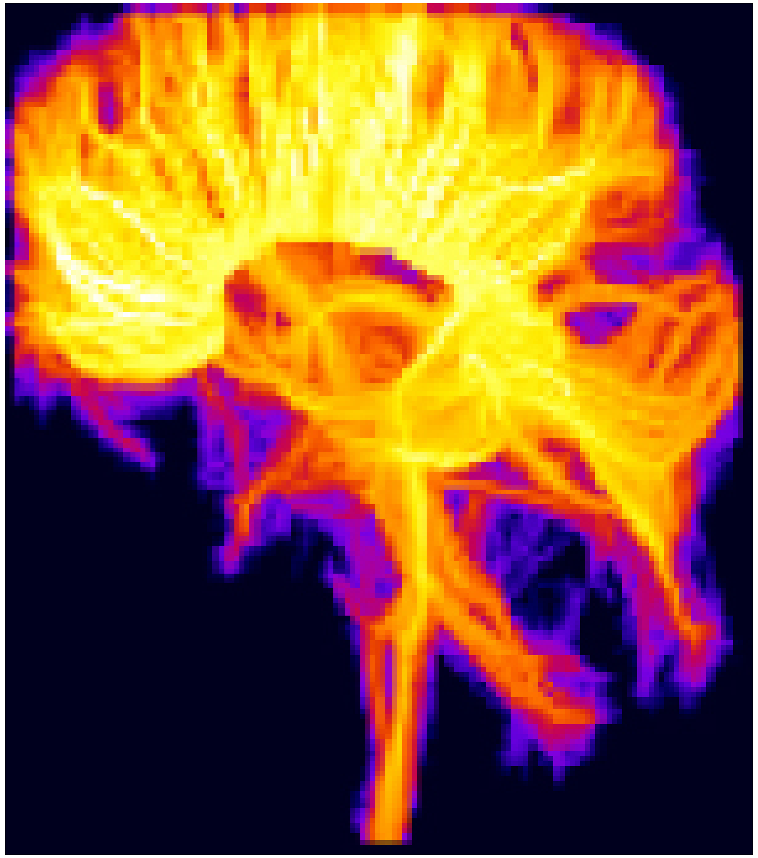
# Probabilistic Tractography

- For each sample of the directional PDF we can produce a track (or streamline).
- Repeat this for a large number of samples.
- The probability of voxels A and B being connected can be calculated by dividing the number of streamlines that reach B, by the total number of streamlines generated from A.



# Probabilistic Tractography in the Brain





**Probabilistic tractography dataset obtained for a healthy volunteer.**

# Multiple fibres

## Beyond the Diffusion Tensor

# Multiple fibre approaches

## Model-Based Approaches

- The multi-tensor model

## Non-Parametric Approaches

- Diffusion Spectrum Imaging (DSI)
- Q-ball Imaging
- Constrained Spherical Deconvolution (CSD)
- Persistent Angular Structure (PAS)

# Multiple fibre approaches

## Model-Based Approaches

- The multi-tensor model

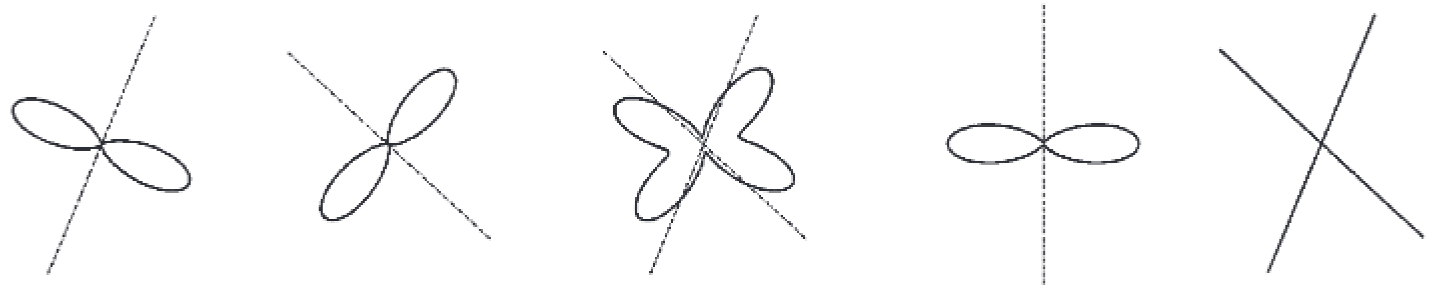
## Non-Parametric Approaches

- Diffusion Spectrum Imaging (DSI)
- Q-ball Imaging
- Constrained Spherical Deconvolution (CSD)
- Persistent Angular Structure (PAS)

# Constrained Spherical Deconvolution (CSD)

- CSD is able to estimate the distribution of fibre orientations within a voxel without making assumptions about the number of fibres present.
- The original method (Tournier et al. 2007) requires a single-shell high angular resolution diffusion data (>60 directions).
- Ideally, the *b*-value used should be in the region of 2,500 – 3,000 s/mm$^2$ (for *in vivo* human brains).
- Multi-shell multi-tissue CSD (MSMT-CSD) was introduced by Jeurissen et al. in 2014.
- MSMT-CSD requires multi-shell high angular resolution diffusion data, containing multiple *b*-values.
- To resolve WM, GM & CSF the acquisition should contain at least 2 shells plus the *b*=0 volumes (i.e. 3 unique *b*-values).

# Constrained Spherical Deconvolution (CSD)



$$f_1S_1(\theta,\phi) \quad + \quad f_2S_2(\theta,\phi) \quad = \quad S(\theta,\phi) \quad = \quad R(\theta) \quad \otimes \quad F(\theta,\phi)$$

Tournier et al. 2007

- Overall diffusion weighted signal attenuation

- Fibre orientation density function describing the fibre orientations present in the voxel

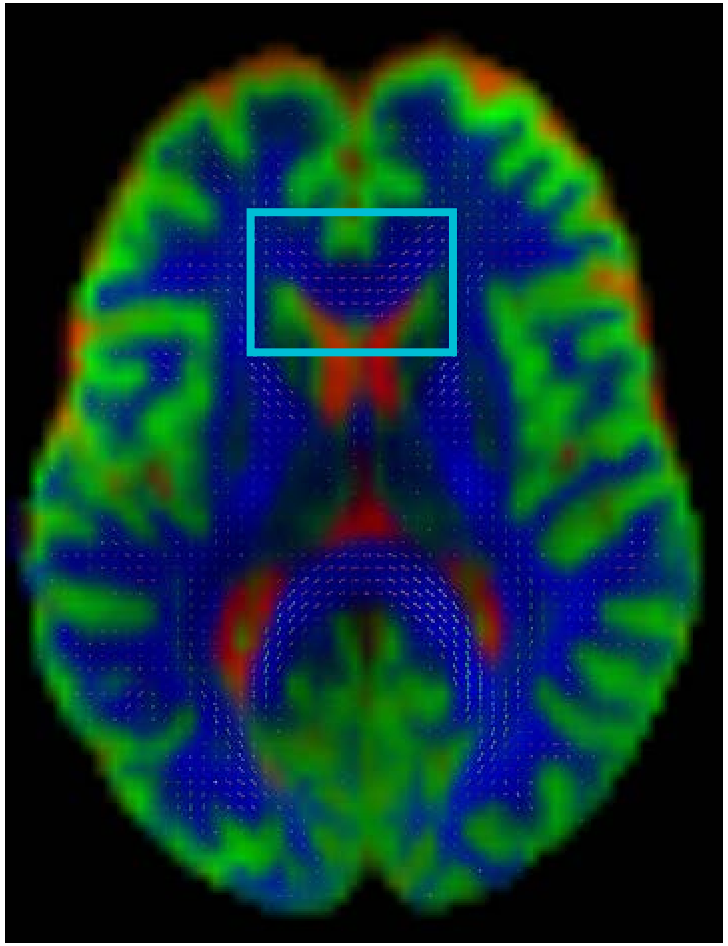
- Two distinct fibre orientations

- $S_1(\theta,\phi)$, $S_2(\theta,\phi)$ – diffusion weighted signal attenuation

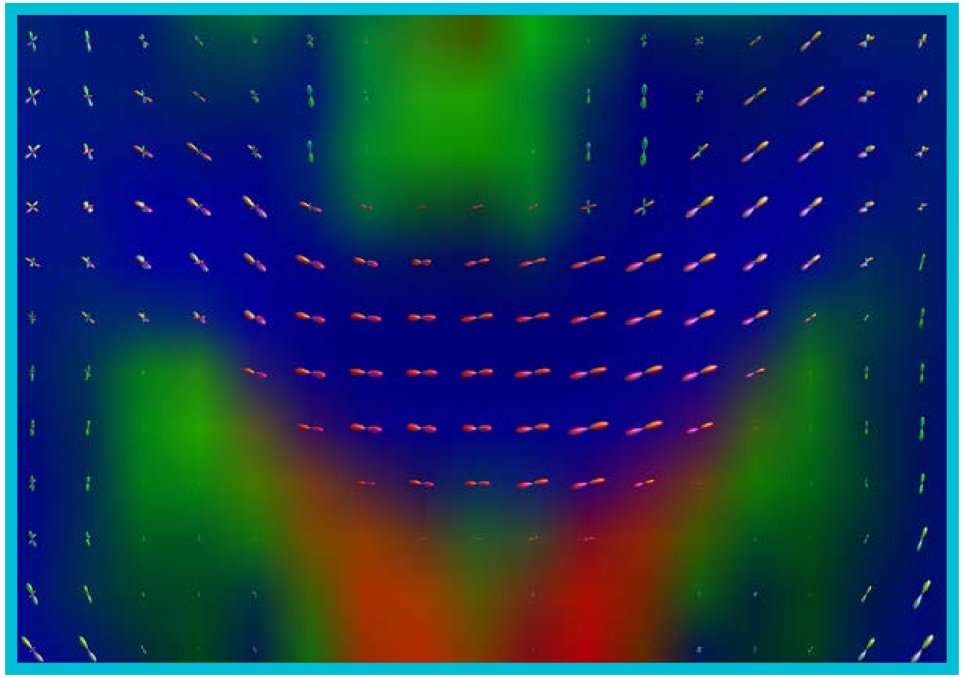
- $f_1,f_2$ – volume fractions

- Axially symmetric response function describing the signal attenuation measured for a single fibre population.

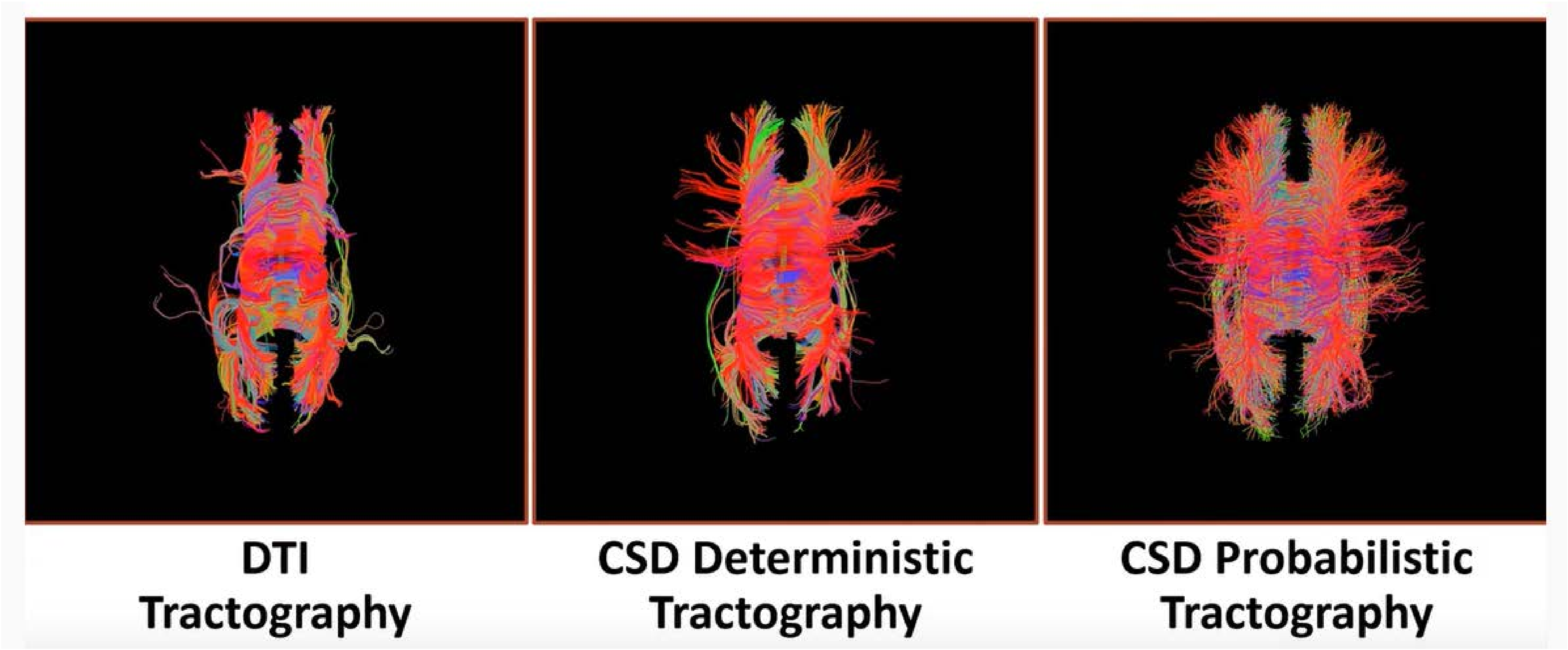
# Constrained Spherical Deconvolution (CSD)



White matter
Grey matter
CSF



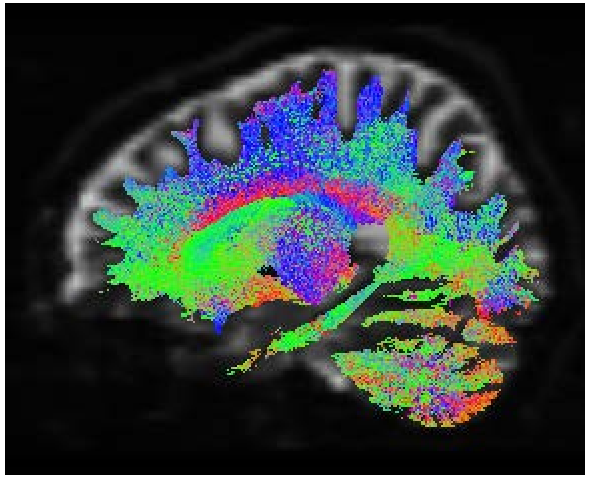
# Constrained Spherical Deconvolution (CSD)




From Gabriel Girard, DIPY tutorial 2021

# Creating the Connectome

- Parcellate the brain using Freesurfer
- Apply parcellation to the tractogram to generate a connectivity matrix, representing the number of streamlines connecting each pair of ROIs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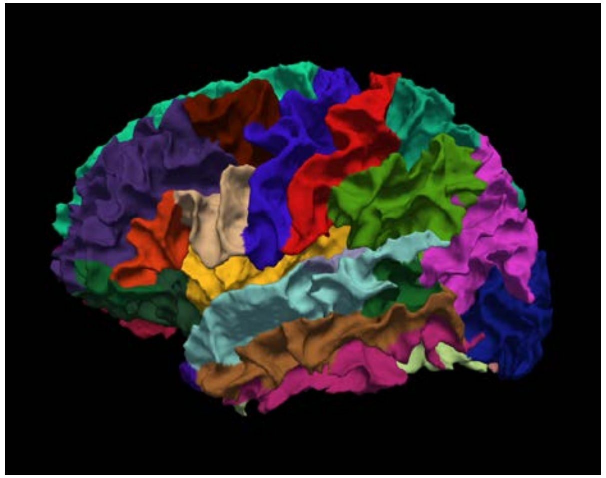
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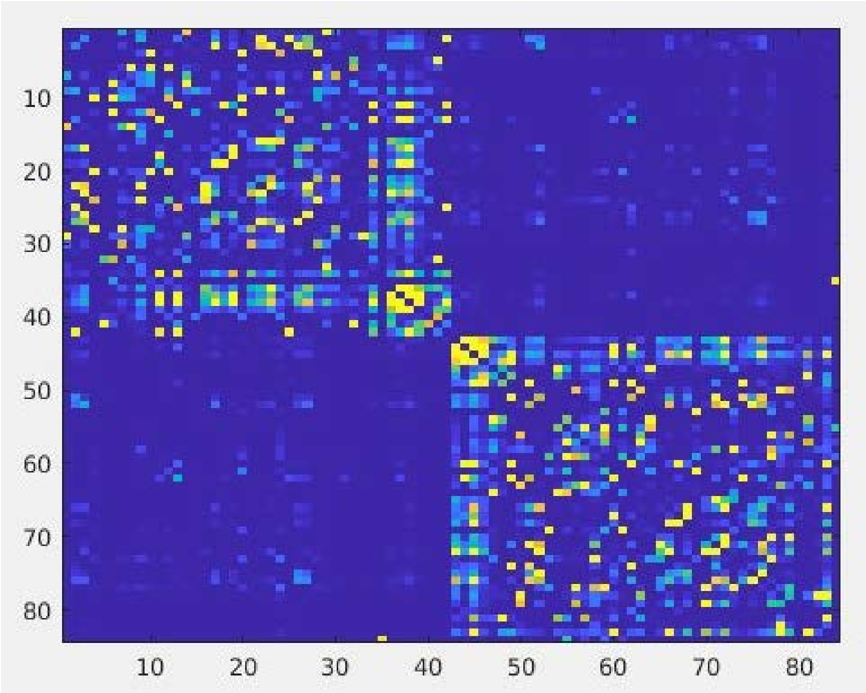
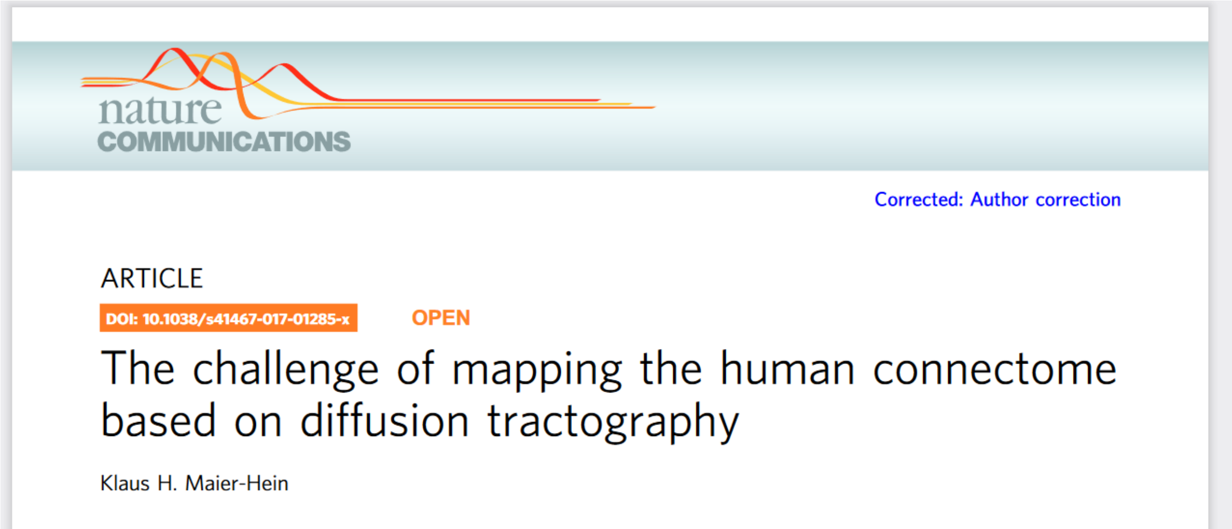


# Interpretation of results

- Streamlines generated with diffusion MRI tractography lack polarity
- Even the best fiber orientation reconstruction algorithm cannot resolve all crossing fibers
- Structural connectomes are dominated by false positives
- Choice of fitting model, tracking algorithm, stopping criteria, etc, can also influence the connectome


nature COMMUNICATIONS

Corrected: Author correction

ARTICLE

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The challenge of mapping the human connectome based on diffusion tractography

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# Questions?