Neuroimage Processing

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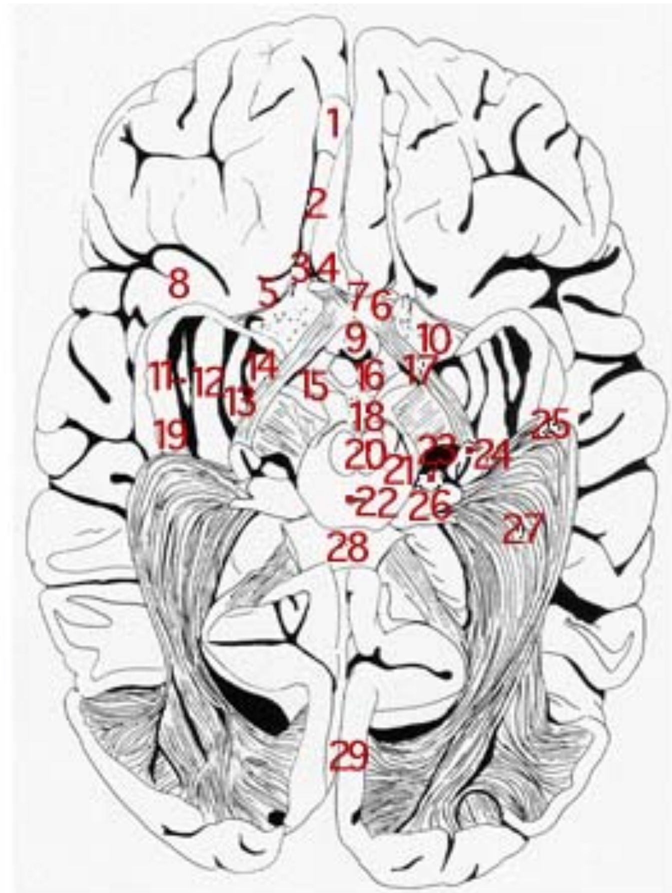
Lecture 06-07.

Diffusion Tensor Imaging

October 16, 2009

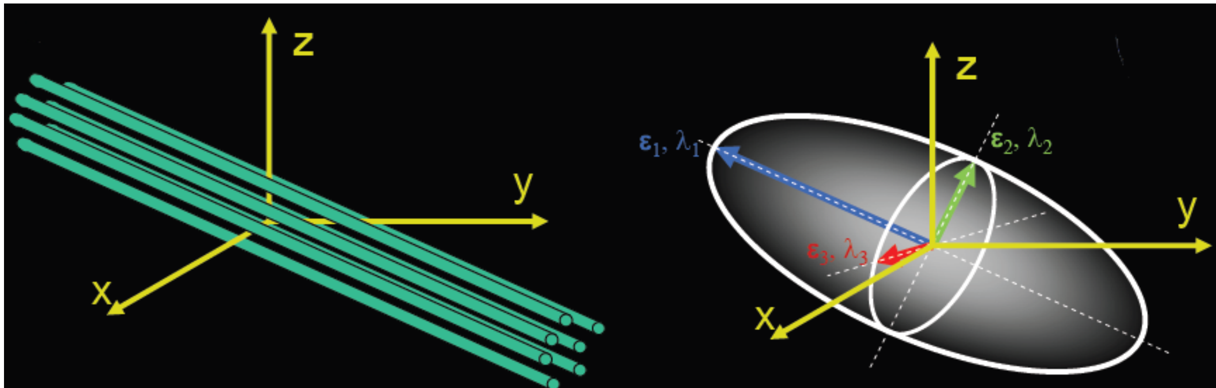
White matter fibers



1. Olfactory bulb
2. Olfactory tract
3. Olfactory trigone
4. Medial olfactory stria
5. Lateral olfactory stria
6. Optic nerve

www.vh.org

Diffusion Tensor Imaging



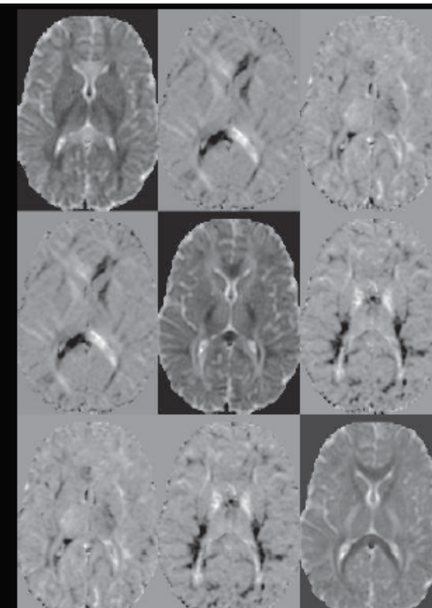
$$p(x\,|\,x_o,\tau) = \frac{1}{\sqrt{(4\pi\tau)^3\,|\underline{D}|}}\,exp\left(\frac{-(x-x_0)^T\,\underline{D}^{-1}(x-x_0)}{4\tau}\right)$$

$$\mathbf{D} = \underbrace{\begin{pmatrix} D_{xx} & D_{xy} & D_{xz} \\ D_{yx} & D_{yy} & D_{yz} \\ D_{zx} & D_{zy} & D_{zz} \end{pmatrix}}_{\text{Diffusion Tensor}} = \mathbf{E}\begin{pmatrix} \lambda_1 & 0 & 0 \\ 0 & \lambda_2 & 0 \\ 0 & 0 & \lambda_3 \end{pmatrix}\mathbf{E}$$

Eigenvalues

Matrix of 3 eigenvectors

$$\mathbf{D} = \begin{pmatrix} D_{xx} & D_{xy} & D_{xz} \\ D_{yx} & D_{yy} & D_{yz} \\ D_{zx} & D_{zy} & D_{zz} \end{pmatrix} =$$



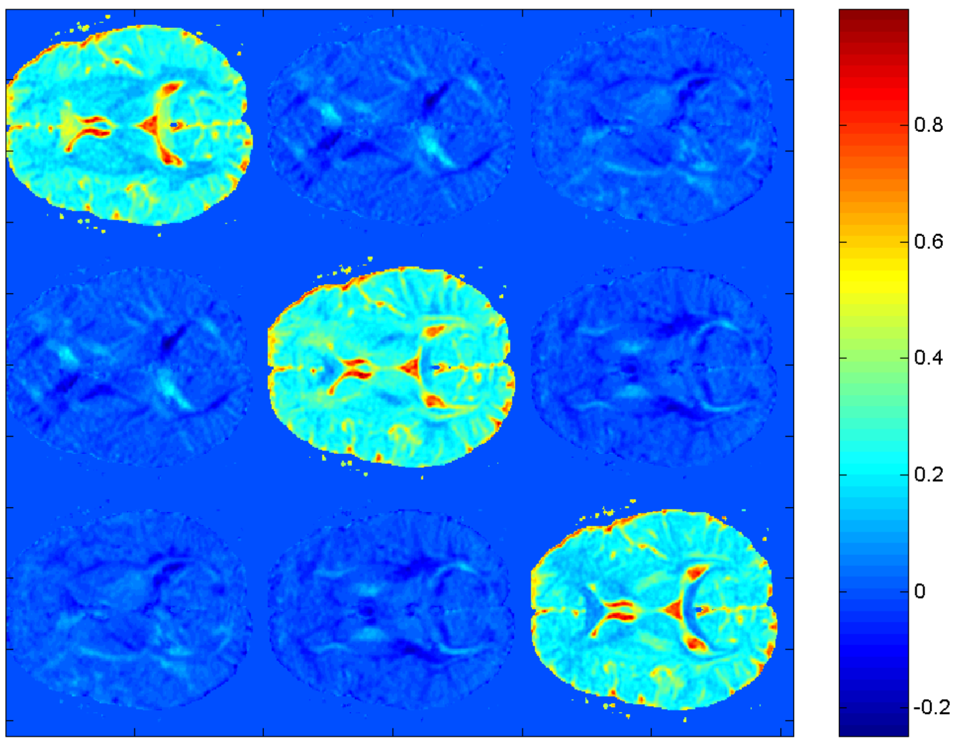
$D_{xx}, D_{yy}, D_{zz} > 0$

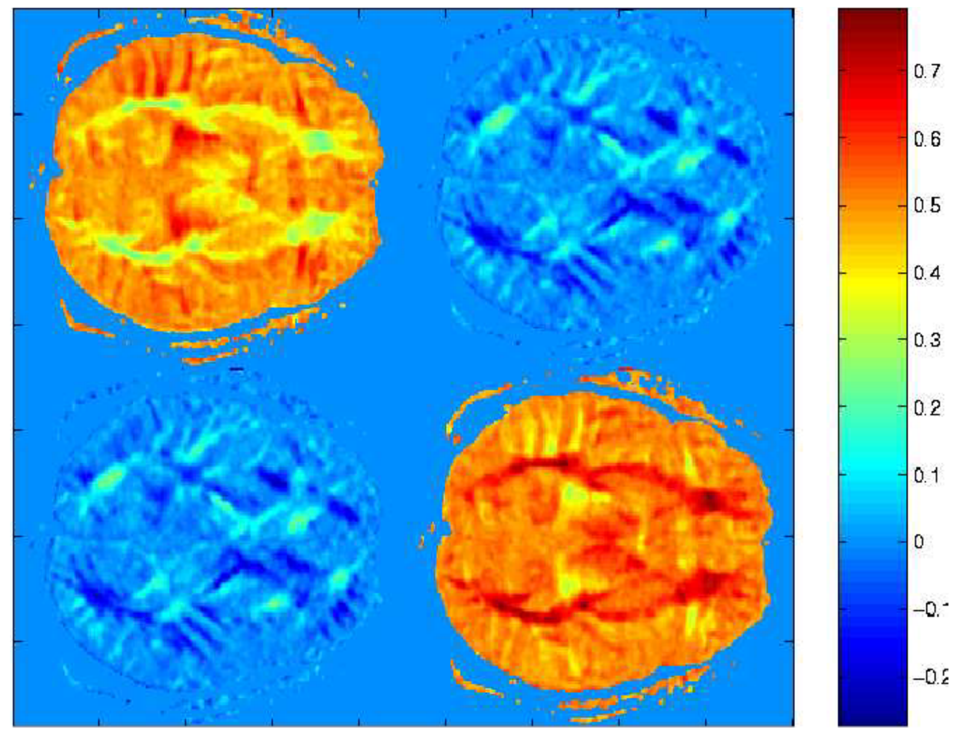
$D_{xy} = D_{yx}; D_{xz} = D_{zx}; D_{yz} = D_{zy}$

DTI data

$$D = (d_{ij})$$

6 diffusion coefficient matrix D_xx, D_xy, D_xz, D_yy, D_yz, D_zz





- Diffusion coefficient measures the diffusion of water molecules.
- The principal eigenvector = direction of water molecules.
- This gives indirect information about white matter fibers.

Fractional Anisotropy (FA) map

Read Alexander.2007….. : review paper

You need to know the difference between FA-map and MD-map.

Tractography

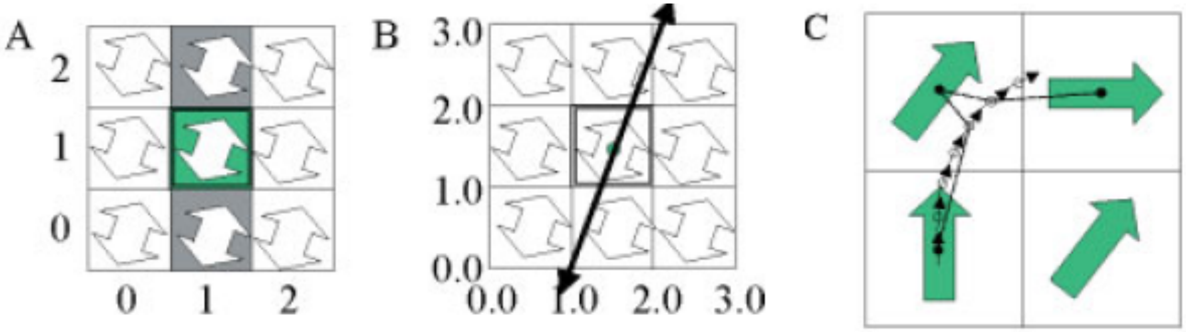
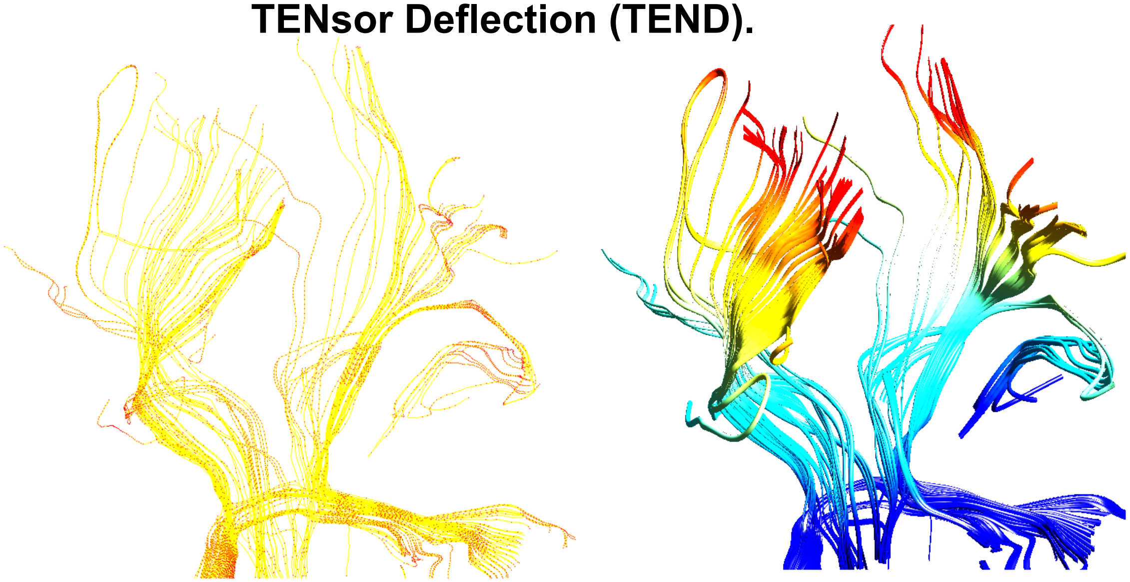


Figure 2. Schematic diagram of the linear line-propagation approach. Double-headed arrows indicate fiber orientations at each pixel. Tracking is initiated from the center pixel. In the discrete number field (A), the coordinate of the seed pixel is {1, 1}. If it is judged that the vector is pointing to {1, 2} and {1, 0}, shaded pixels are connected. In the continuous number field (B), the seed point is {1.50, 1.50} and a line, instead of a series of pixels, is propagated. (C) shows an example of the interpolation approach to perform nonlinear line propagation. Large arrows indicate the vector of the largest principal axis. For every step size, a distance-weighted average of nearby vectors is calculated. In this example, the vector orientations of two nearest pixels are averaged as the line is propagated

TENsor Deflection (TEND).

Mori and van Zijl NMR Biomed 2002



Camino software package

http://en.wikipedia.org/wiki/Camino_(diffusion_MRI_toolkit)

Second order Runge-Kutta algorithm with TEND (Lazar et al., HBM 2003).

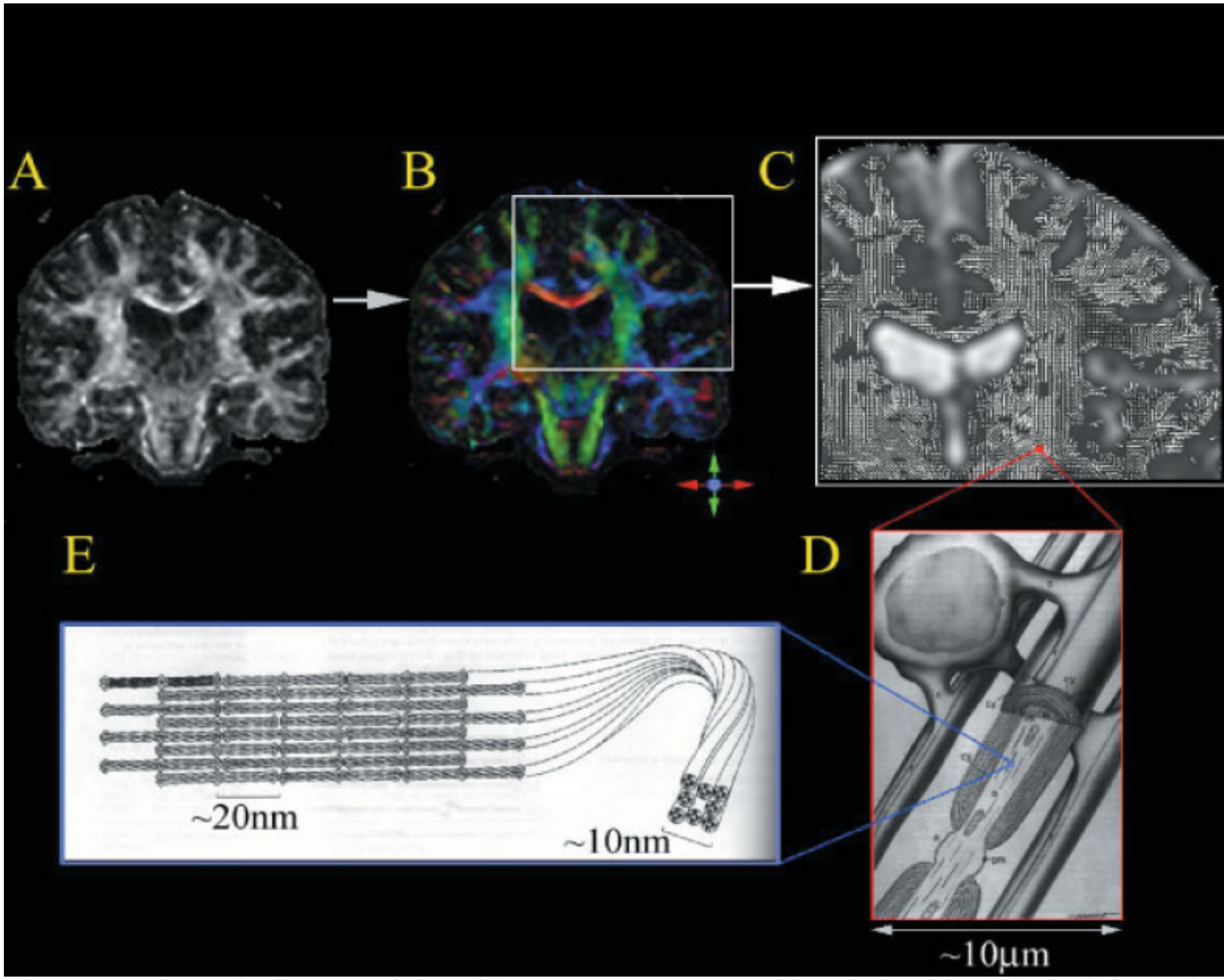
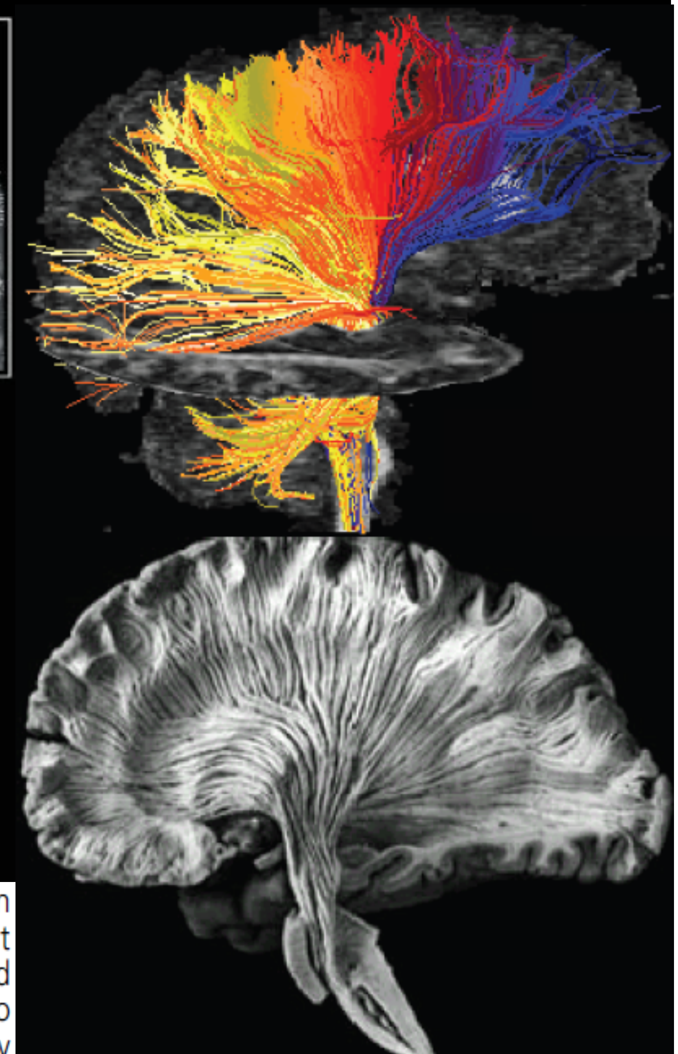
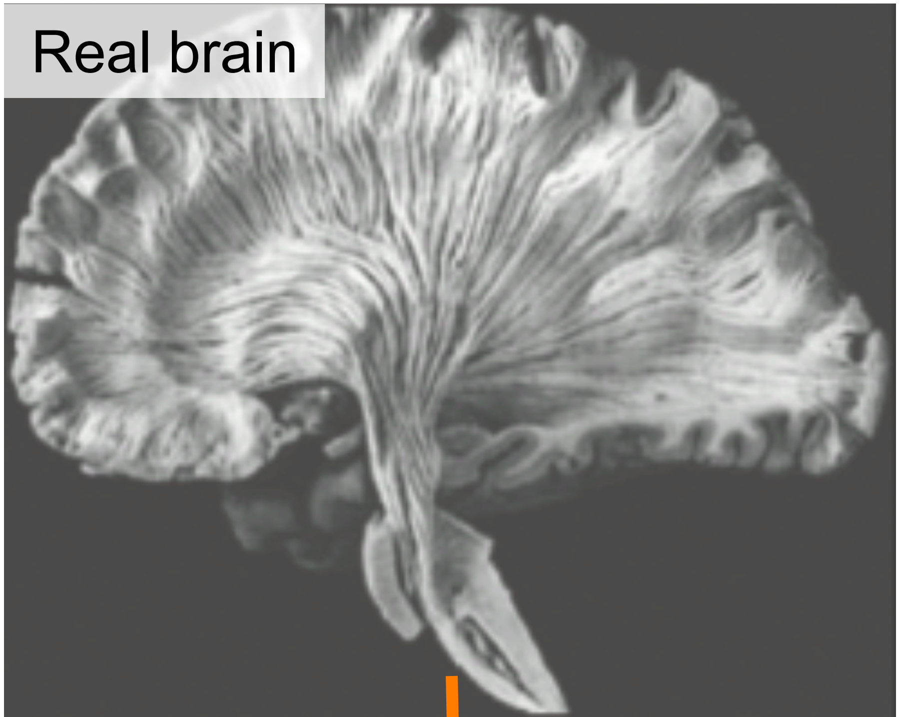


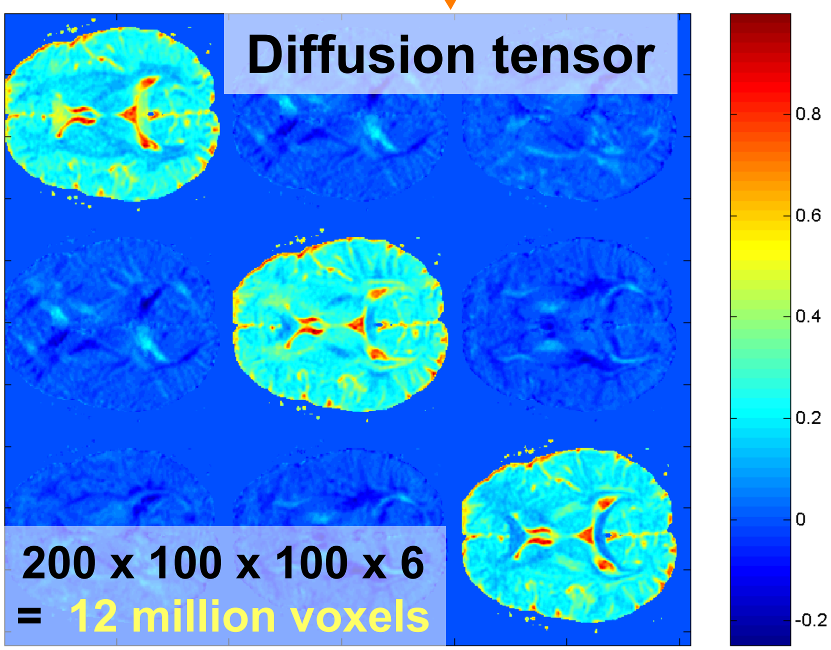
Figure 1. Schematic diagram of the white matter structure and its relationship with the information provided by DTI-based images, such as anisotropy maps (A), have sufficient resolution to segment white and gray matter. By incorporating DTI orientation information, white matter can be parcellated into various tracts using a color-coded map (B) or a vector map (C). The image resolution is sufficient to delineate large white matter tracts, which mostly consist of neuroglia and axons that are largely running parallel. A pixel thus contains bundles of axons and neuroglial cells (D). Note that the size of a pixel (C) is on the order of mm but that the size of the cells (D) is on the order of μm. The axon is filled with neuronal filaments (E) running along its longitudinal axis, which may contribute in superimposing anisotropy on the direction of water diffusion. In the color-coded map, red indicates fibers running along the right–left direction, green inferior–superior, and blue anterior–posterior (perpendicular to the plane). The figures (D) and (E) were reproduced from Carpenter[49] and Alberts *et al.*[64] respectively with permission



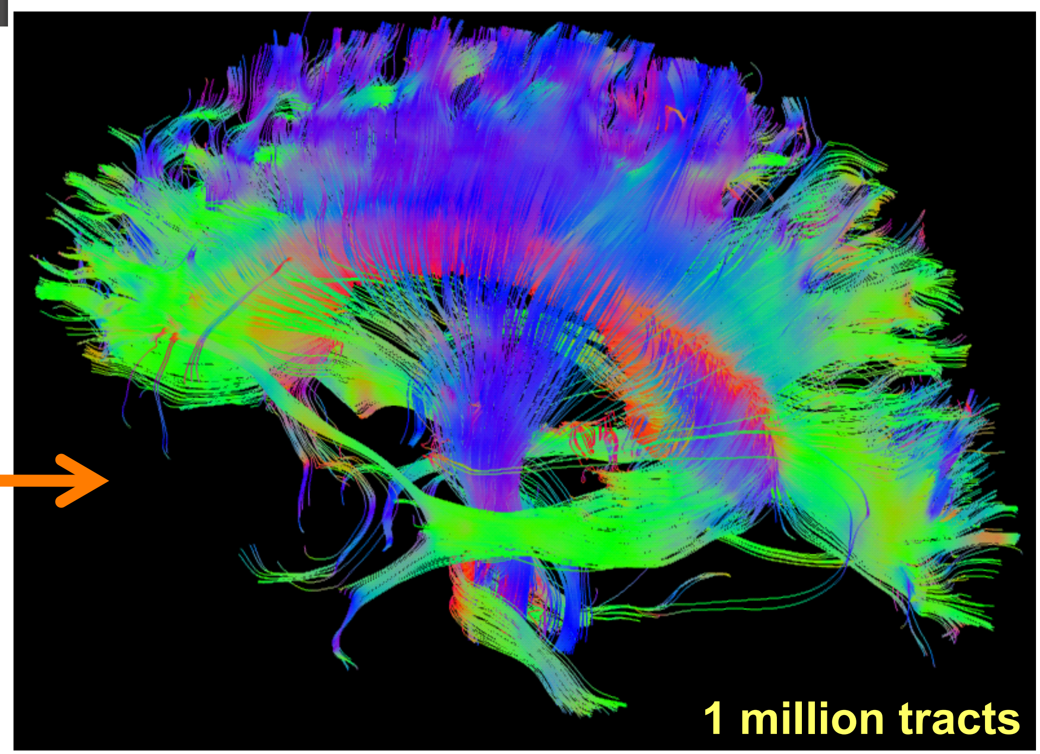
Mori and van Zijl NMR Biomed 2002

Diffusion Tensor Imaging

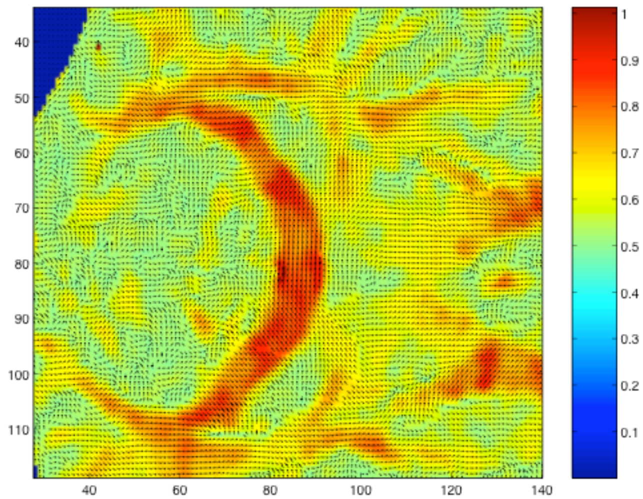


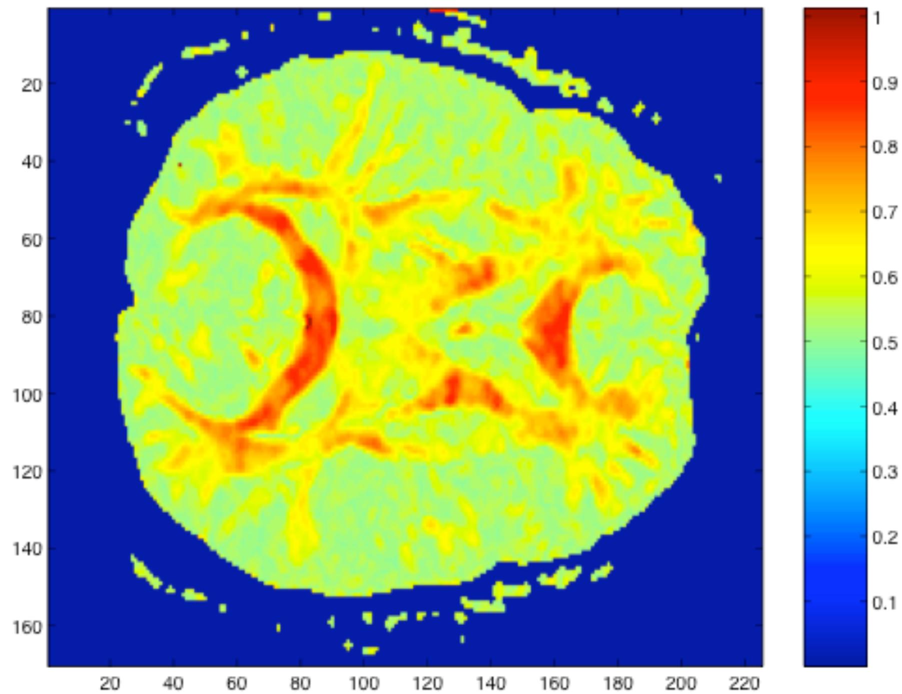


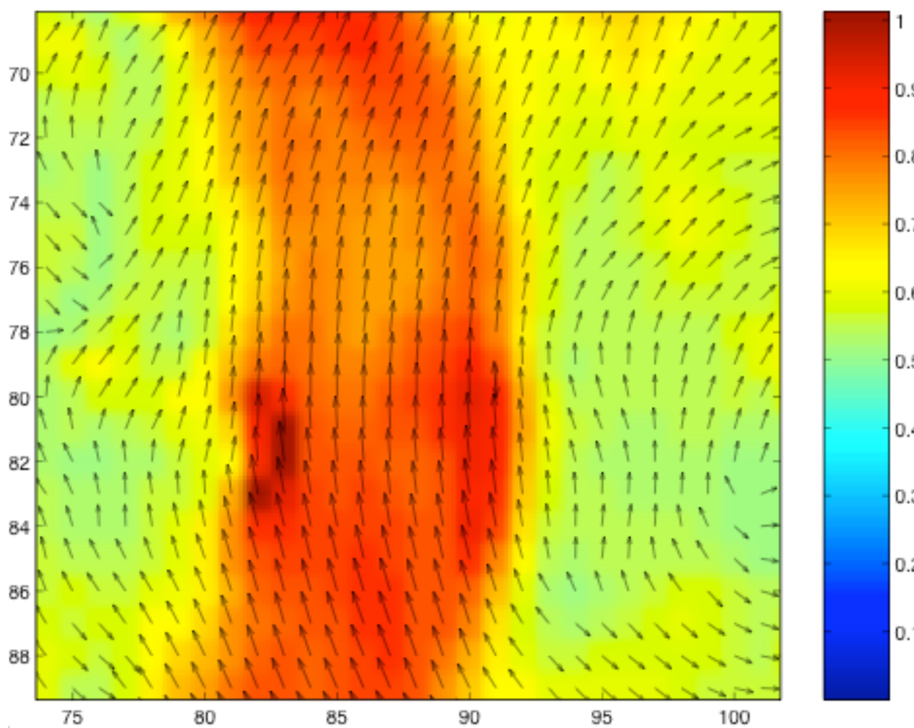
White matter fiber tractography

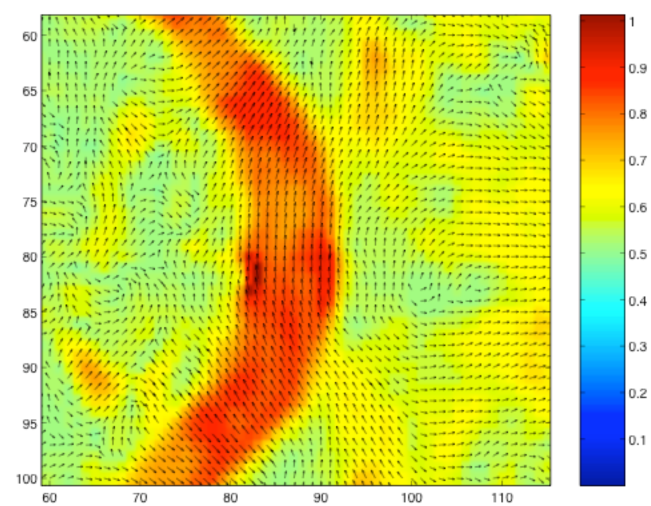


Principal eigenvectors

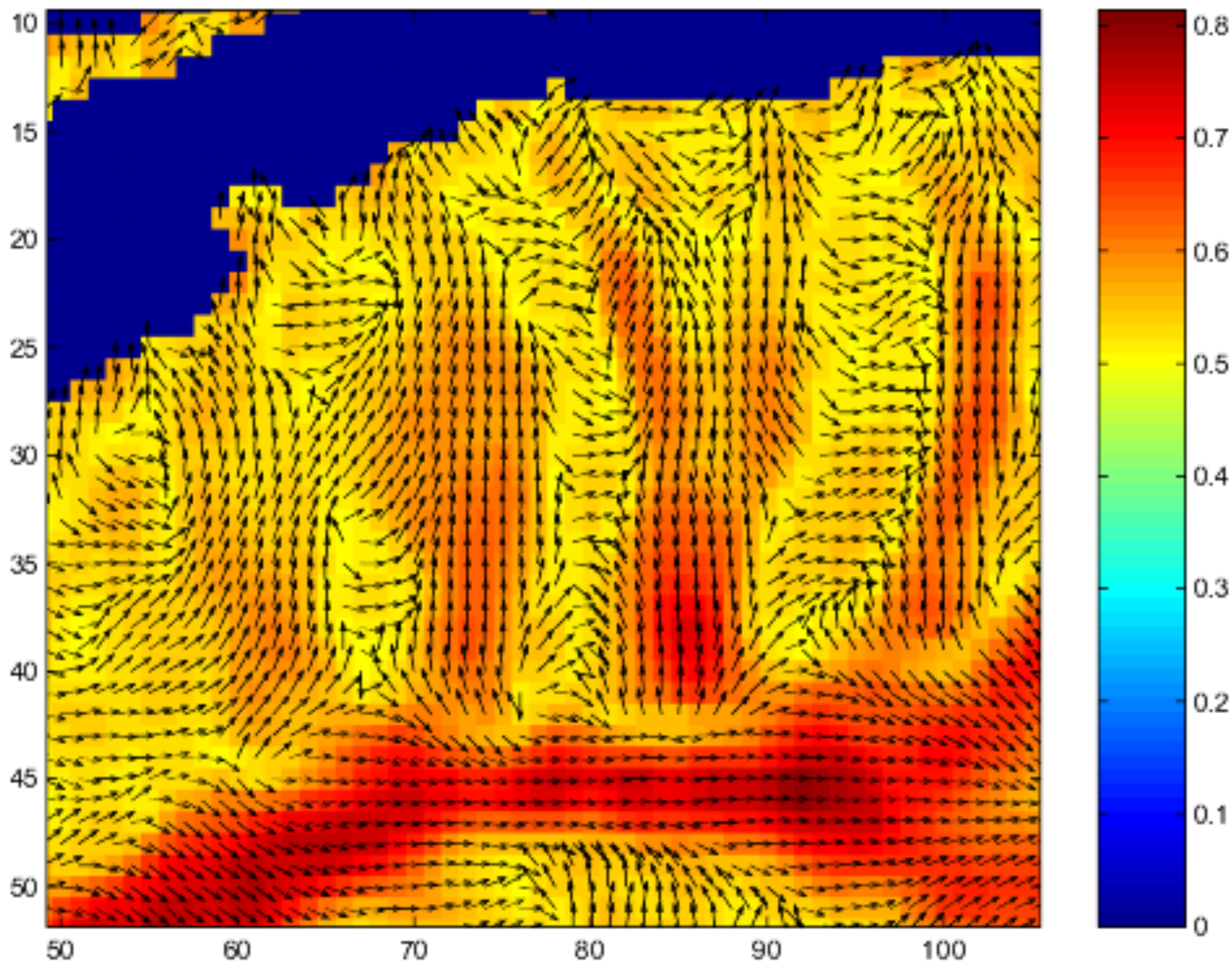




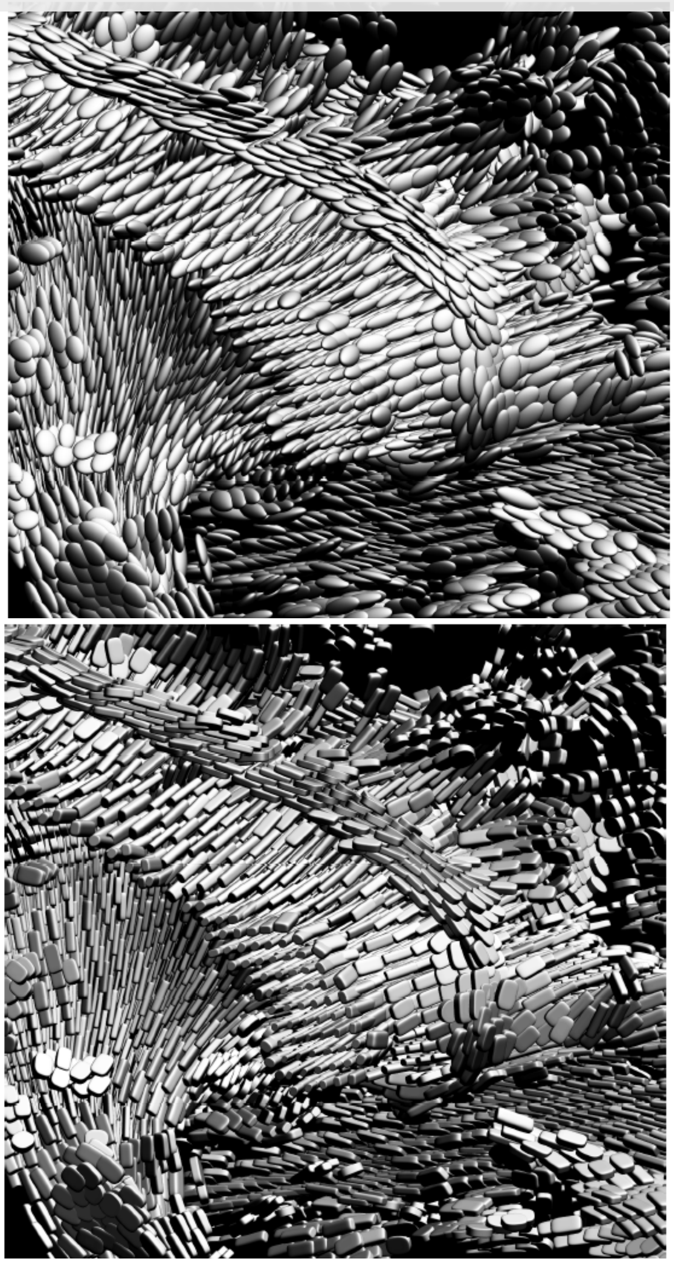


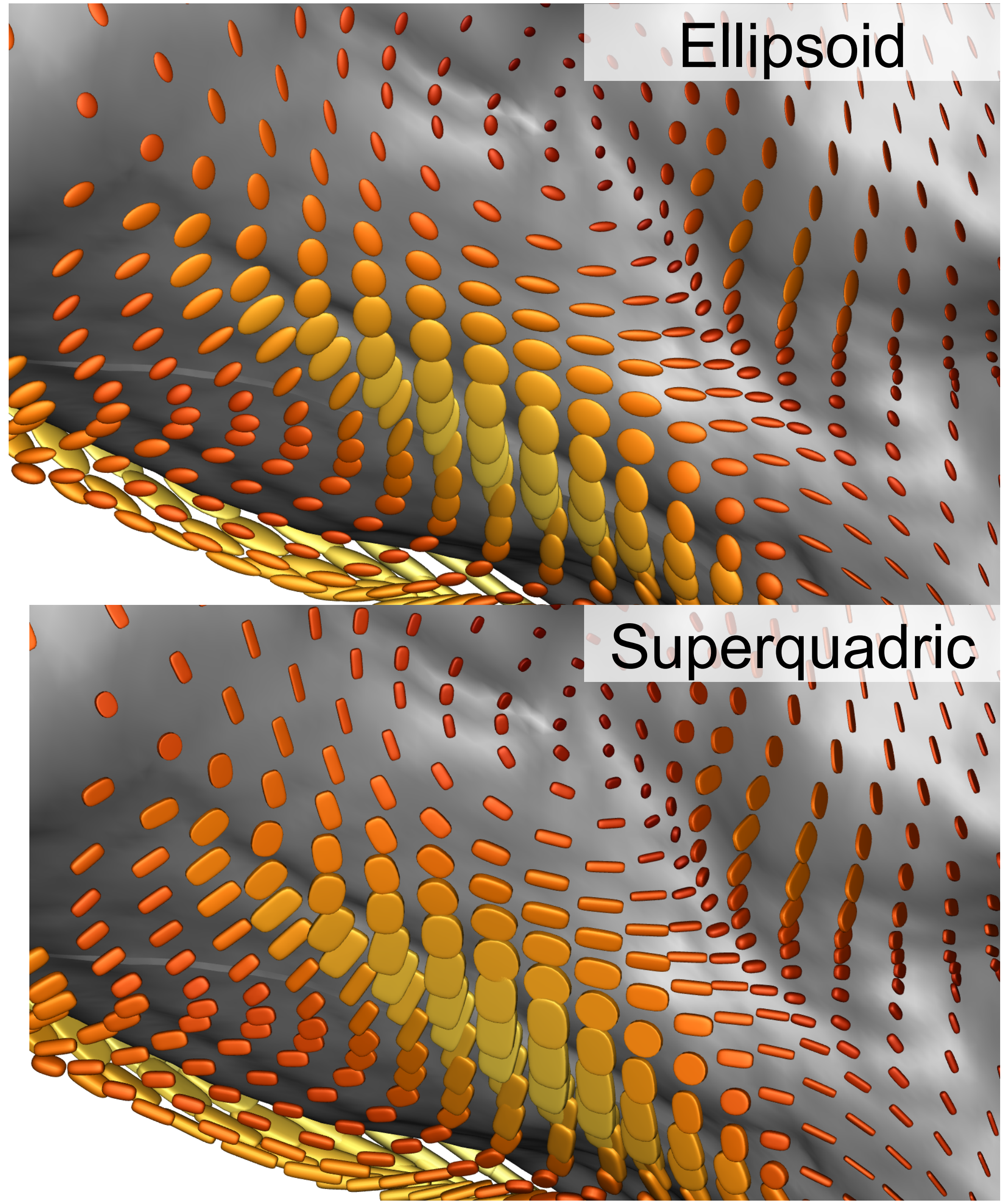


principal eigenvectors



Tensor field visualization





Kindlmann, "Superquadric Tensor Glyphs", Joint Eurographics , IEEE TCVG Symposium on Visualization 2004

Scientific Computing and Imaging Institute

Figure 11: *3-D region of DT-MRI dataset of brain visualized with ellipsoids (top) and superquadrics (bottom).*

Diffusion tensor imaging (DTI) is a new technique that provides the directional information of water diffusion in the white matter of the brain. The directional information is usually represented as a symmetric positive definite 3×3 matrix $D = (d_{ij})$ which is usually termed as the *diffusion tensor* or *diffusion coefficients*. The diffusion tensors are usually normalized by the transpose, i.e. $D/\mathrm{tr}D$. This normalization guarantees that the sum of eigenvalues of D to be 1.

The eigenvectors and eigenvalues are obtained by solving

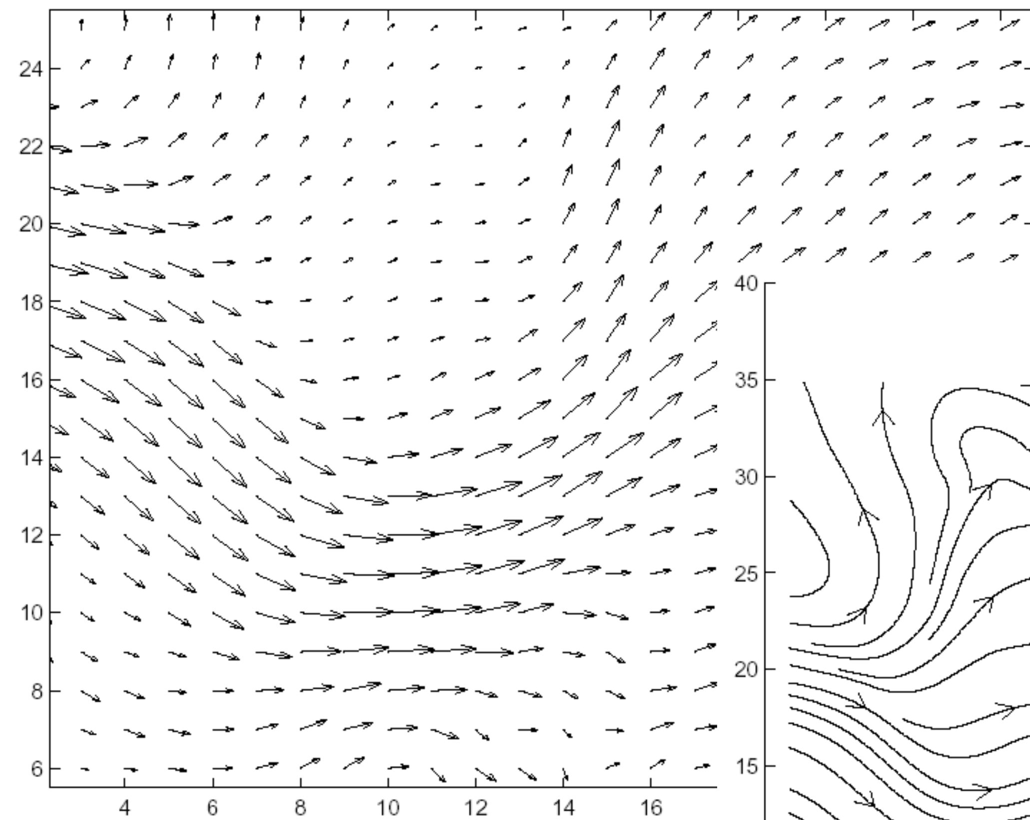
$$D\mathbf{V} = \lambda\mathbf{V}.$$

Consider a vector field $\mathbf{V}$ which is the principal eigenvector of D with $\|\mathbf{V}\| = 1$ with the corresponding principal eigenvalue λ. Now suppose that we would like to smooth signals along the vector fields $\lambda\mathbf{V}$ such that we smooth more along the larger vector fields. Suppose that the stream line or flow $\mathbf{x} = \psi(t)$ corresponding to the vector field is given by

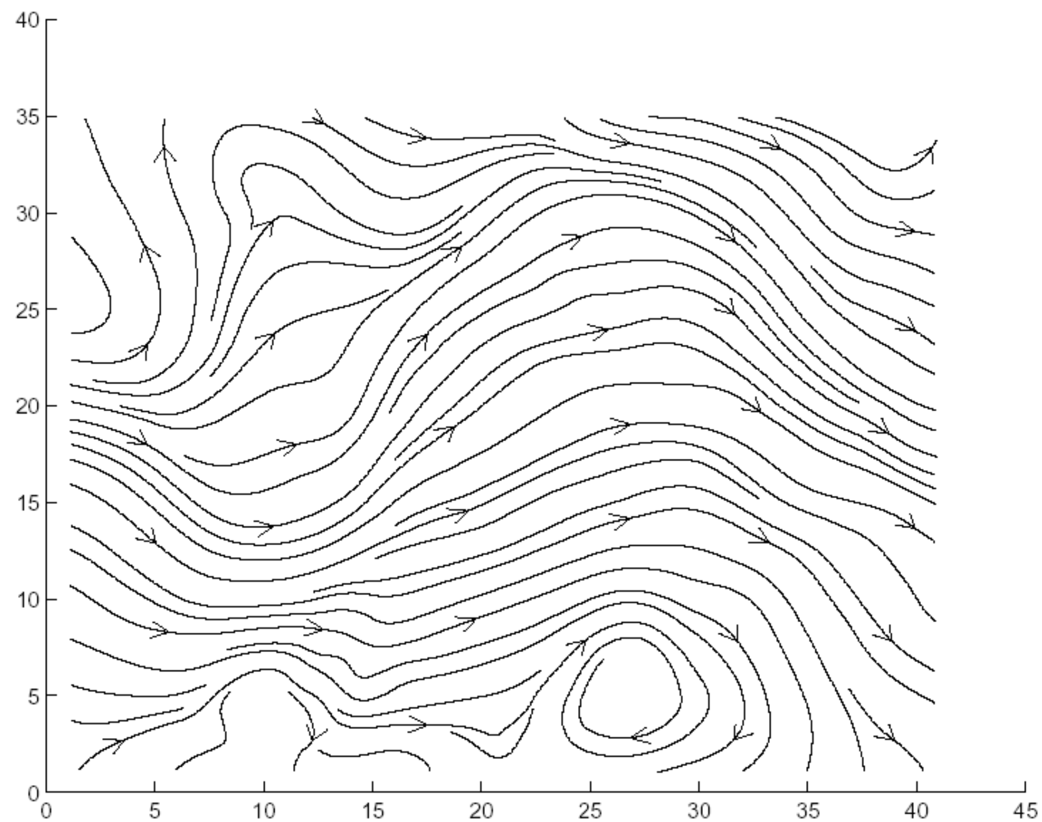
$$\frac{d\psi}{dt} = (\lambda\mathbf{V}) \circ \psi(t).$$

This ordinary differential equation gives a family of integral curves whose tangent vector is $\lambda\mathbf{V}$ (Betounes, 1998).

For given vector fields there exists a family of curves whose tangent is given by the vector fields.



Stream lines generated by built in MATLAB function



Streamline based tractography

second order Runge-Kutta algorithm (Lazar et al., HBM. 2003).

MATLAB demonstration

Parametric model of white fiber tracts

Clayden et al. IEEE TMI 2007

Cubic B-spline is used to model and match tracts.

:computational nightmare

Batchelor et al. MRM 2006

Sine and cosine Fourier descriptors are used to extract global shape features for classification

: inefficient representation

Main contribution of Chung et al. 2010

1. More efficient Fourier descriptor (uses less number of basis than before).

2. Developed registration and averaging framework for 3D curves without numerically demanding optimization routines as in splines.

Orthonormal basis in [0,1]

$$\Delta f + \lambda f = 0$$ Eigenfunctions form orthonormal basis

$$f(t) = f(-t)$$ Sine and cosine basis

$$f(t+2) = f(t)$$ Cosine basis: more compact representation

$$\lambda_l = -l^2\pi^2$$

$$\psi_0 = 1, \psi_l = \sqrt{2}\cos(l\pi t)$$

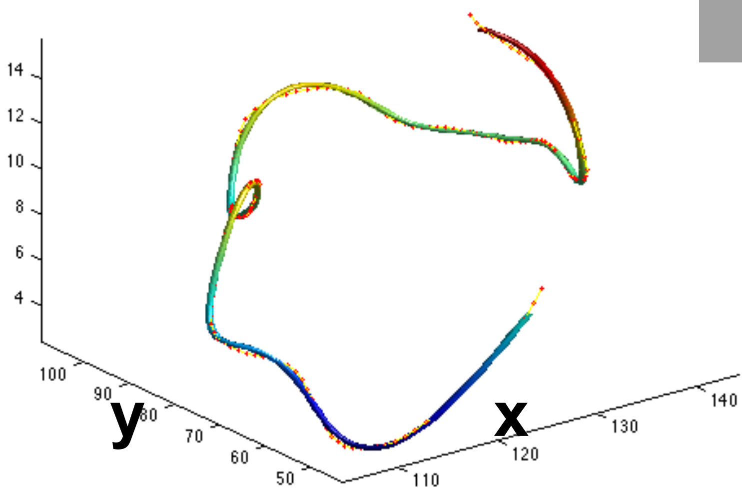
Fourier analysis in [0,1]

$$\sum_{l=0}^{k} f_l \psi_l(t) \to f$$

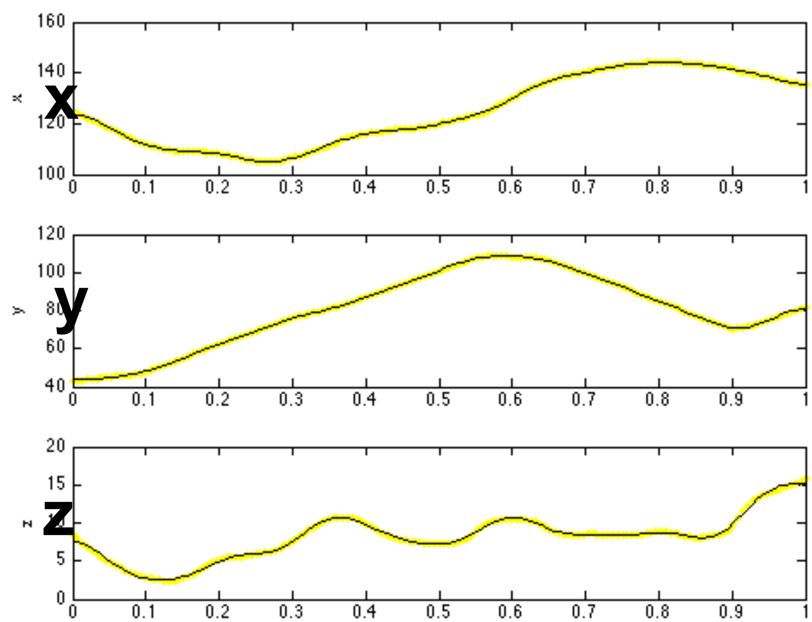
$$f_l = \langle f, \psi_l \rangle = \int_0^1 f(t)\psi_l(t)\, dt$$

This integral can be magically computed by matrix inversion

White matter fiber tract model



parameterization



88.1799	56.6336	5.7367
-12.4775	-11.2552	-2.0791
2.4336	-15.4428	-0.4021
4.3956	2.2733	-0.9354
-0.0106	-0.0674	0.6999
2.1773	-2.4194	-0.1176
0.5808	0.8390	1.2942
0.0615	-0.1893	0.1188
-0.2629	0.7524	0.1089
0.7909	-0.7276	-0.1901
0.5458	0.6236	0.6939
0.4295	-0.4337	0.2185
0.2150	0.4157	0.0254
0.1584	-0.1973	0.0762
-0.1557	0.2466	-0.1086
0.0632	-0.0978	-0.0208
0.0389	-0.0143	-0.0284
-0.0014	-0.1193	0.1970
0.0004	0.0129	-0.0198
0.1342	0.0002	0.0260

Any tract can be compactly parameterized with only 60 coefficients.

Tract registration is done by matching these parameters.

basis expansion

$$(x, y, z)' = \sum_{l=0}^{19} \beta_l \cos(l\pi t)$$

Least squares estimation

x, y, z coordinate vector $\longrightarrow$ $f(p_i) = \sum_{j=0}^{k} \beta_j \psi_j(p_i)$

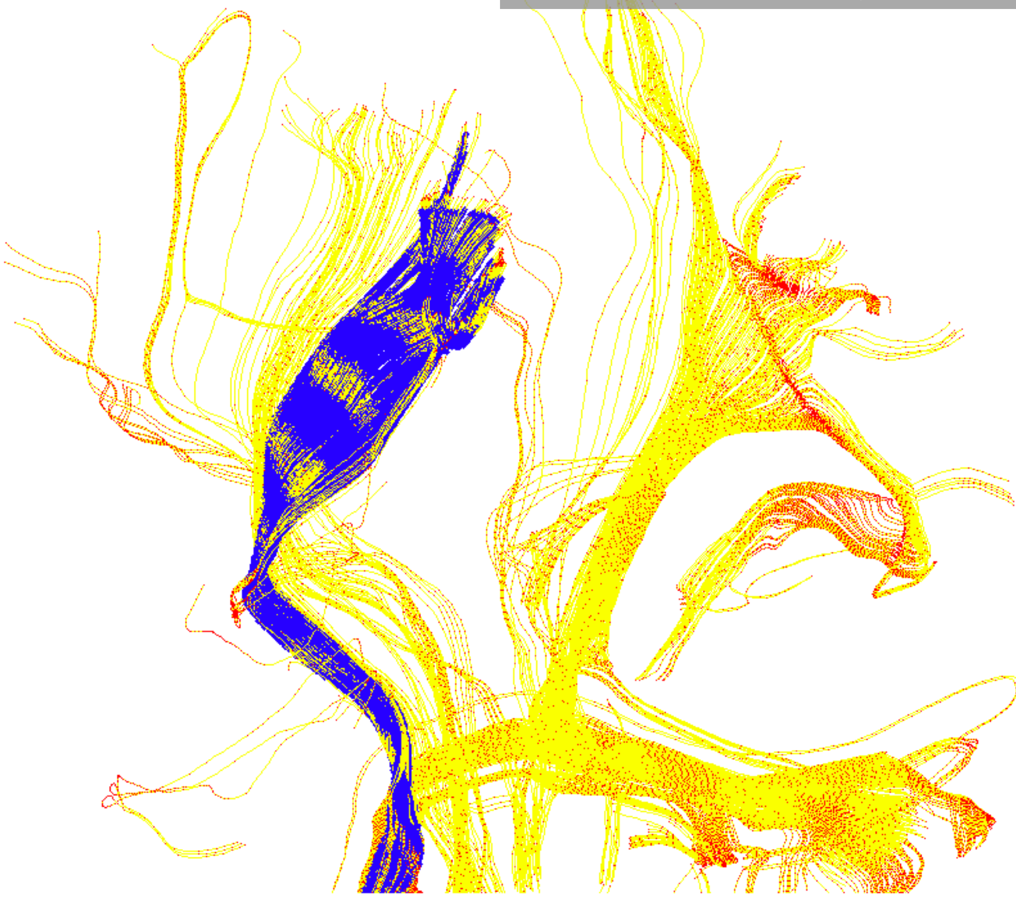
$$\mathbf{f} = (f(p_1), \cdots, f(p_n))' \quad \beta = (\beta_0, \cdots, \beta_k)'$$

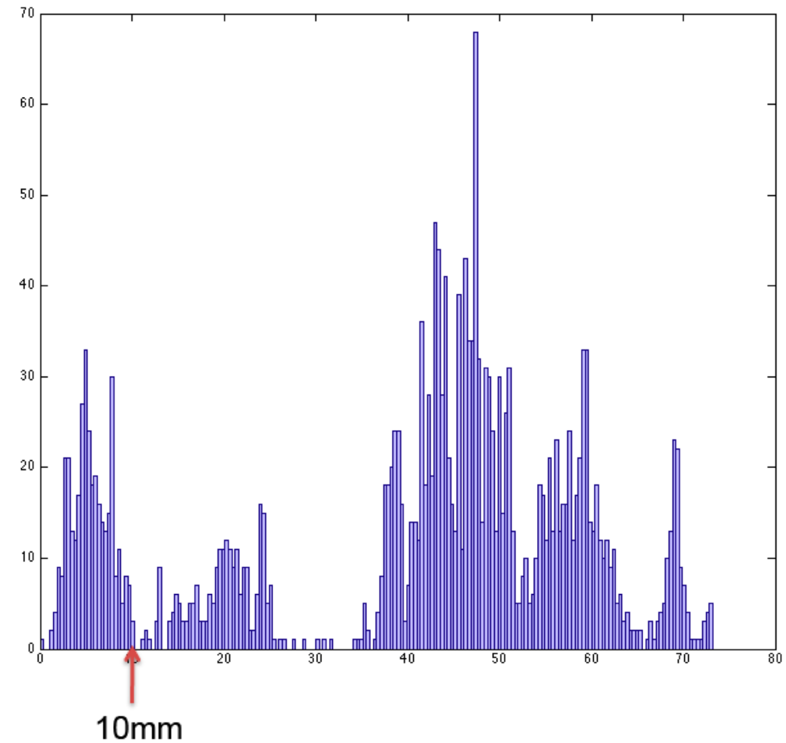
$$\mathbf{Y} = \begin{bmatrix} \psi_0(p_1) & \cdots & \psi_k(p_1) \\ \vdots & \ddots & \vdots \\ \psi_0(p_n) & \cdots & \psi_k(p_n) \end{bmatrix}$$

$$\mathbf{f} = \mathbf{Y}\beta \longrightarrow \beta = (\mathbf{Y}'\mathbf{Y})^{-1}\mathbf{Y}'\mathbf{f}$$

MATLAB demonstration

Discrepancy measure: distance between tracts



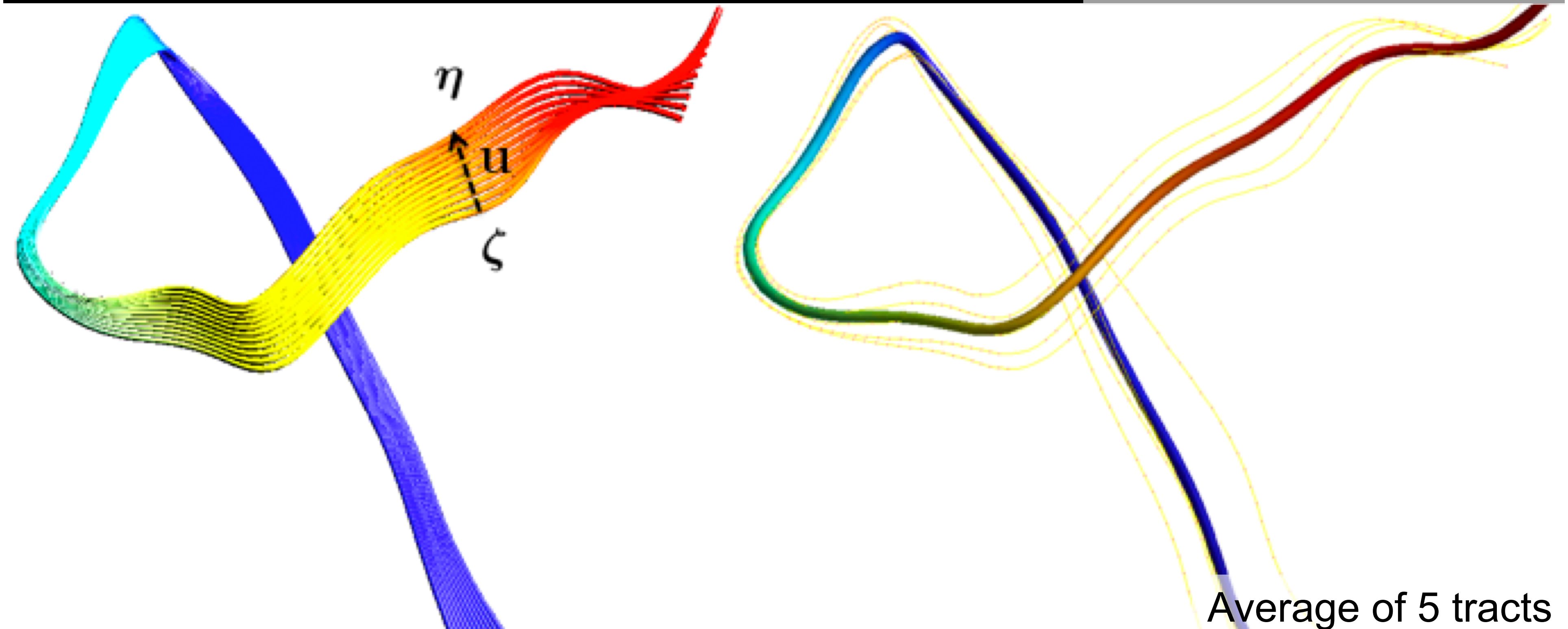


Histogram of discrepancy measure

$$\rho(\boldsymbol{\zeta}, \boldsymbol{\eta}) = \int_0^1 \|\boldsymbol{\zeta}(t) - \boldsymbol{\eta}(t)\|^2 \, dt$$

$$= \int_0^1 \sum_{j=1}^{3} \left[\sum_{l=0}^{k} (\zeta_{lj} - \eta_{lj}) \psi_l(t) \right]^2 dt \;\; = \sum_{j=1}^{3} \sum_{l=0}^{k} (\zeta_{lj} - \eta_{lj})^2$$

Tract alignment



$$\boldsymbol{\eta}(t) = \sum_{l=0}^{k} \boldsymbol{\eta}_l \psi_l(t)$$

$$\boldsymbol{\zeta}(t) = \sum_{l=0}^{k} \boldsymbol{\zeta}_l \psi_l(t)$$

→

optimal displacement

$$\mathbf{u}^*(t) = \arg \min_{u_1, u_2, u_3} \rho(\boldsymbol{\zeta} + \mathbf{u}, \boldsymbol{\eta})$$

Minimum is taken over the subspace spanned by the basis functions.

Define average tract

Given m cosine series representations $\zeta^1, \cdots, \zeta^m$

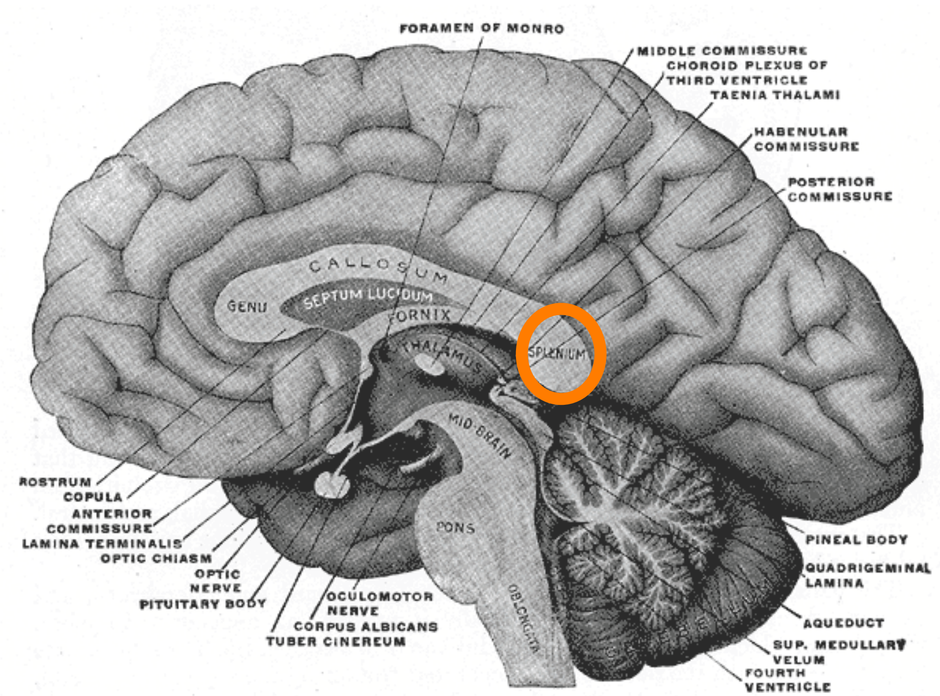
we define the average tract as

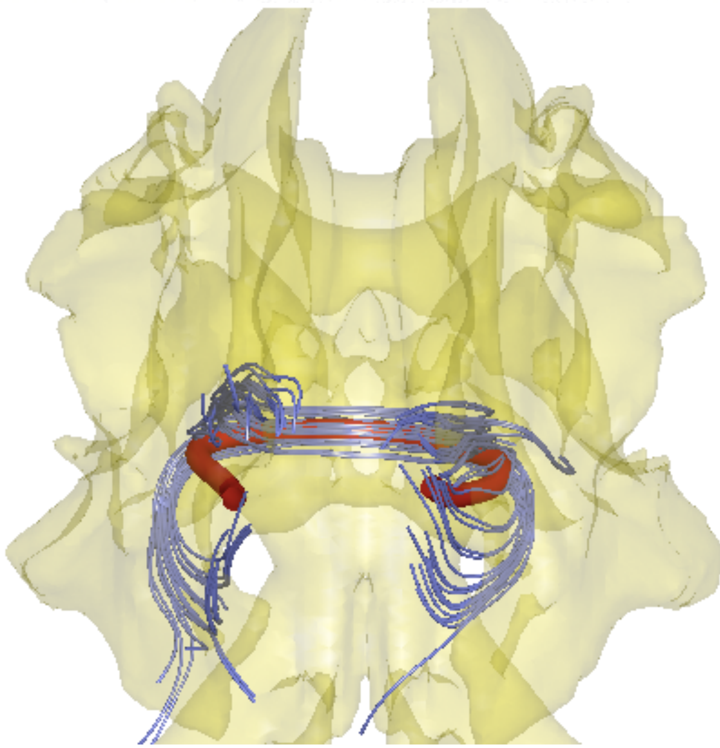
$$\overline{\zeta}(t) = \arg\min_{\zeta} \sum_{j=1}^{m} \rho(\zeta^j, \zeta)$$

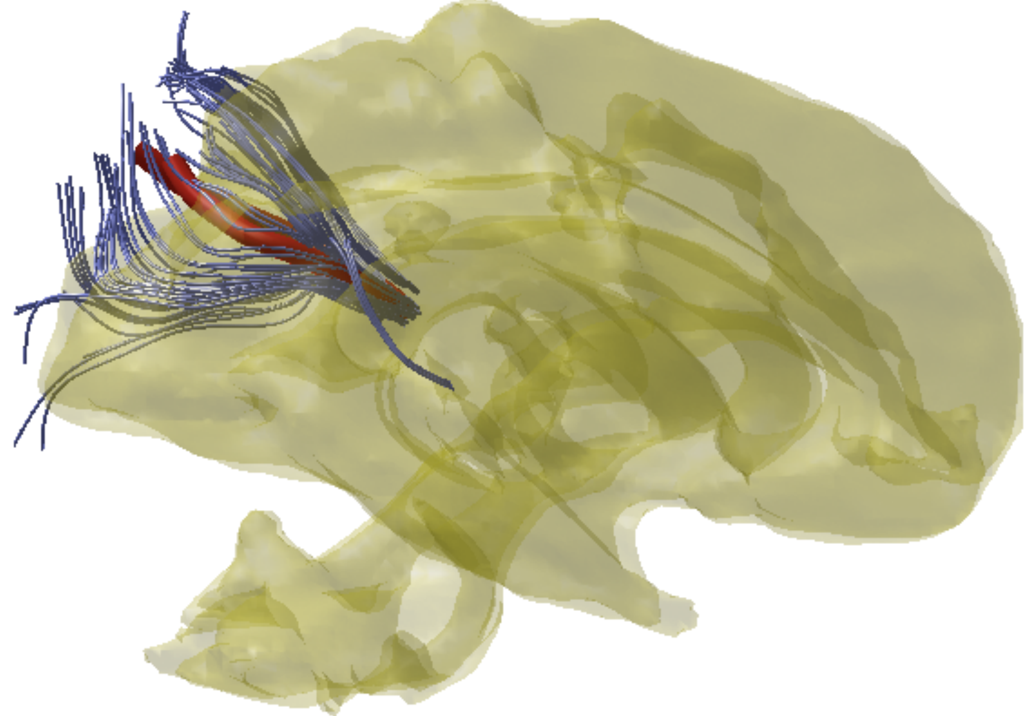
$$= \sum_{l=0}^{k} \overline{\zeta}_l \psi_l(t)$$

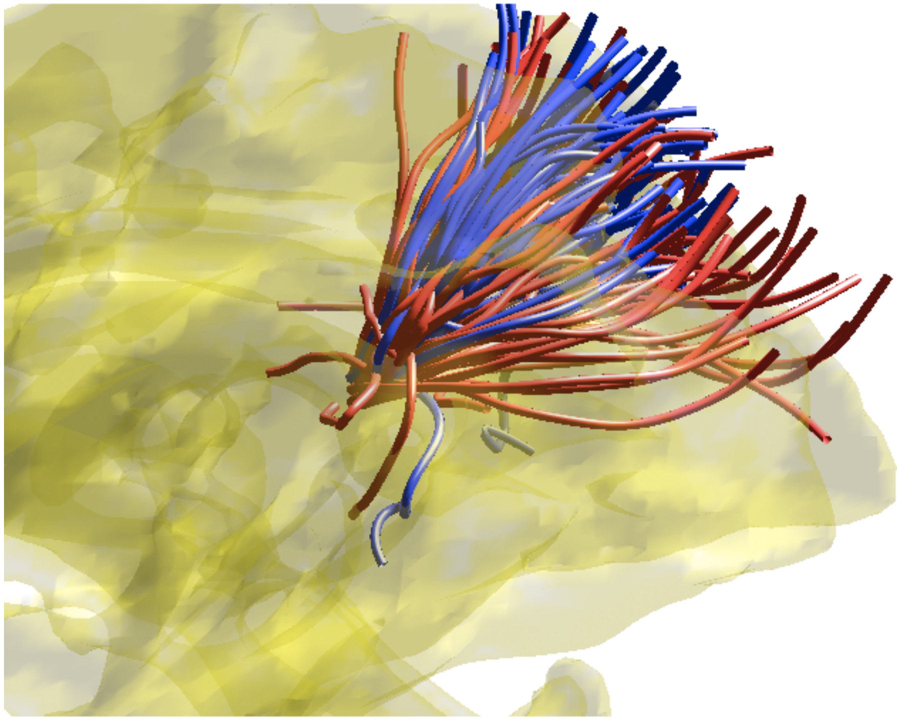
The average tract is simply given by averaging coefficients.

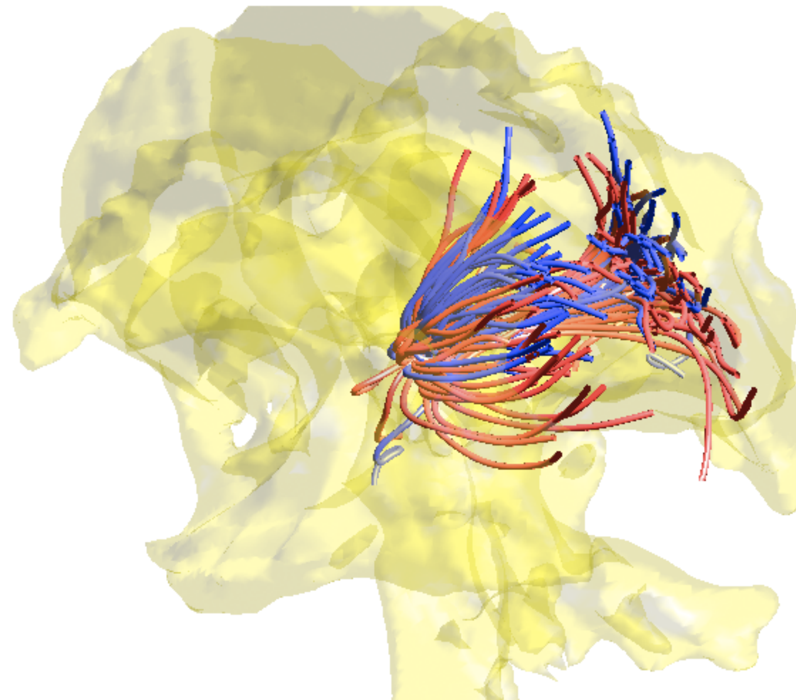
Average tracts passing through the splenium of the corpus callosum



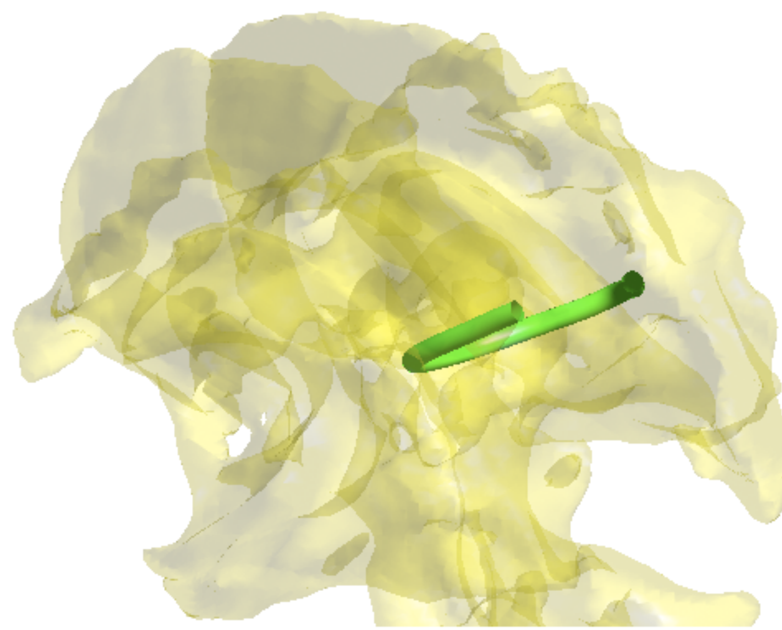




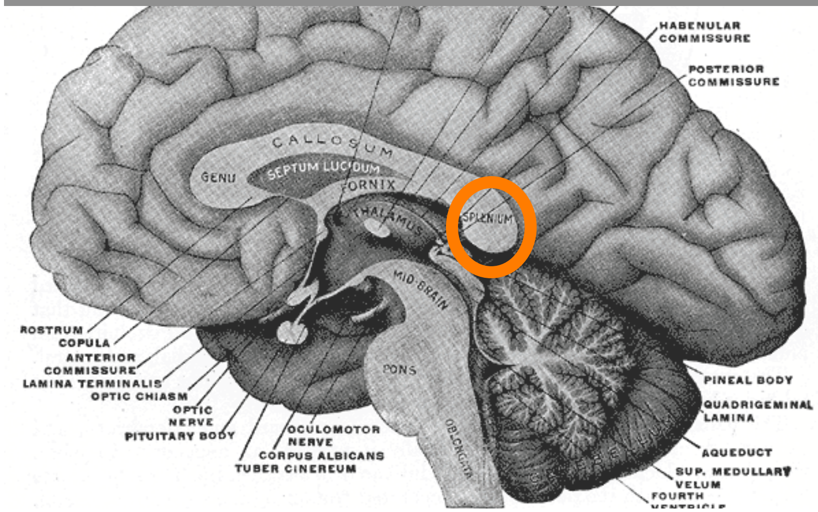




Average tracts across 74 subjects. Averaged within each subject (42 autistic 32 control)

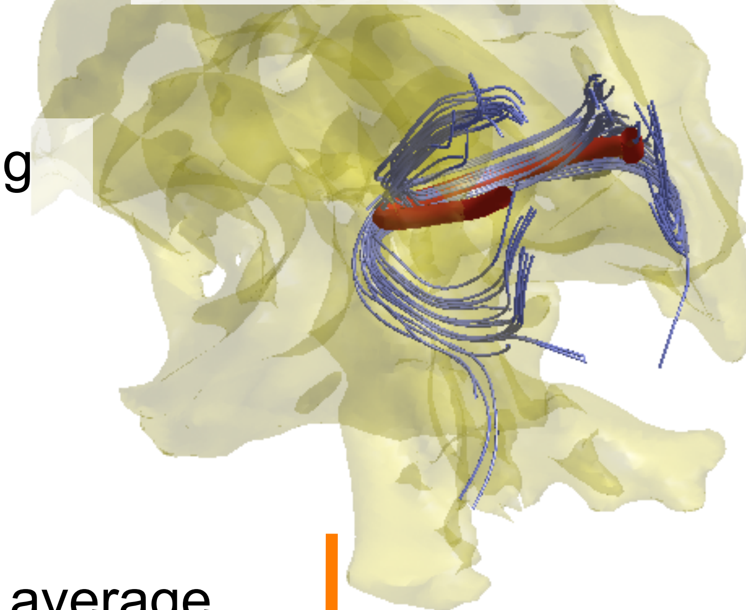


Fiber concentration analysis using cosine series representation

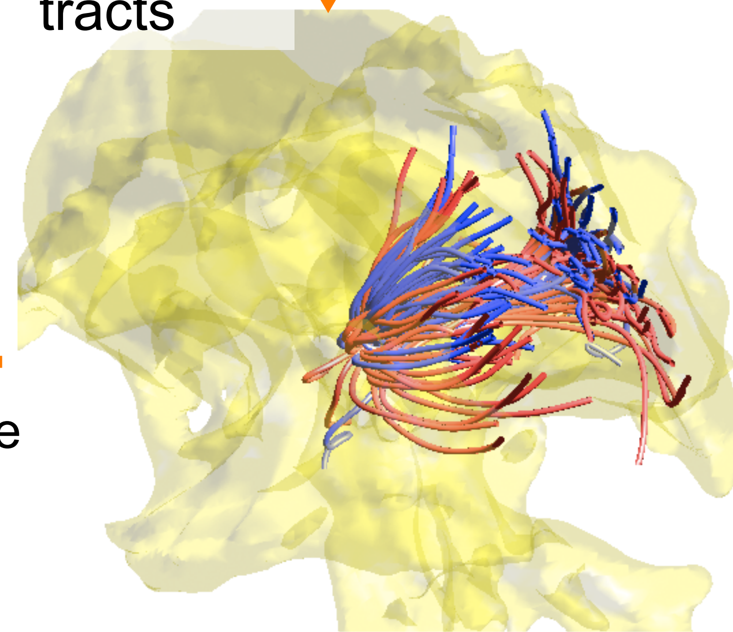


tracts passing through spleninum

Chung et al., 2009, EMBC

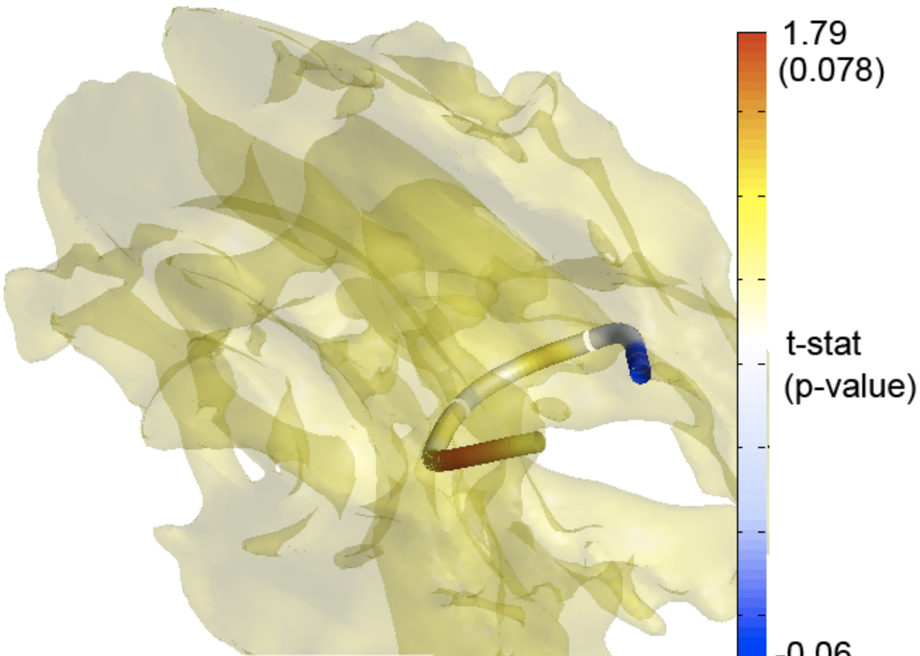


average tracts



42 autistic & 32 control

two sample t-test



control - autism

Inference on representation

Compare tract shapes between the groups

$$\zeta^1, \cdots, \zeta^m \longleftrightarrow \eta^1, \cdots, \eta^n$$

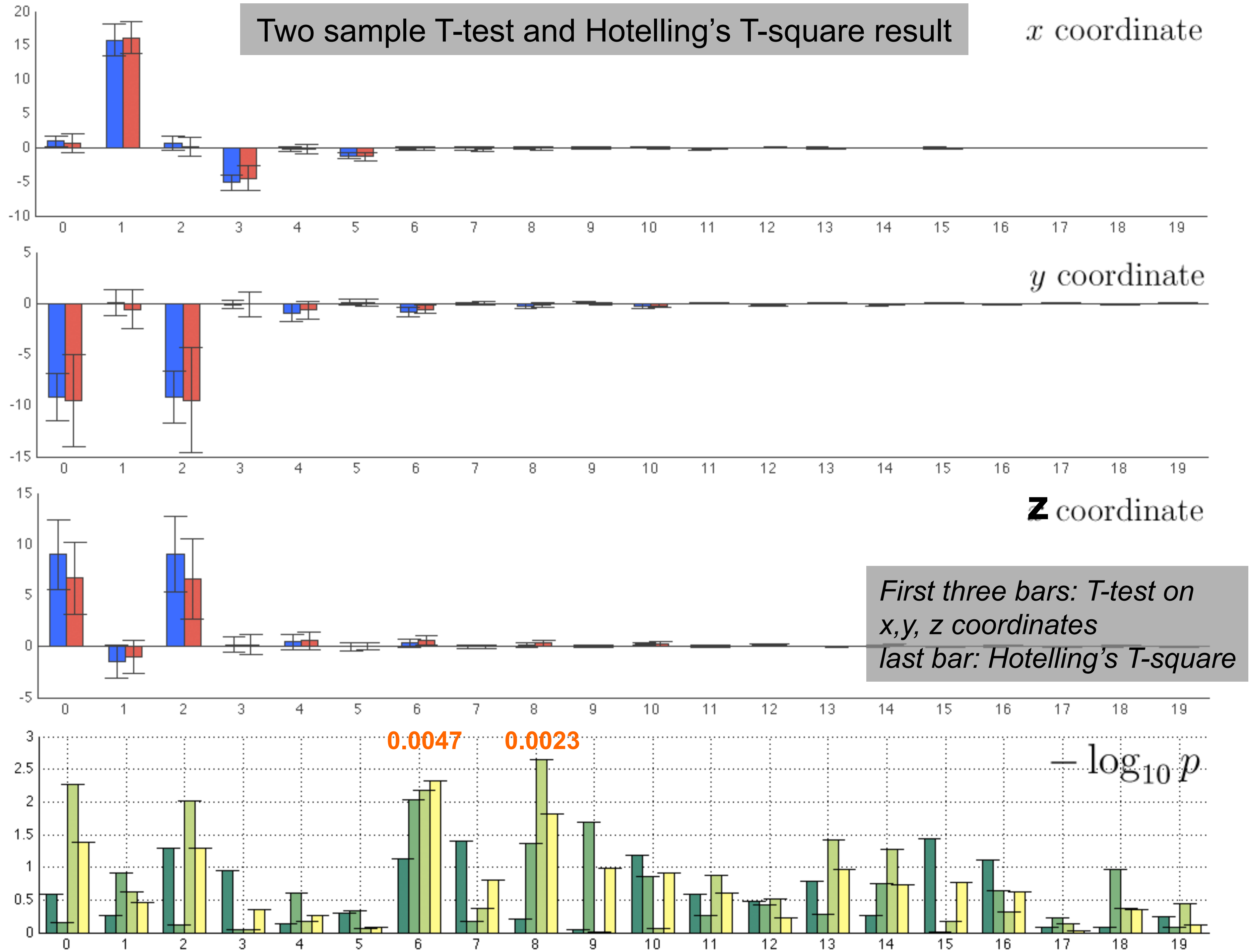
This is done by testing the equality of mean tracts between the groups

$$H_0 : \overline{\zeta} = \overline{\eta}$$

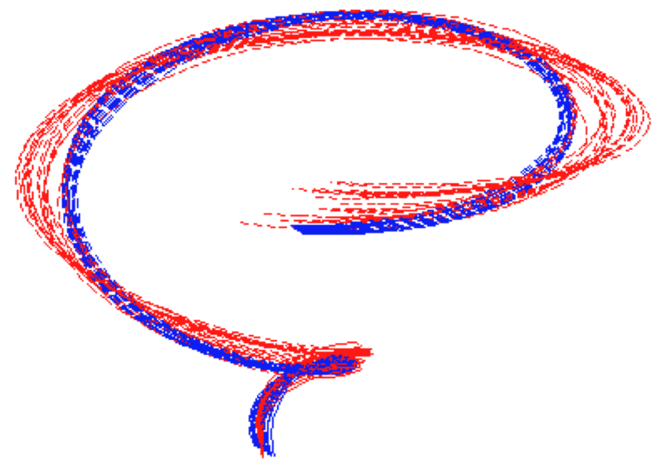
Equivalent hypothesis

$$H_0' : \overline{\zeta}_1 = \overline{\eta}_1, \cdots, \overline{\zeta}_k = \overline{\eta}_k$$

Two cosine representations are equivalent if and only if the coefficients match


Two sample T-test and Hotelling's T-square result
x coordinate
y coordinate
z coordinate
First three bars: T-test on x,y, z coordinates
last bar: Hotelling's T-square
$-\log_{10} p$
0.0047
0.0023

Validation via Random Simulation



We have performed a simulation study to proposed framework can detect small tract between two collection of similarly shaped the parametric curve

$$(18) \qquad (x, y, z) = (s \sin s, s \cos s, s), s \in [0, 10]$$

as a basis for simulation, we have generated two groups of random curves. This gives a shape of a spiral with increasing radius along the z-axis. The first group consists of 20 curves generated by

$$(x, y, z) = (s \sin(s + e_1), s \cos(s + e_2), s + e_3),$$

where $e_1, e_2, e_3 \sim N(0, 1)$. The second group consists of 20 curves generated by

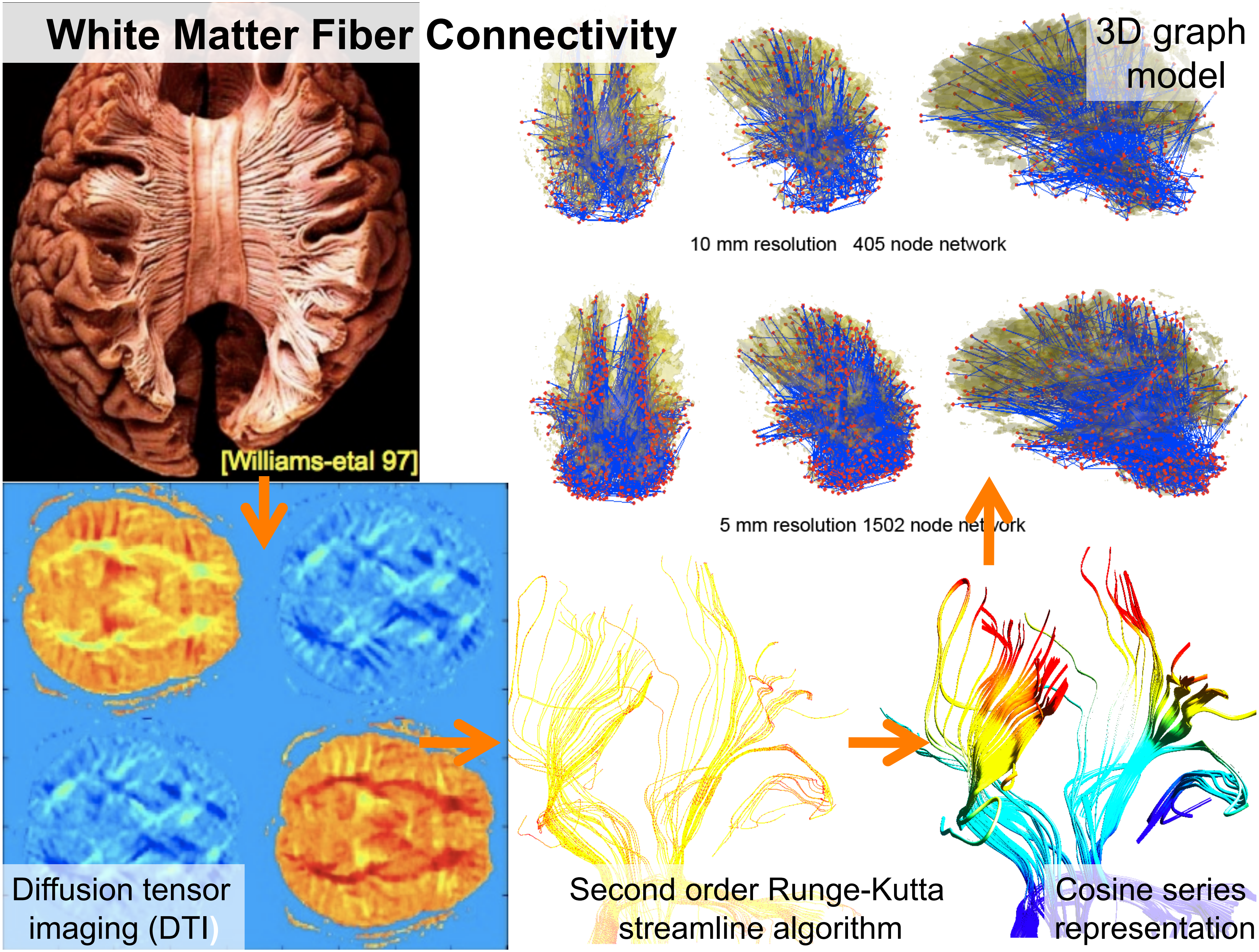
$$(x, y, z) = ((s + e_4) \sin(s + 0.1), (s + e_5) \cos(s - 0.1), s - 0.1),$$

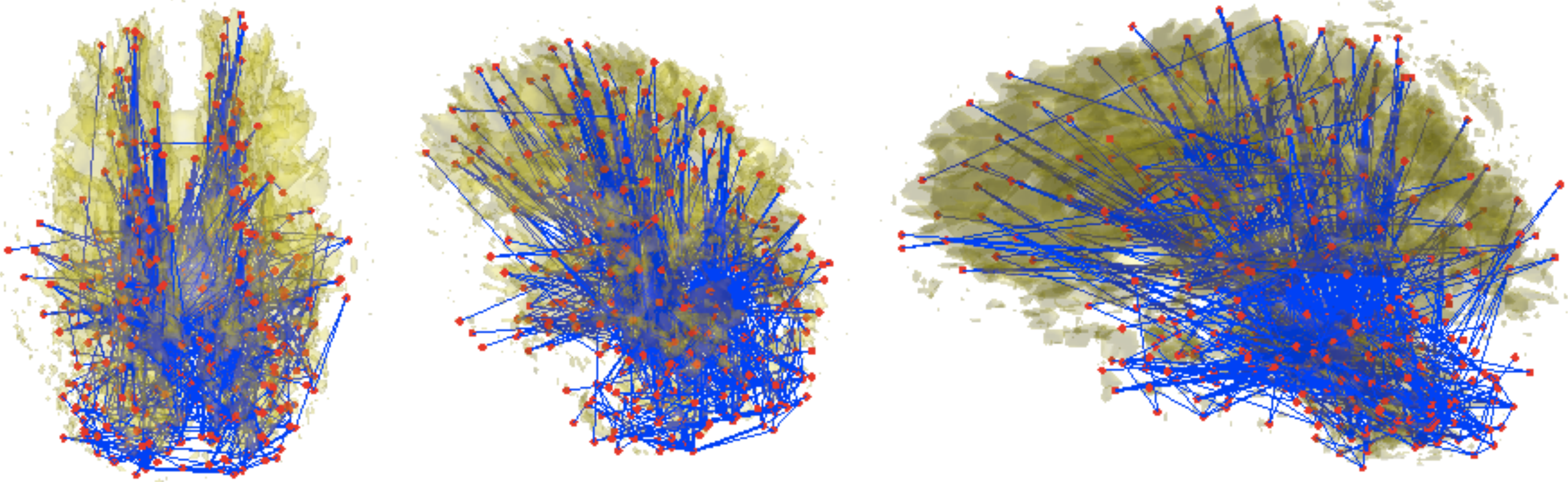
where $e_4, e_5 \sim N(0, 0.2^2)$. The non-additive noise is given

MATLAB demonstration

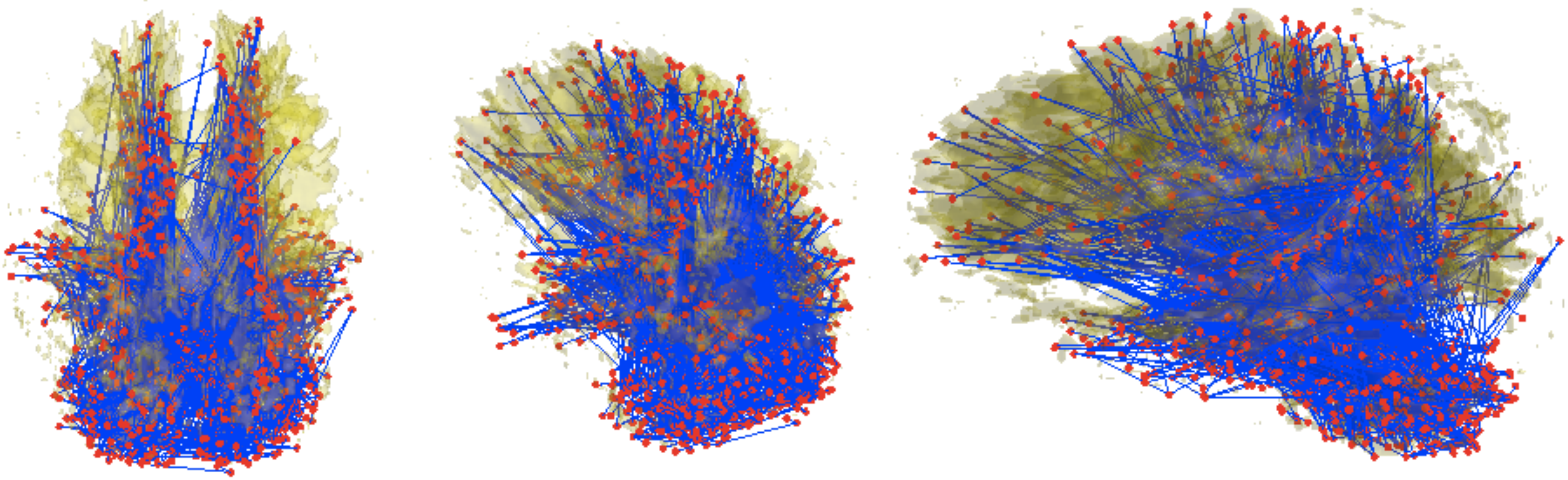
DTI-based brain connectivity analysis

White Matter Fiber Connectivity



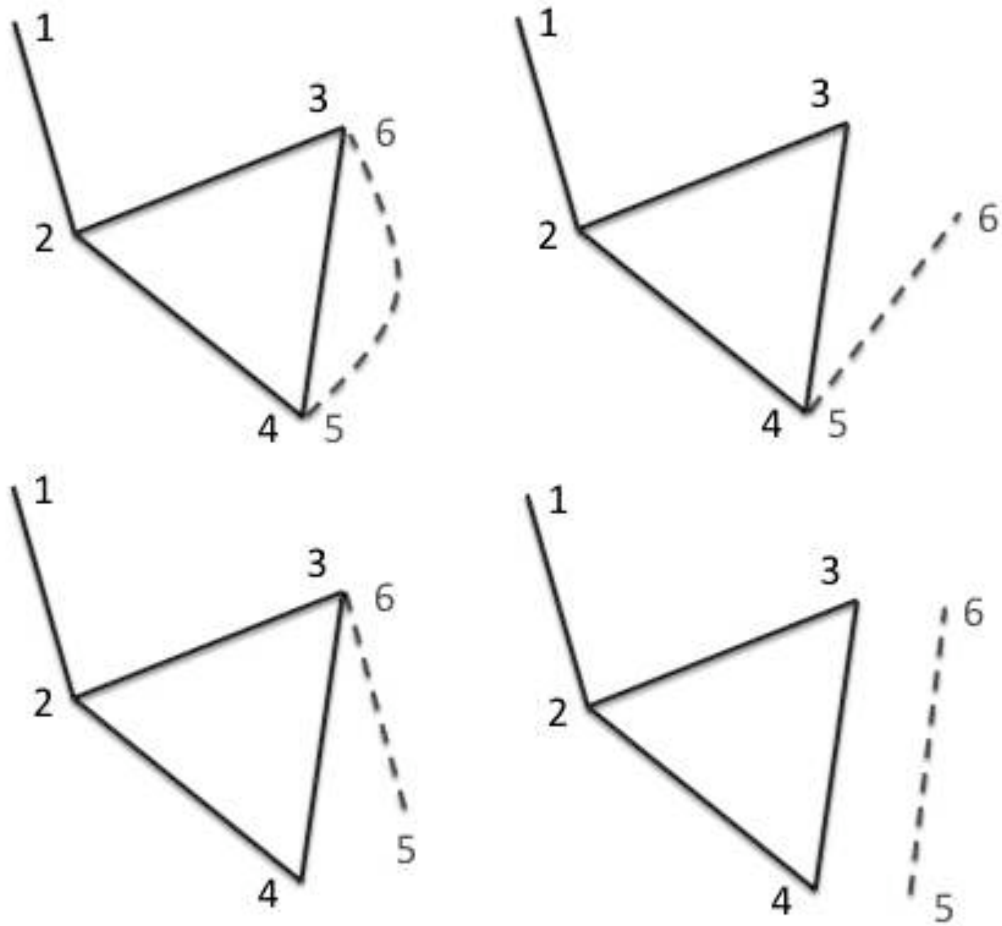


10 mm resolution   405 node network

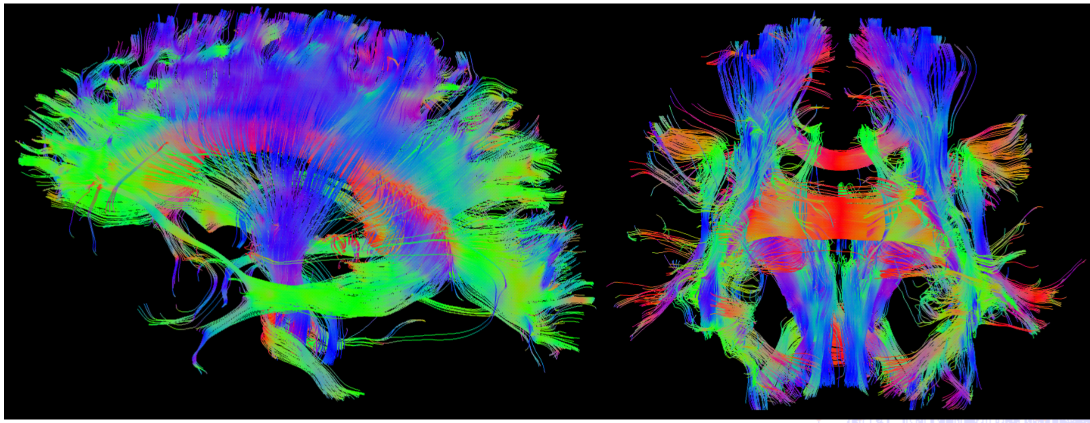


5 mm resolution 1502 node network

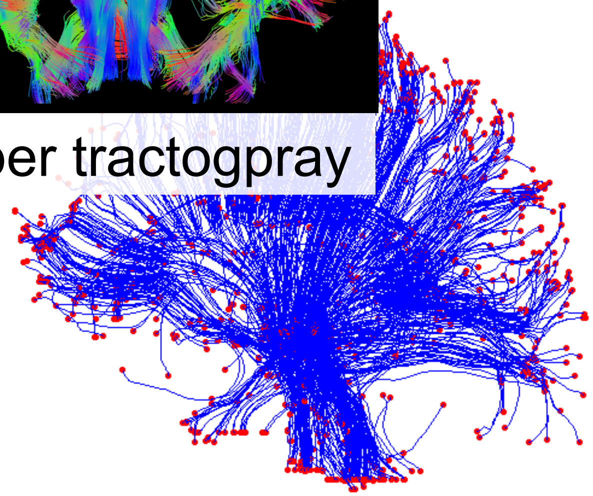
Building DTI-based brain network graph



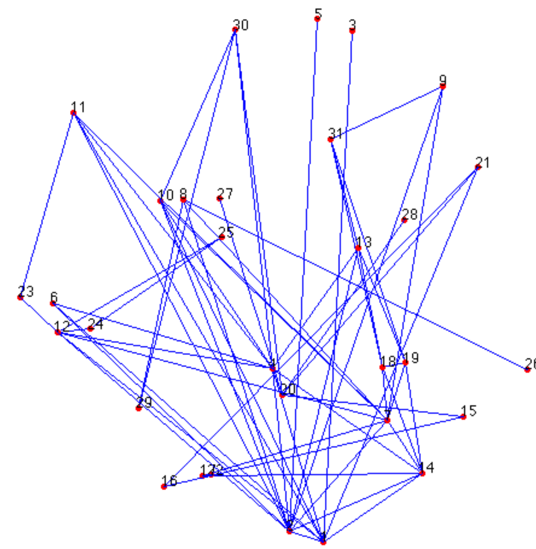
Scalable iterative structural network construction

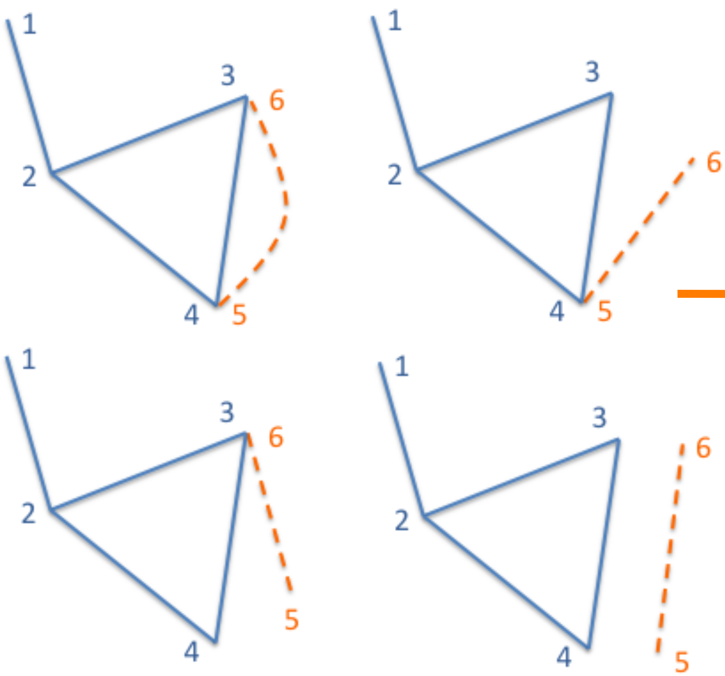


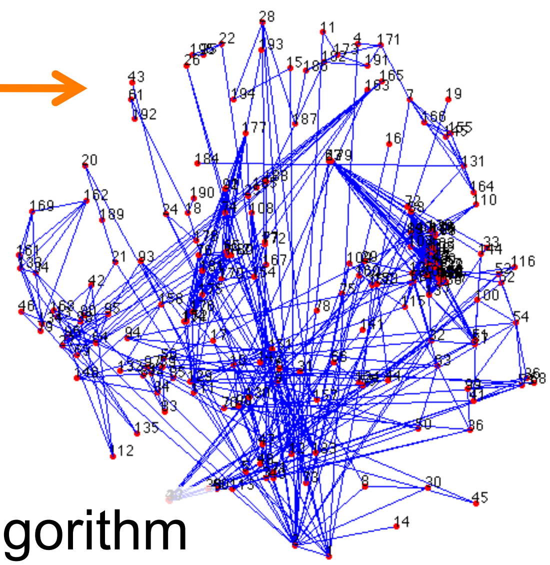
Whole brain white matter fiber tractogpray

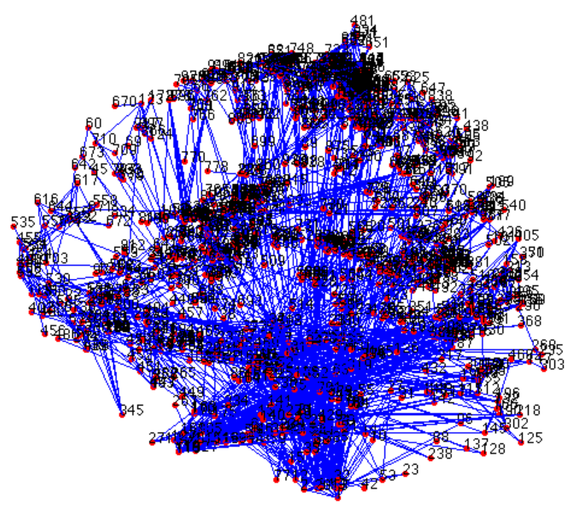


Scalable 3D graph









Iterative graph construction algorithm

MATLAB demonstration

Brain connectivity analysis

Predicting human resting-state functional connectivity from structural connectivity

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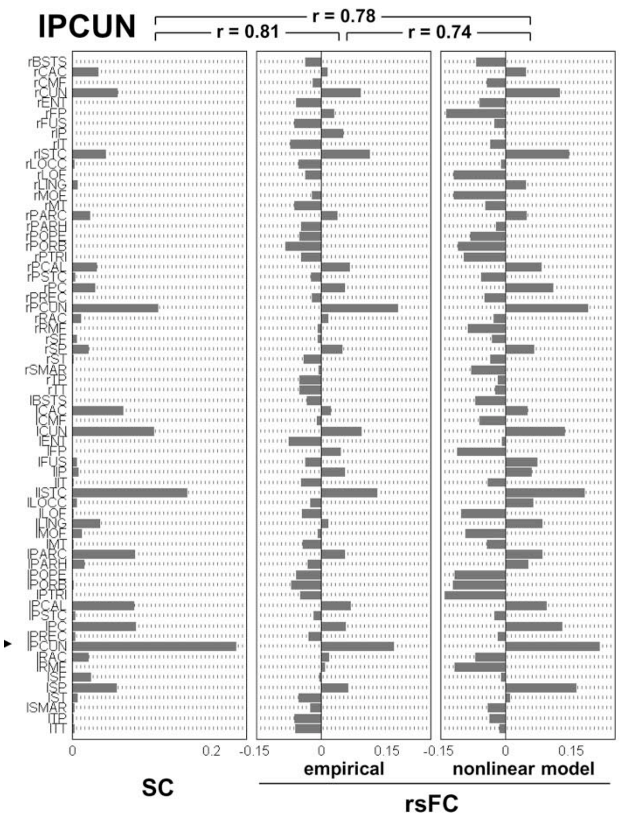

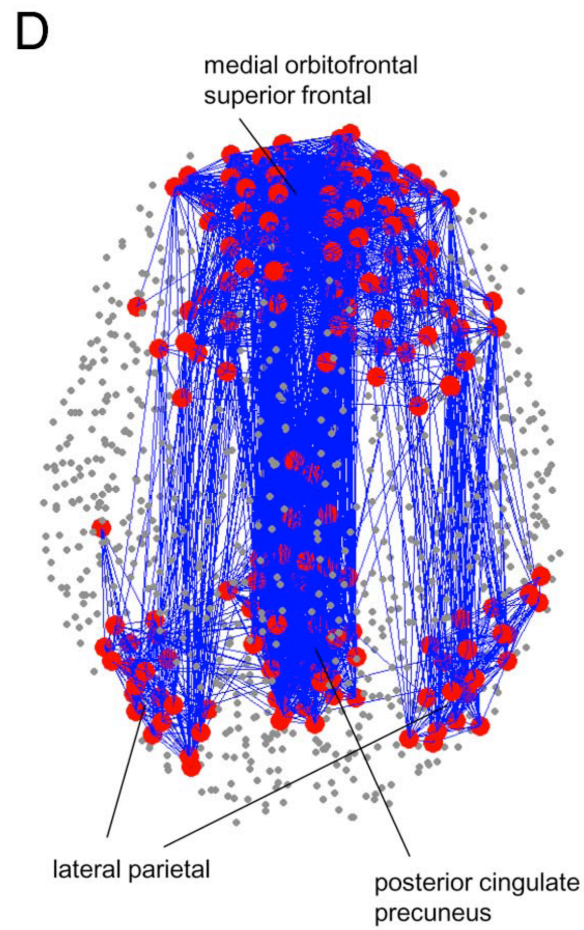

NeuroImage

www.elsevier.com/locate/ynimg
NeuroImage 32 (2006) 228 – 237

Partial correlation for functional brain interactivity investigation in functional MRI

Guillaume Marrelec,[a,b,c,*] Alexandre Krainik,[d,e] Hugues Duffau,[a,b,f] Mélanie Pélégrini-Issac,[a,b] Stéphane Lehéricy,[g] Julien Doyon,[a,b,c] and Habib Benali[a,b,c]

Originally Keith J. Worsley's idea

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NeuroImage 31 (2006) 993 – 1003

Mapping anatomical correlations across cerebral cortex (MACACC) using cortical thickness from MRI

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MACACC methods—correlations

Cortical cross-correlations are obtained using simple linear correlations whose strength is measured using Pearson's r.

$$r = \frac{\sum T_i T_j - \frac{\sum T_i \sum T_j}{N_s}}{\sqrt{\left(\sum T_i^2 - \frac{\left(\sum T_i\right)^2}{N_s}\right)\left(\sum T_j^2 - \frac{\left(\sum T_j\right)^2}{N_s}\right)}} \qquad (1)$$

Cross correlation on cortical thickness

Seminar on October 23, 2009

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Research field: Statistical geometry and applications

Wishart Mixtures and Diffusion Tensor Imaging

The Wishart distribution is a natural distribution on the space of positive definite symmetric matrices. It is derived from the sample covariance matrix coming from a multivariate normal distribution. Combining several Wishart distributions with different covariance parameters therefore leads to Wishart mixtures which has practical relevance to Diffusion Tensor Imaging which is a modern in vivo brain imaging technique that tracts the whole brain white matter fibers. Statistical estimation of the mixing distribution will be presented.

Forward model selection framework

$$\zeta_i(t) = \sum_{l=0}^{k} c_{li}\psi_l + \epsilon_i(t)$$

When do we stop the expansion?
Why did we choose degree 19?

first presented in [10] [11]. Although increasing the degree of the representation increases the goodness-of-fit, it also increases the number of estimated coefficients linearly. So it is necessary to stop the series expansion at the degree where the goodness-of-fit and the number of coefficients balance out.

Assuming up to the $(k-1)$-degree representation is proper in (9), we determine if adding the k-degree term is statistically significant by testing

$$H_0 : c_{ki} = 0.$$

Let the k-th degree *sum of squared errors* (SSE) for the i-th coordinate be

$$\mathrm{SSE}_k = \sum_{j=1}^{n} \left[\zeta_i(t_j) - \sum_{l=0}^{k} \widehat{c_{li}} \psi_l(t_j) \right]^2,$$

optimal degree = 13.94 ± 7.02
upper 80 percentile = 19

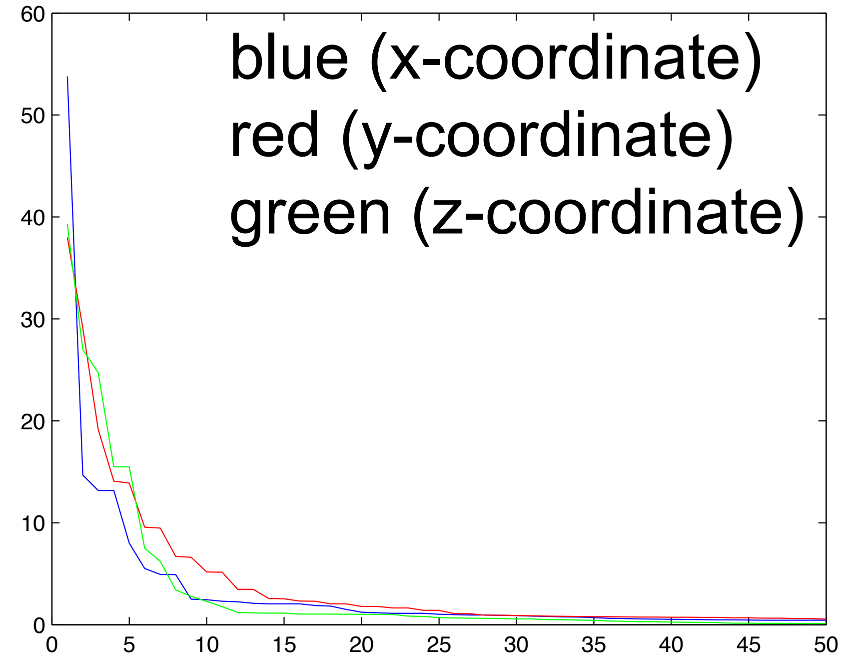
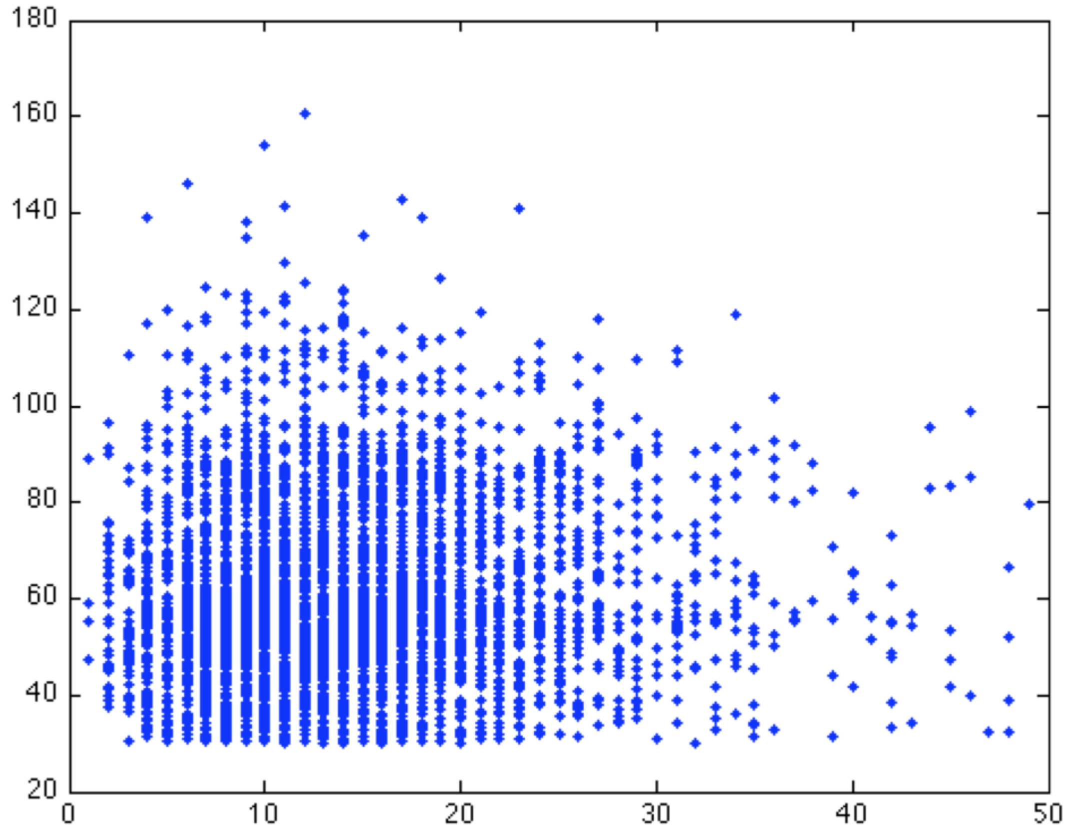


Figure 3. As the degree k increases, SSE decreases until it flattens out. So it is reasonable to stop the series expansion when the decrease in SSE is no longer significant. Under H_0, the test statistic F follows

$$F = \frac{\mathrm{SSE}_{k-1} - \mathrm{SSE}_k}{\mathrm{SSE}_{k-1}/(n-k-2)} \sim F_{1,n-k-2},$$

the F-distribution with 1 and $n-k-2$ degrees of freedom. We compute the F statistic at each degree and stop increasing the degree of expansion if the corresponding p-value first becomes bigger than the pre-specified significance $\alpha = 0.01$.

Is the optimal degree dependent on the length of a tract? No!



It's more related to bending and curvature, which in turn is related to spatial frequency of tract shape.

length of tract (vertical axis) vs. optimal degree (horizontal axis)