

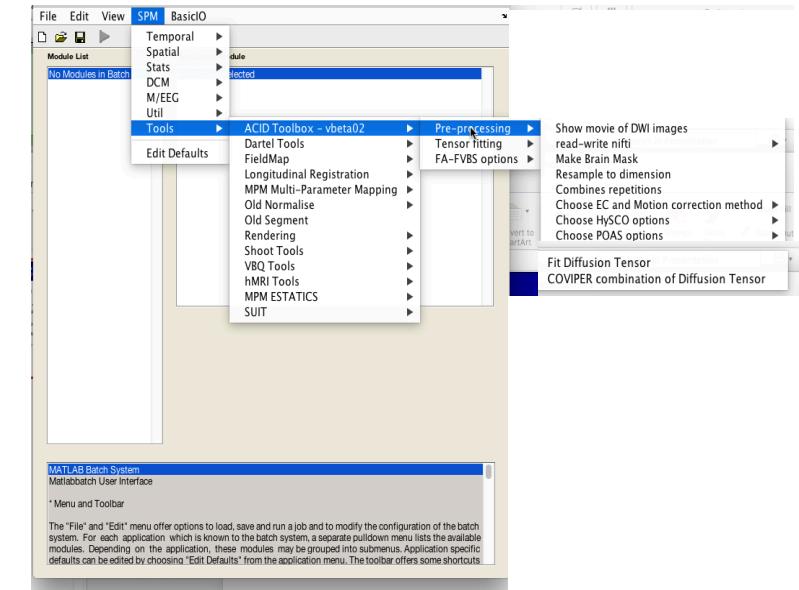


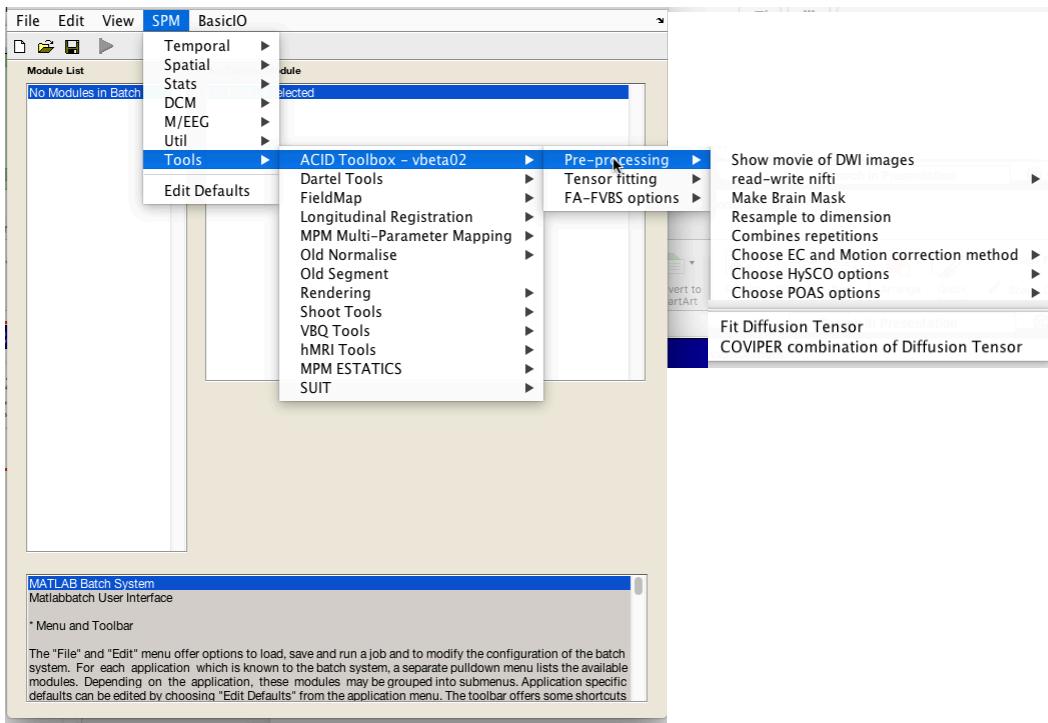
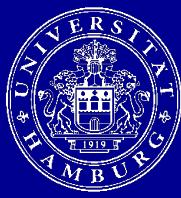
# Artefact Correction In Diffusion MRI

## ACID SPM toolbox

Siawoosh Mohammadi

Department of Systems Neuroscience  
University Medical Center Eppendorf  
Hamburg, Germany  
[s.mohammadi@uke.de](mailto:s.mohammadi@uke.de)





## Preprocessing:

- Eddy current and motion
- HySCO (EPI distortions)
- msPOAS (adaptive smoothing)
- Vibration Artifacts ( DTI model)
- Spinal Cord Branch – *in prep*
- Rican Noise Bias Correction – *in prep.*

## Signal Models:

- DTI (ols, wols, robust fitting)
- Diffusion Kurtosis Imaging
- NODDI-DTI

**Open-Access: [www.diffusiontools.com](http://www.diffusiontools.com)**

**Questions/queries to Siawoosh Mohammadi**  
**s.mohammadi@uke.de**



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Hamburg-Eppendorf

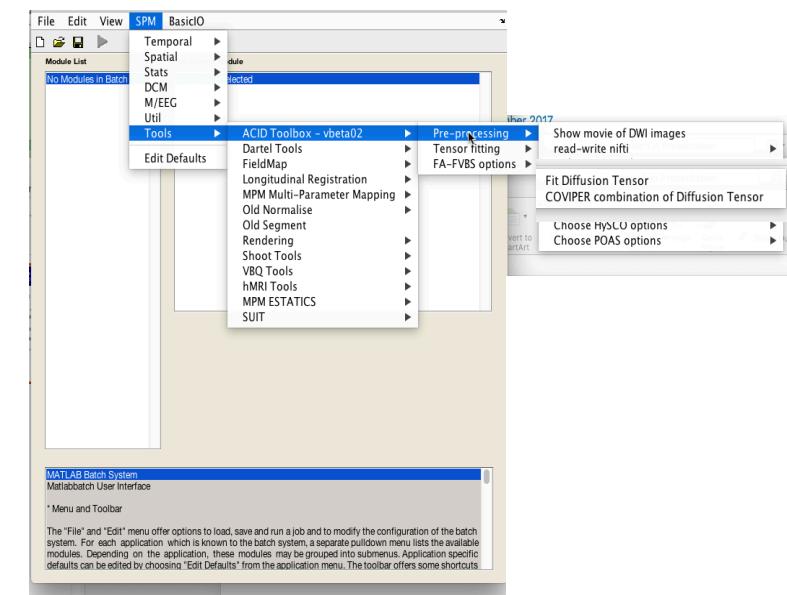
# Artefact Correction In Diffusion MRI

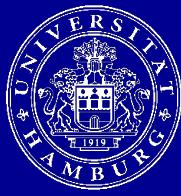
## ACID SPM toolbox



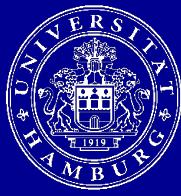
Siawoosh Mohammadi

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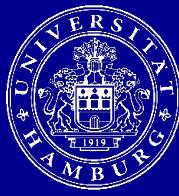




- 30-60 min intro to ACID toolbox
- hands-on application:
  - Installation,
  - ECMOCO,
  - msPOAS,
  - HySCO,
  - Tensor fitting
- Open discussion

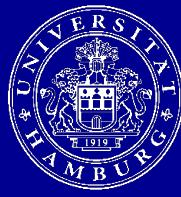


- One main goal of our group: "*In-vivo histology using MRI*"
- Standard DTI is sensitive to microstructure but unspecific
- Advanced diffusion MRI might improve specificity
- Diffusion MRI suffers from various artifacts
- Advanced diffusion MRI requires correcting artifacts
- ACID toolbox provides ***principled, model-based, and peer-reviewed correction methods*** to correct artifacts and thus enable advanced diffusion MRI



# Outline of this talk

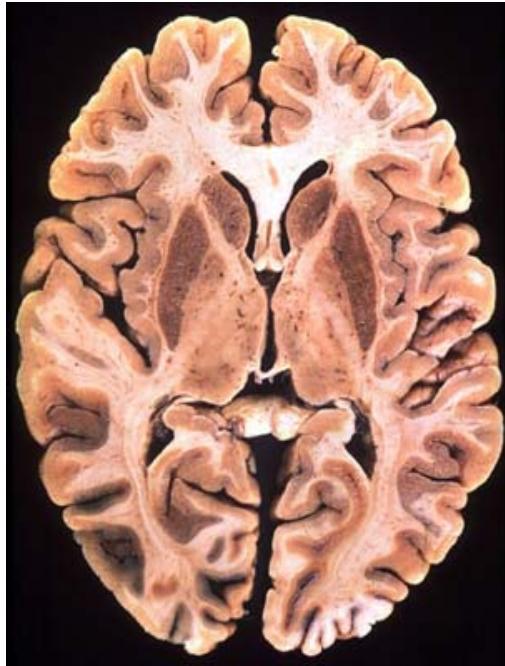
- Diffusion MRI: why, how, and what does it mean?
- Pre-processing steps
  - Eddy current and motion correction
  - Susceptibility artefacts correction
  - Vibration artefact correction
  - Position-orientation adaptive smoothing
- Diffusion models
  - Weighted Ordinary Least Squares, Robust Tensor Fitting
  - Kurtosis Tensor Imaging
  - NODDI-DTI



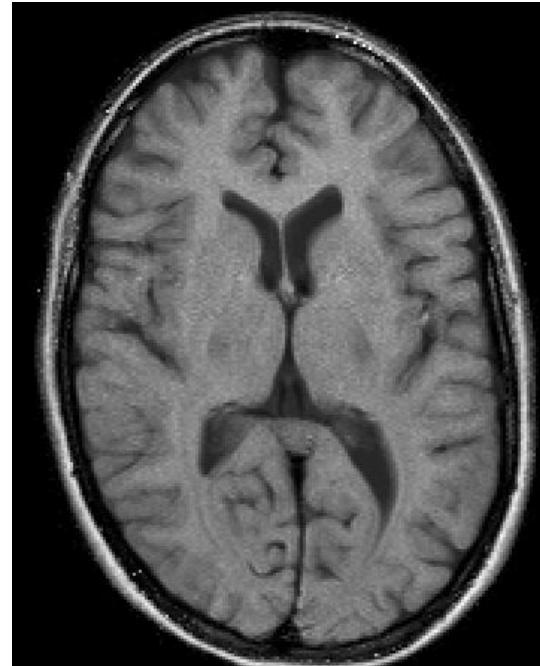
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# Why is diffusion more interesting than standard structural imaging?



**Histology**

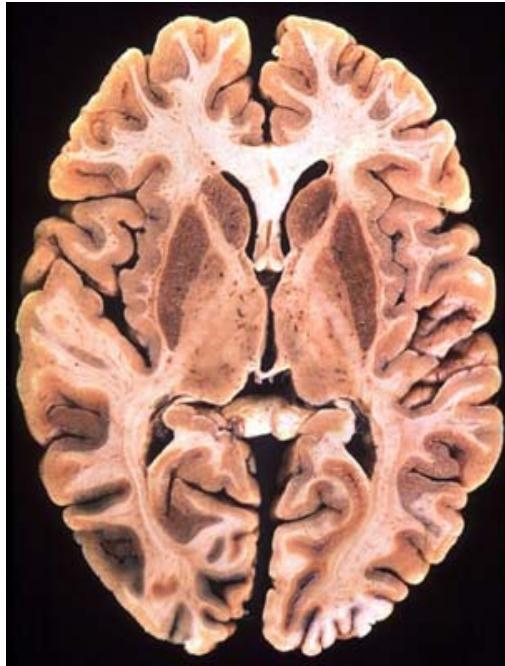


**T1w image**

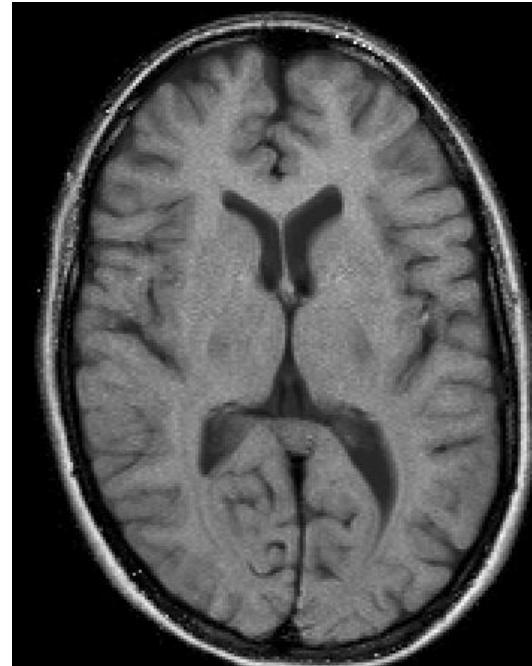


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# Diffusion MRI reveals microstructural information



**Histology**



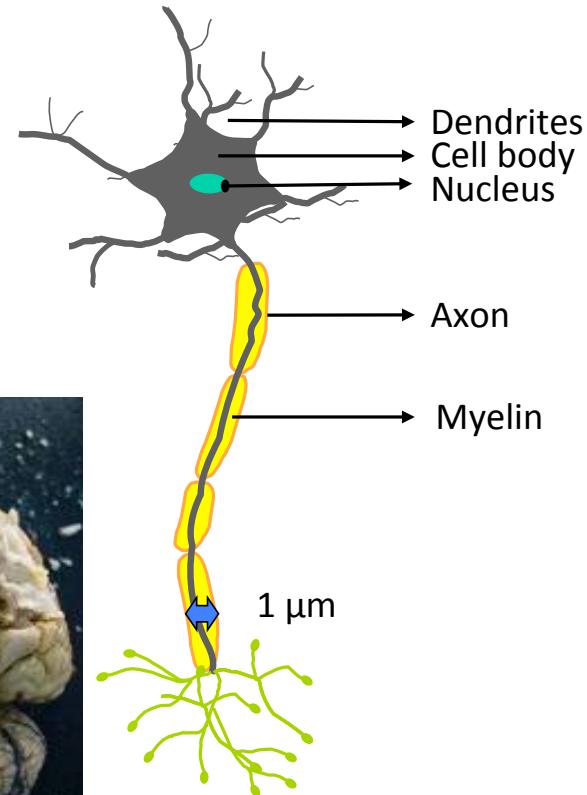
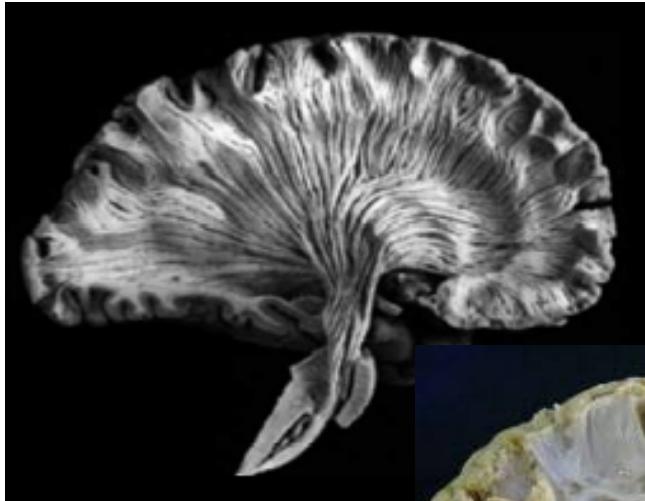
**T1w image**



**DTI index map**

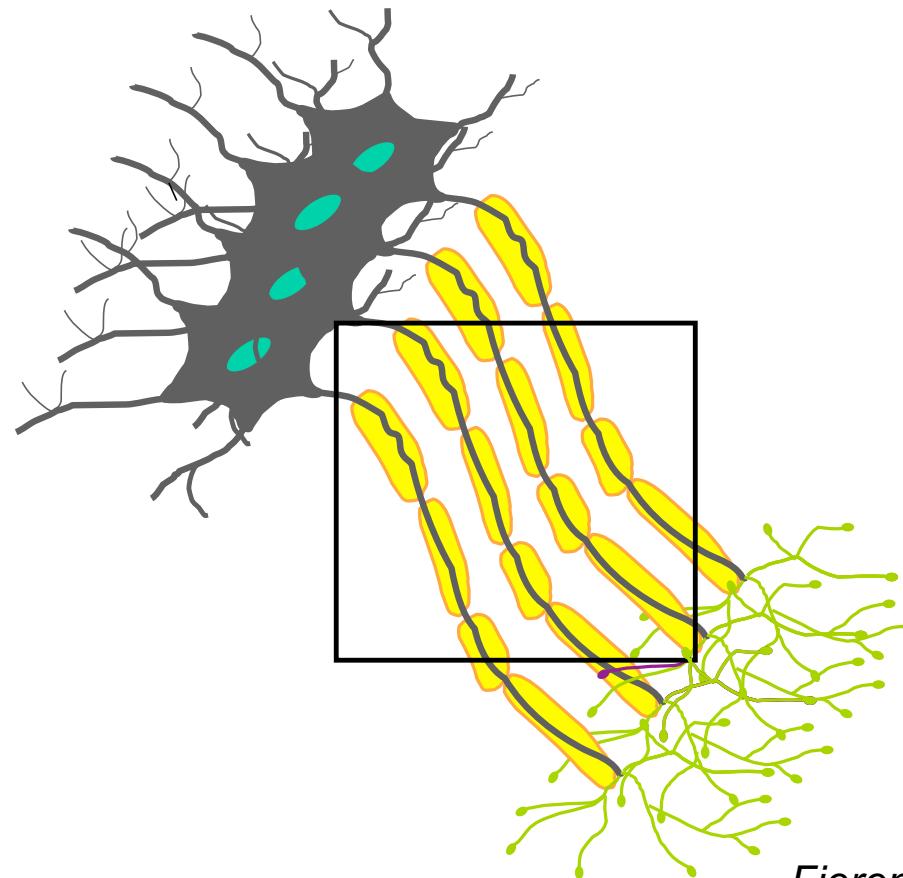


# Main features of fibers in the white matter

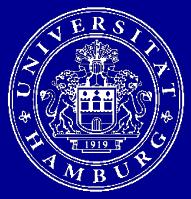


*Fieremans, ESMRMB, 2015*

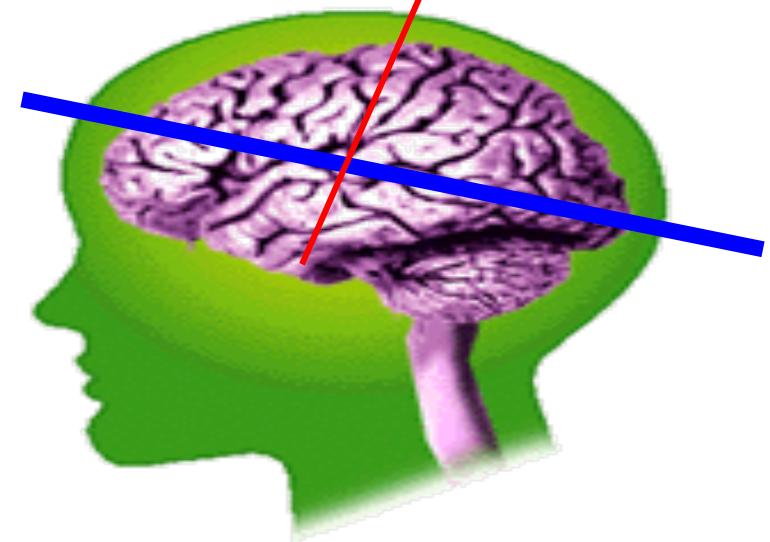
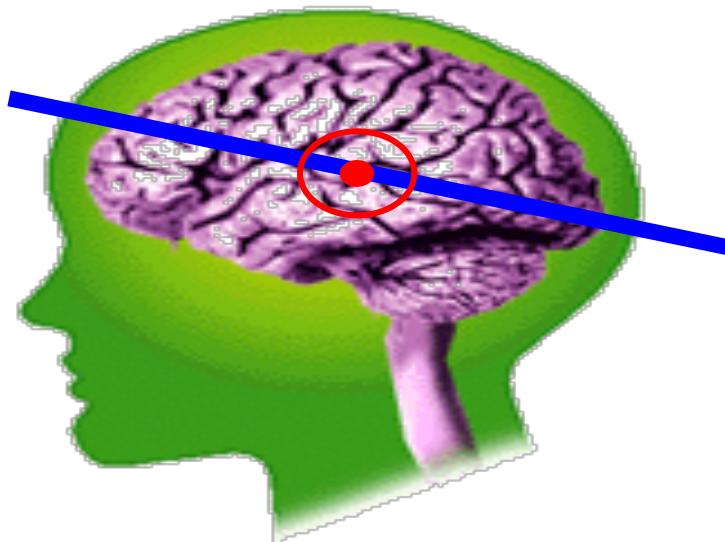
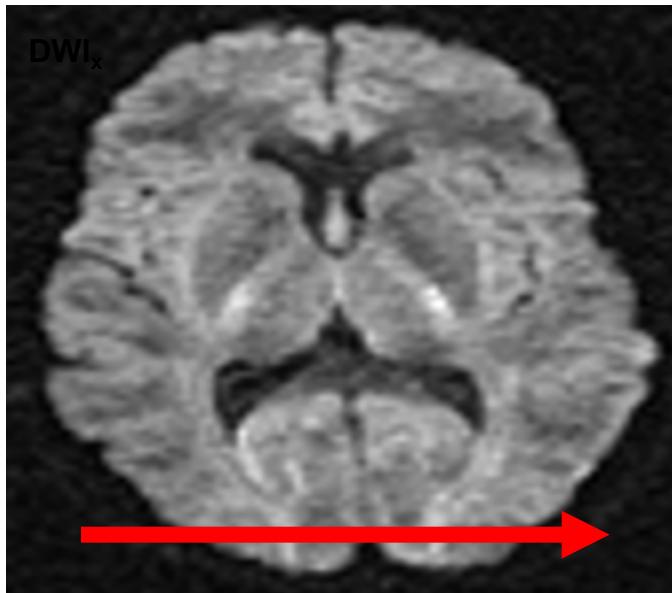
## Aligned axons in fiber pathways

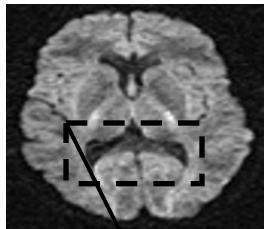


*Fieremans, ESMRMB, 2015*

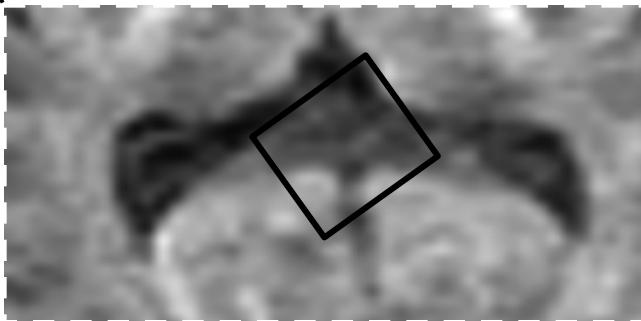


# Diffusion weighted images

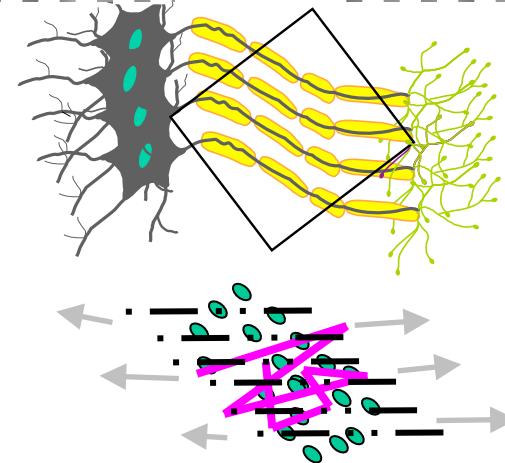
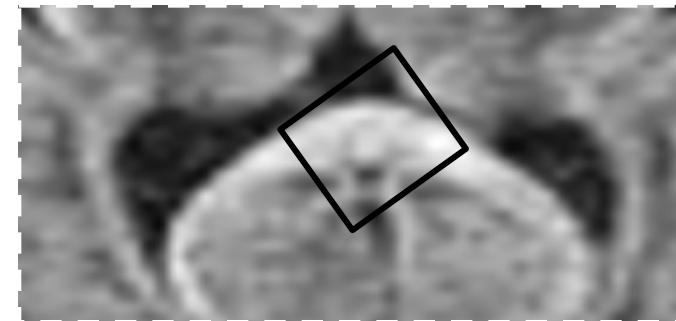




$$\vec{G}^D = \begin{pmatrix} G_x & 0 & 0 \end{pmatrix}$$



$$\vec{G}^D = \begin{pmatrix} 0 & 0 & G_z \end{pmatrix}$$

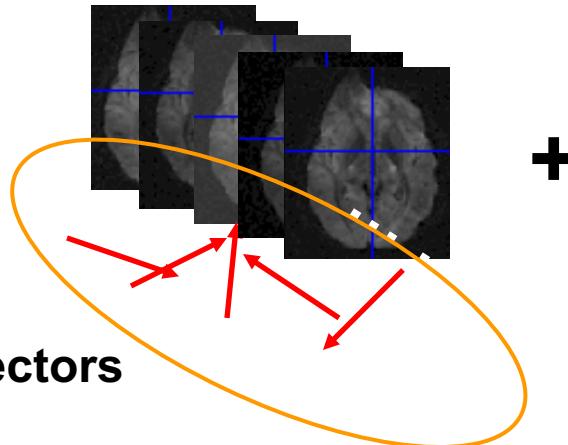




# What do we need for diffusion MRI?

**Shell 1**  
(b-value e.g 1000 s/mm<sup>2</sup>)

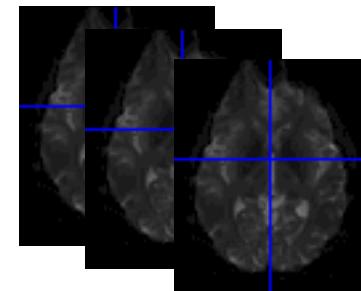
*n* DW images



+

**Shell 0**  
(b-value e.g 0 or 100 s/mm<sup>2</sup>)

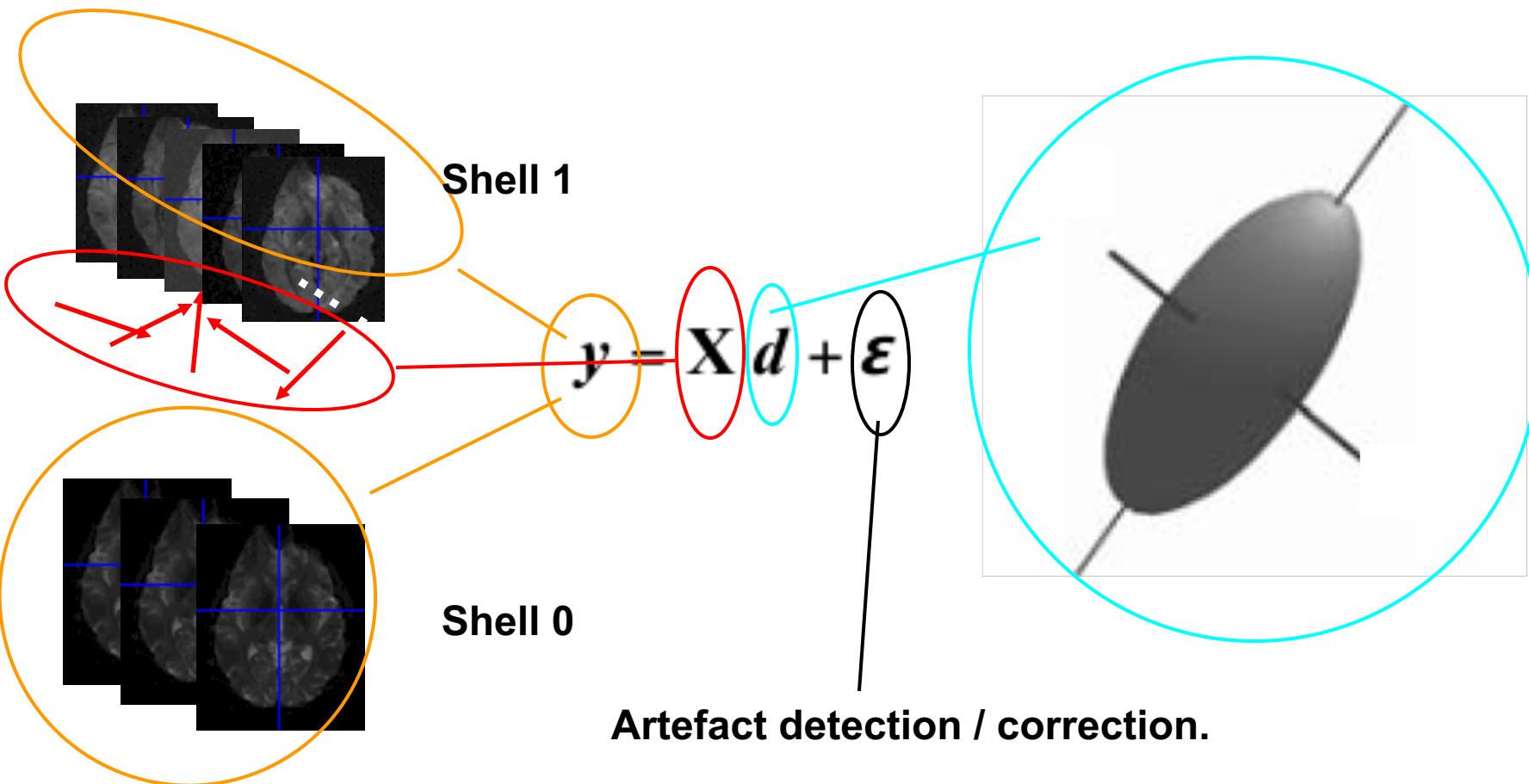
*m* reference images

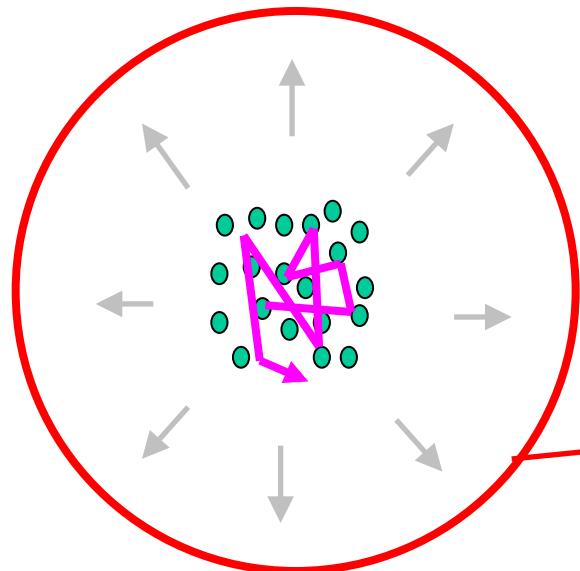


+

**Model**

# The general linear model framework for diffusion MRI





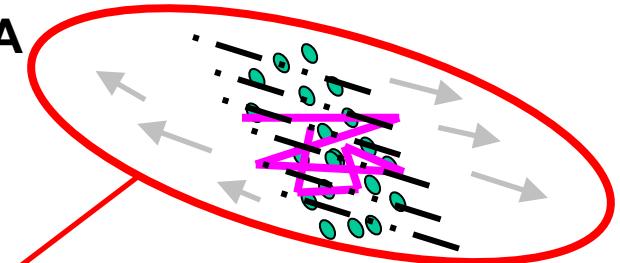
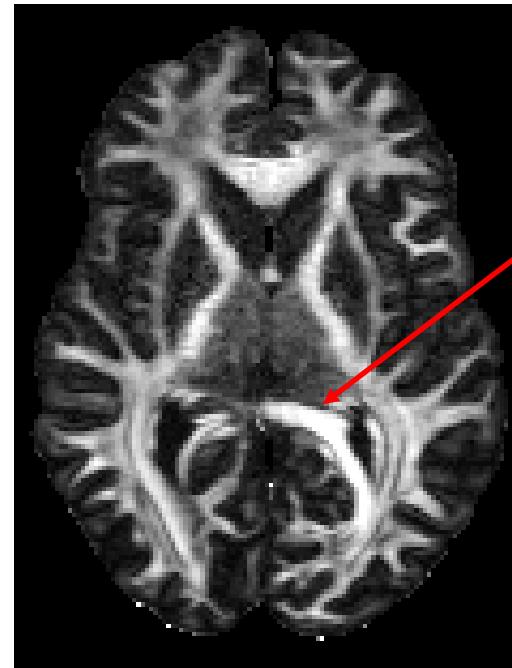
CSF: Isotropic diffusion

## Fractional anisotropy - FA





## Fractional anisotropy - FA

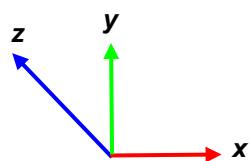
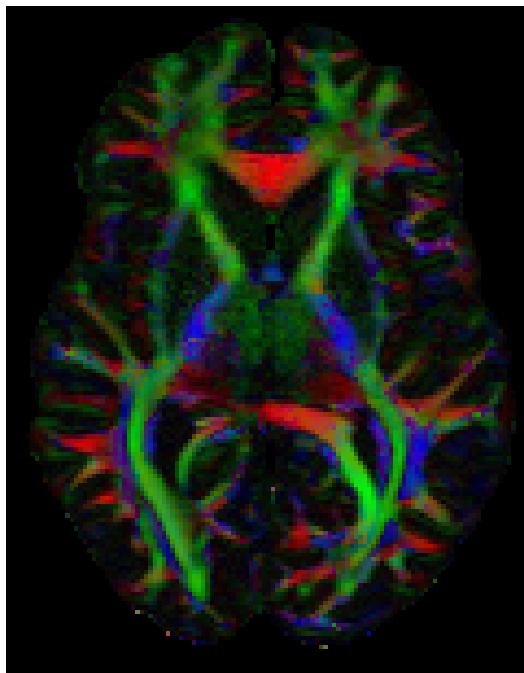


**WM: Anisotropic diffusion**



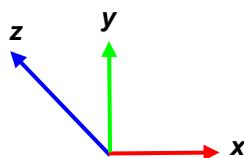
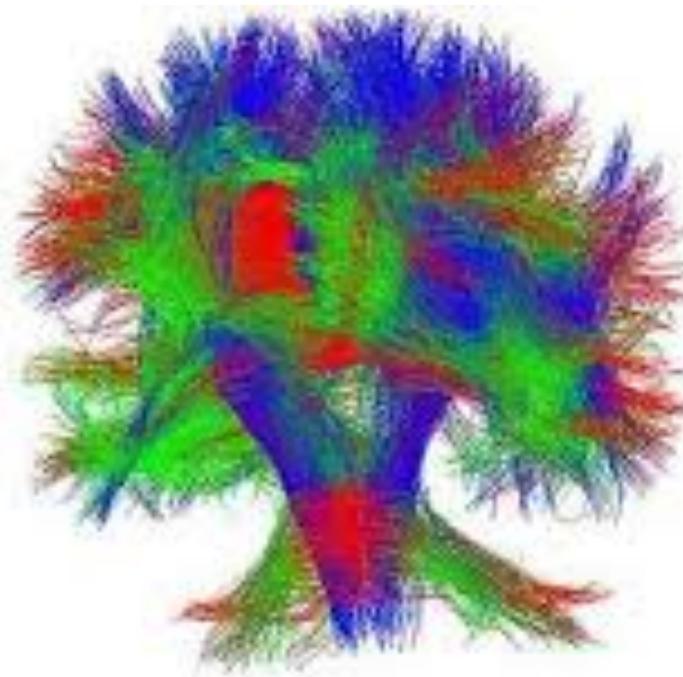
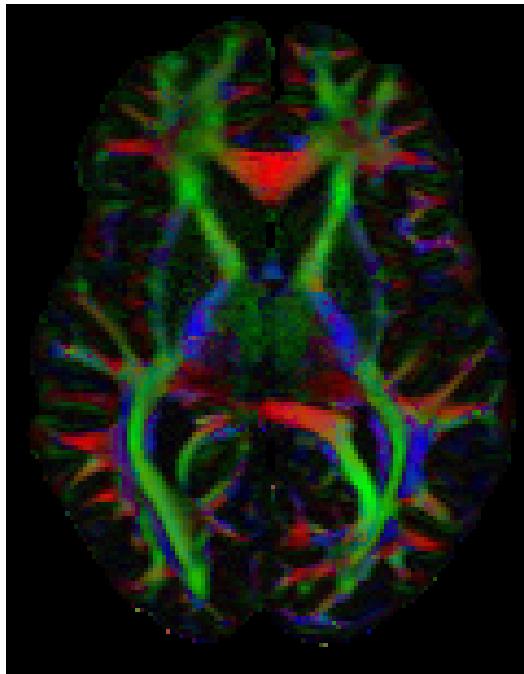


# Diffusion MRI reveals orientation information



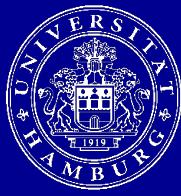


# Diffusion MRI reveals orientation information



**For tractography in SPM contact Marco Reisert:**

<https://www.uniklinik-freiburg.de/mren/members/current/reisert/>



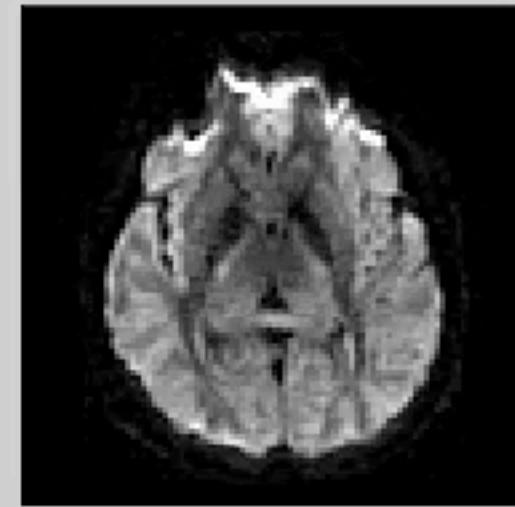
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Single spin echo

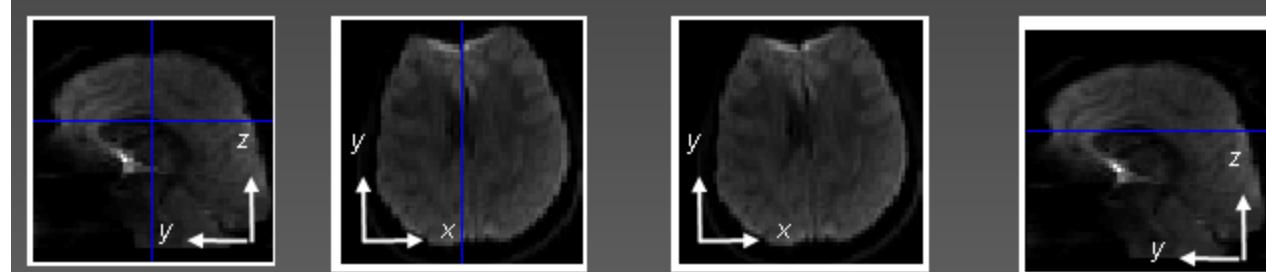
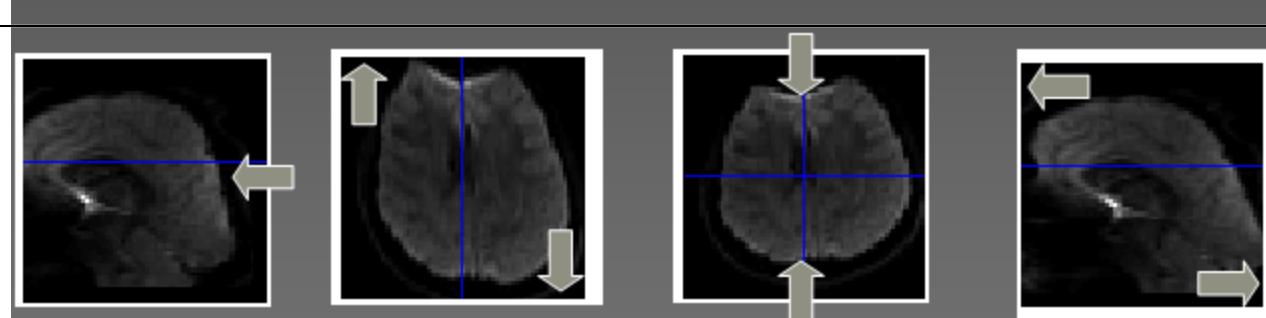


Double spin echo



*Stejskal & Tanner, JCP, 1965*

*Reese et al., MRM, 2003*

original  
imagedistorted  
image

translation

in-plane shearing

scaling

through-plane shearing

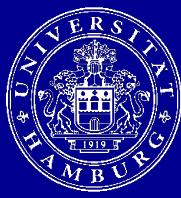
eddy current  
field  
components

$$B_0^{\text{EC}}$$

$$\longrightarrow \begin{pmatrix} G_x^{\text{EC}} \\ 0 \\ 0 \end{pmatrix}$$

$$\uparrow \begin{pmatrix} 0 \\ G_y^{\text{EC}} \\ 0 \end{pmatrix}$$

$$\uparrow \begin{pmatrix} 0 \\ 0 \\ G_z^{\text{EC}} \end{pmatrix}$$



The screenshot shows the SPM Batch Editor interface. The menu bar at the top includes File, Edit, View, SPM, and BasicIO. The SPM menu is currently active, displaying a list of tools. A submenu for 'Tools' is open, specifically the 'ACID Toolbox - vbeta02' section. Under this section, the 'EC and Motion Correction multi targets' option is highlighted with a blue selection bar. To the right of this menu, a detailed description of the selected tool is provided, including sub-options like 'Choose EC and Motion correction method', 'Choose HySCO options', and 'Choose POAS options'. The bottom left corner of the window displays the 'MATLAB Batch System' and 'Matlabbatch User Interface' information. A note at the bottom explains the function of the 'File' and 'Edit' menus.

File Edit View SPM BasicIO

Module List

No Modules in Batch

Temporal ►

Spatial ►

Stats ►

DCM ►

M/EEG ►

Util ►

Tools ►

- ACID Toolbox - vbeta02 ►
- Dartel Tools
- FieldMap
- Longitudinal Registration
- MPM Multi-Parameter Mapping
- Old Normalisation
- Old Segment
- Rendering
- Shoot Tools
- VBQ Tools
- hMRI Tools
- MPM ESTATICS
- SUIT

Pre-processing ►

- Tensor fitting
- FA-FVBS options

18:04:08 – 26/09/2017

.....done

Show movie of DWI images

read-write nifti

Make Brain Mask

Resample to dimension

Combines repetitions

Choose EC and Motion correction method

Choose HySCO options

Choose POAS options

PMSK=spm\_se

AMSK=ACID\_r

figure;image

figure;image

mSb0=mean(A)

mSb0=mean(A)

mSb0=mean(A)

mSb0=mean(A)

mSb0\*0.05

mSb0\*0.14

26.09.17,

spm12 mispl

MATLAB Batch System

Matlabbatch User Interface

\* Menu and Toolbar

The "File" and "Edit" menu offer options to load, save and run a job and to modify the configuration of the batch system. For each application which is known to the batch system, a separate pulldown menu lists the available modules. Depending on the application, these modules may be grouped into submenus. Application specific

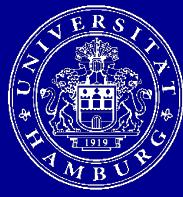


The screenshot shows the SPM Batch Editor interface. The menu bar at the top includes File, Edit, View, SPM, BasicIO, and a toolbar with red, yellow, and green buttons. On the left, a vertical sidebar lists "Module List" items: Temporal, Spatial, Stats, DCM, M/EEG, Util, Tools (which is selected), and Edit Defaults. Below this is a section for the "MATLAB Batch System" and "Matlabbatch User Interface". A note states: "The 'File' and 'Edit' menu offer options for opening and saving files. For each application which has modules. Depending on the application".

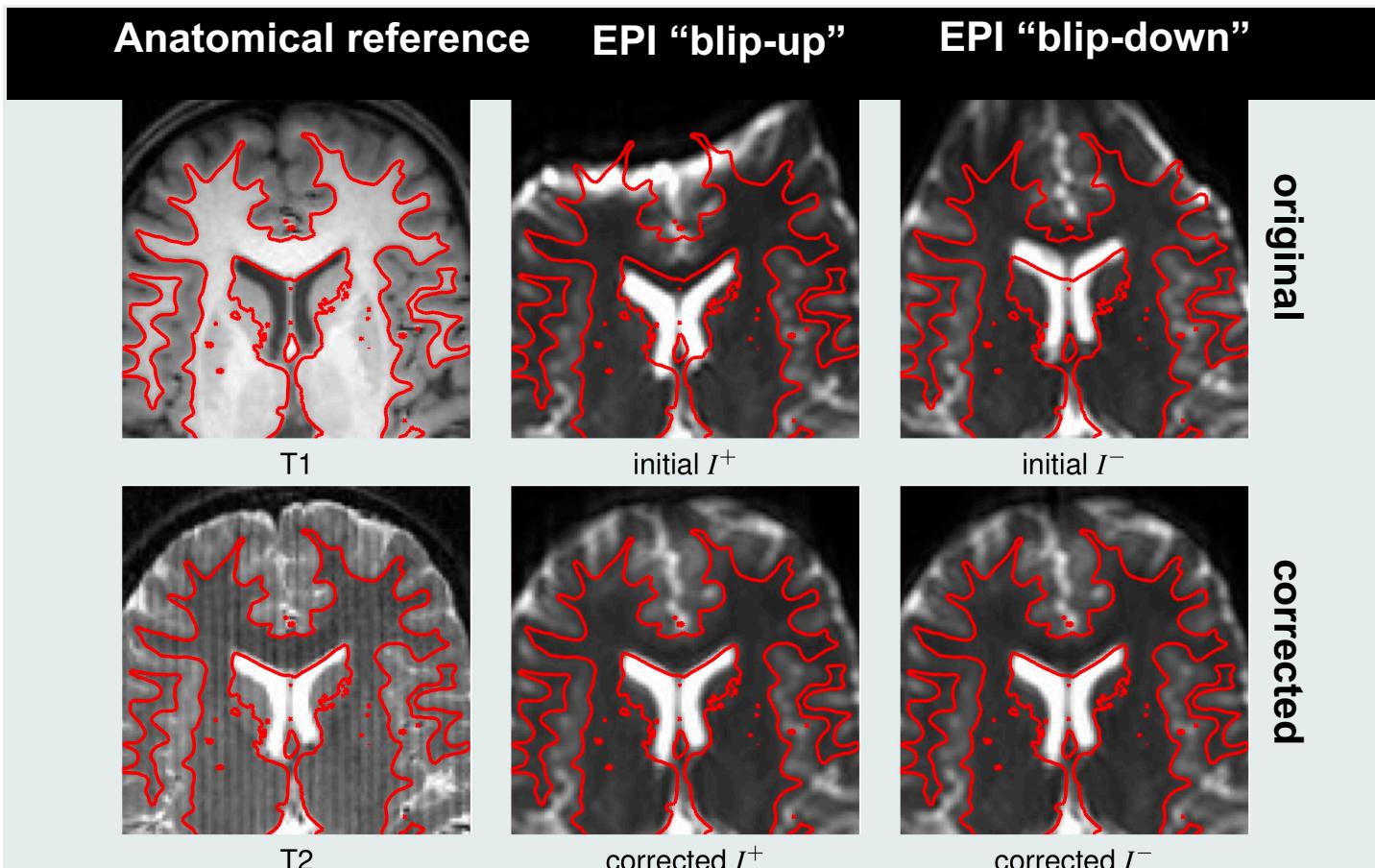
The main workspace is titled "Batch Editor" and contains the "EC and Motion Correction" module. The "Current Module: EC and Motion Correction multi targets" panel displays help text and configuration parameters:

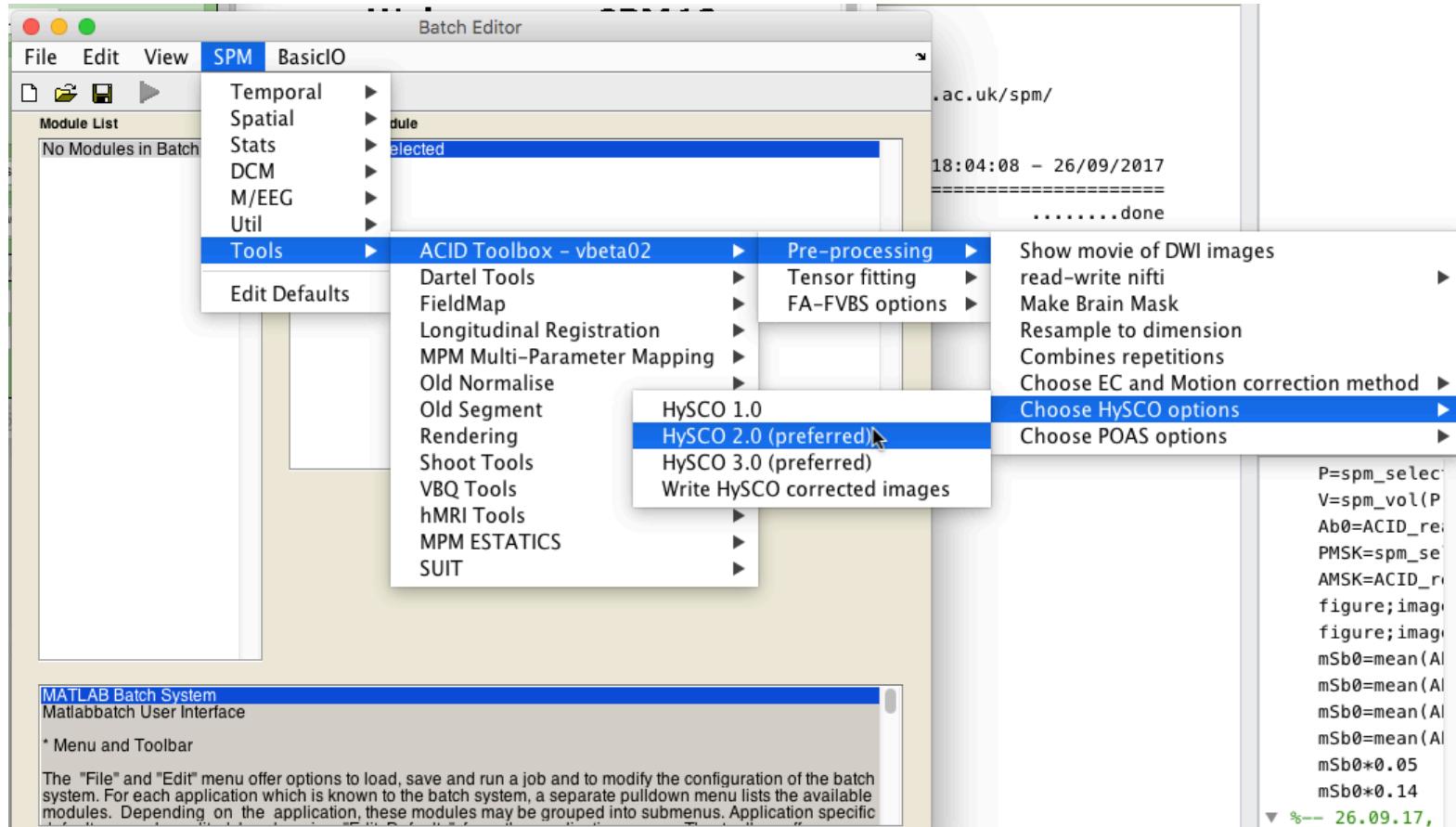
Parameter	Value
Source Images	<-X <-X [5 1000 1000 2000]
Defaults	1x12 double
. Enter 12 binaries	ON
. Choose write option	ON
. Choose display option	y
. Dimension of phase-encoding	3d output
. Output format	Volume-wise
. Registration scheme	ON
. Are b=0 images interspersed?	

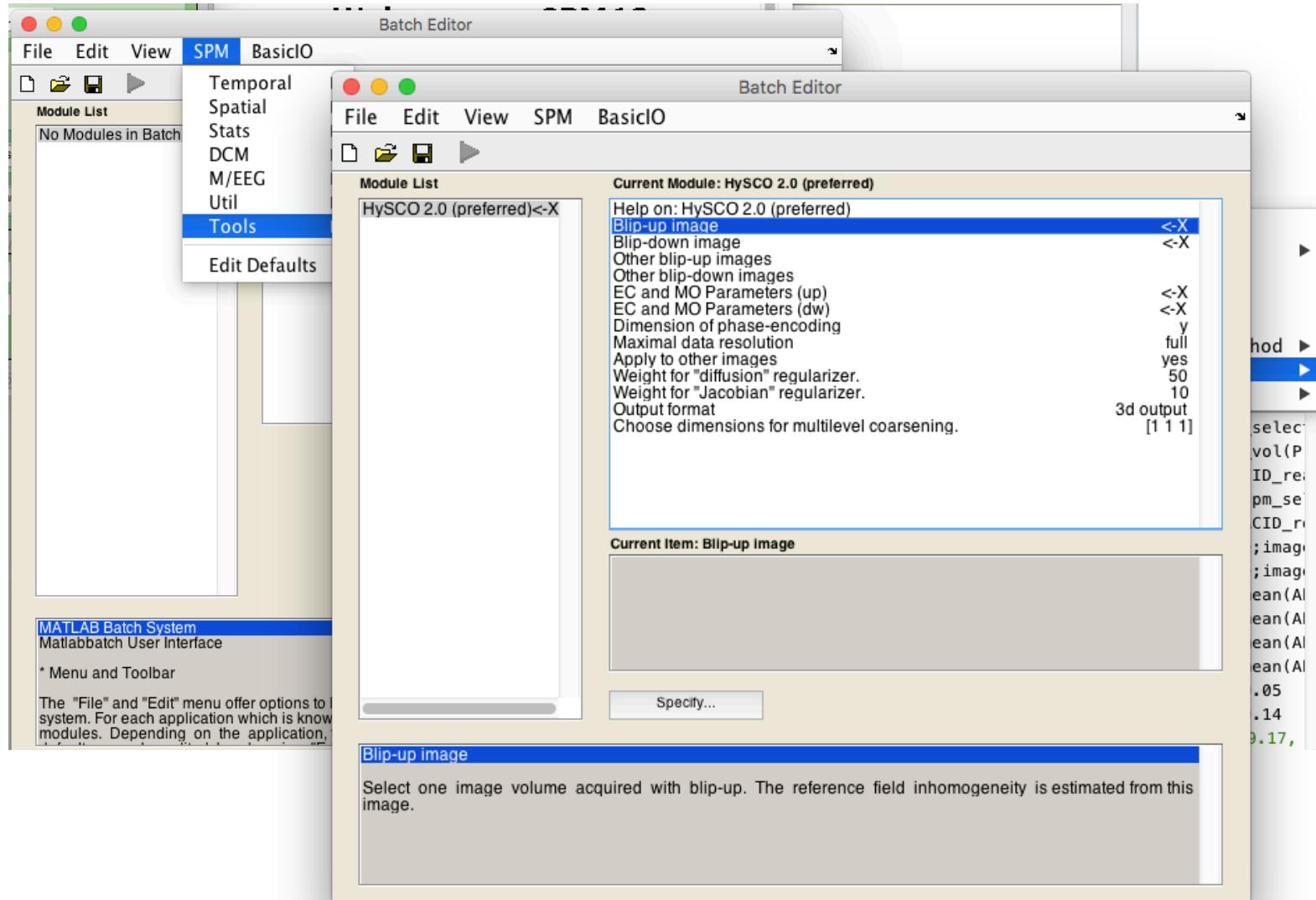
The "Current Item: Source Images" panel contains a "Specify..." button. At the bottom, a note says: "Source Images Select source images. These images will be registered to the sources image."



- Diffusion MRI: why, how, and what does it mean?
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Batch Editor

File Edit View SPM BasicIO

Module List

No Modules in Batch

Temporal  
Spatial  
Stats  
DCM  
M/EEG  
Util  
Tools

Edit Defaults

MATLAB Batch System

Matlabbatch User Interface

\* Menu and Toolbar

The "File" and "Edit" menu offer options to system. For each application which is known modules. Depending on the application,

Batch Editor

File Edit View SPM BasicIO

Module List

HySCO 2.0 (preferred)<-X

Current Module: HySCO 2.0 (preferred)

Help on: HySCO 2.0 (preferred)

Blip-up image <-X  
Blip-down image <-X  
Other blip-up images <-X  
Other blip-down images <-X  
EC and MO Parameters (up) <-X  
EC and MO Parameters (dw) <-X  
Dimension of phase-encoding <-X  
Maximal data resolution y  
Apply to other images full  
Weight for "diffusion" regularizer. yes  
Weight for "Jacobian" regularizer. 50  
Output format 10  
Choose dimensions for multilevel coarsening. 3d output [1 1 1]

Current Item: Blip-up image

Specify...

Blip-up image

Select one image volume acquired with blip-up. The reference field inhomogeneity is estimated from this image.



Batch Editor

File Edit View SPM BasicIO

Module List

No Modules in Batch

Temporal Spatial Stats DCM M/EEG Util Tools Edit Defaults

MATLAB Batch System Matlabbatch User Interface

\* Menu and Toolbar

The "File" and "Edit" menu offer options to system. For each application which is known modules. Depending on the application,

Batch Editor

File Edit View SPM BasicIO

Module List

HySCO 2.0 (preferred)<-X

Help on: HySCO 2.0 (preferred)

Blip-up image <-X  
Blip-down image <-X  
Other blip-up images <-X  
Other blip-down images <-X  
EC and MO Parameters (up) <-X  
EC and MO Parameters (dw) <-X  
Dimension of phase-encoding <-X  
Maximal data resolution <-X  
Apply to other images <-X  
Weight for "diffusion" regularizer. <-X  
Weight for "Jacobian" regularizer. <-X  
Output format <-X  
Choose dimensions for multilevel coarsening. <-X

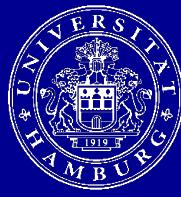
Current Item: Blip-up image

Specify... 3d output [1 1 1]

Blip-up image

Select one image volume acquired with blip-up. The reference field inhomogeneity is estimated from this image.

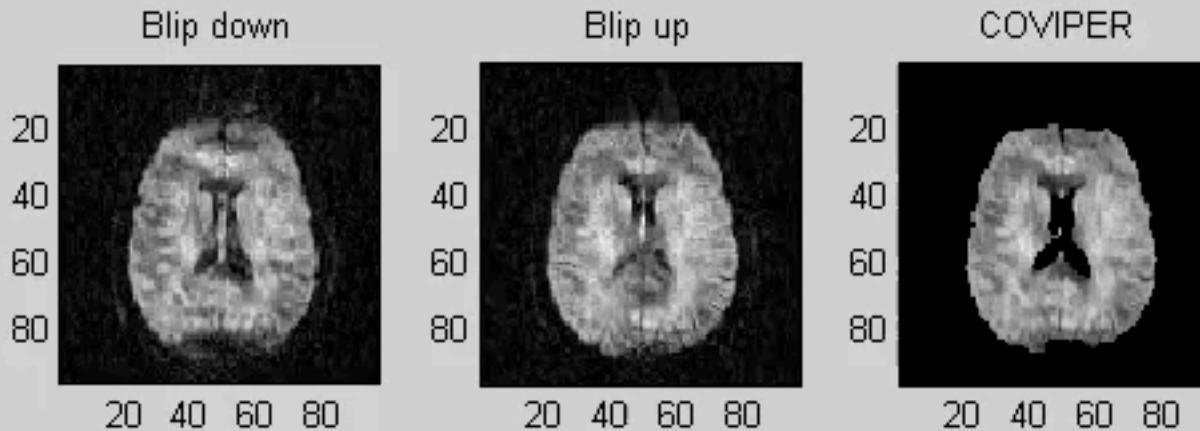
vol(P ID\_re; pm\_se; CID\_r; ;image; ;image; ean(AI ean(AI ean(AI ean(AI .05 .14 9.17,



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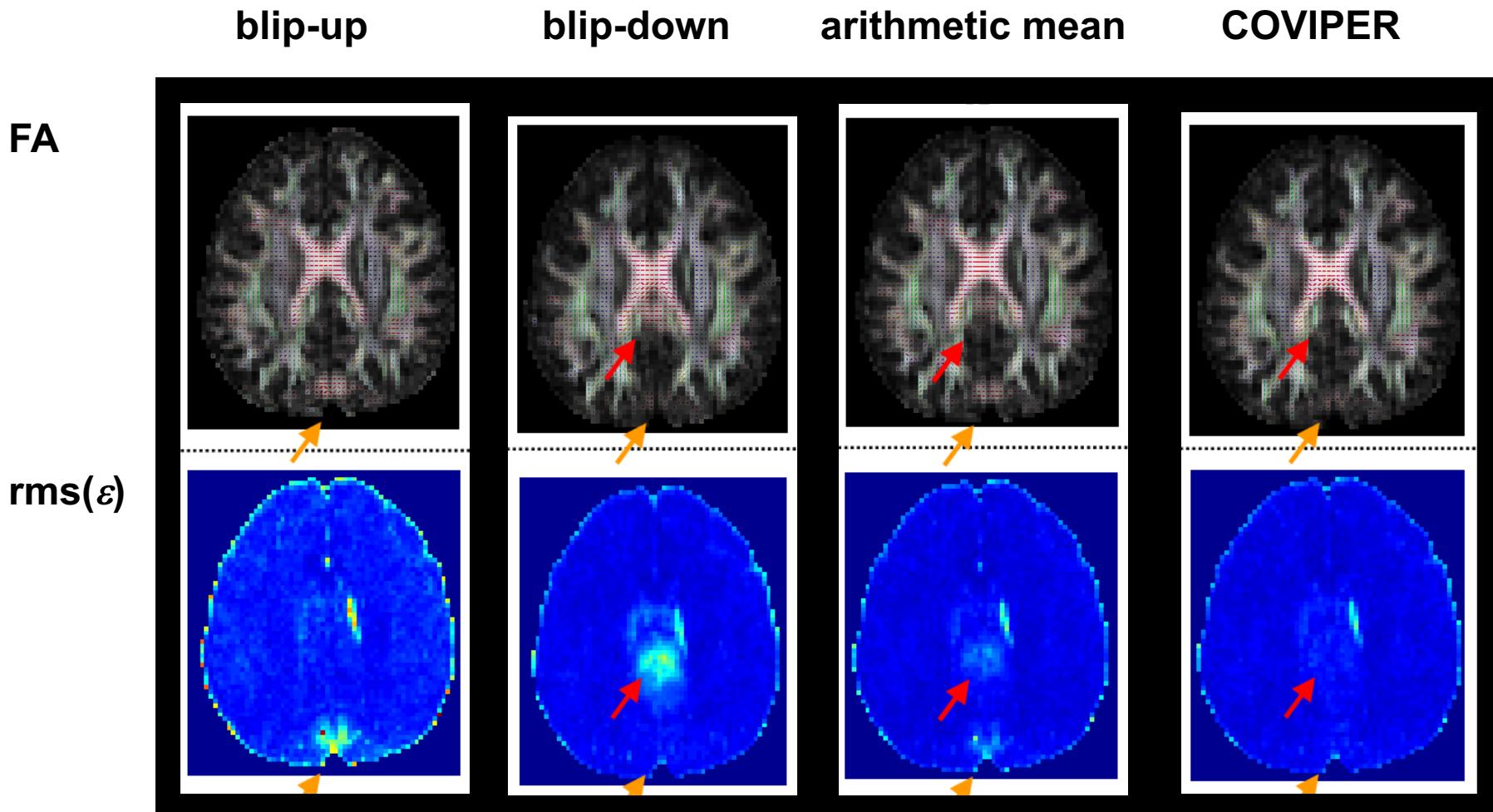


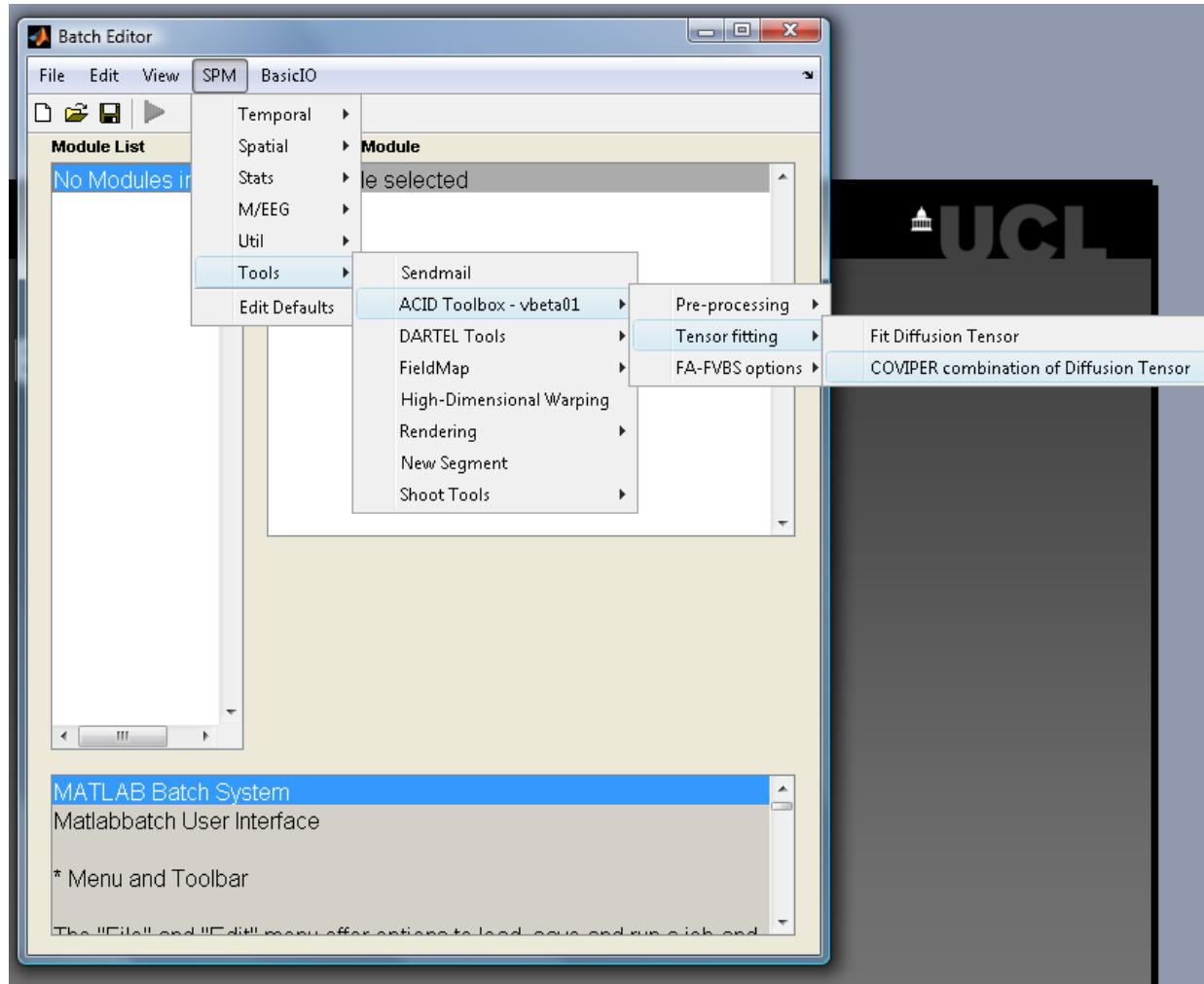
# Vibration artifacts and its correction



**Correction of Vibration Artifacts in DTI  
Using Phase-Encoding Reversal  
(COVIPER)**

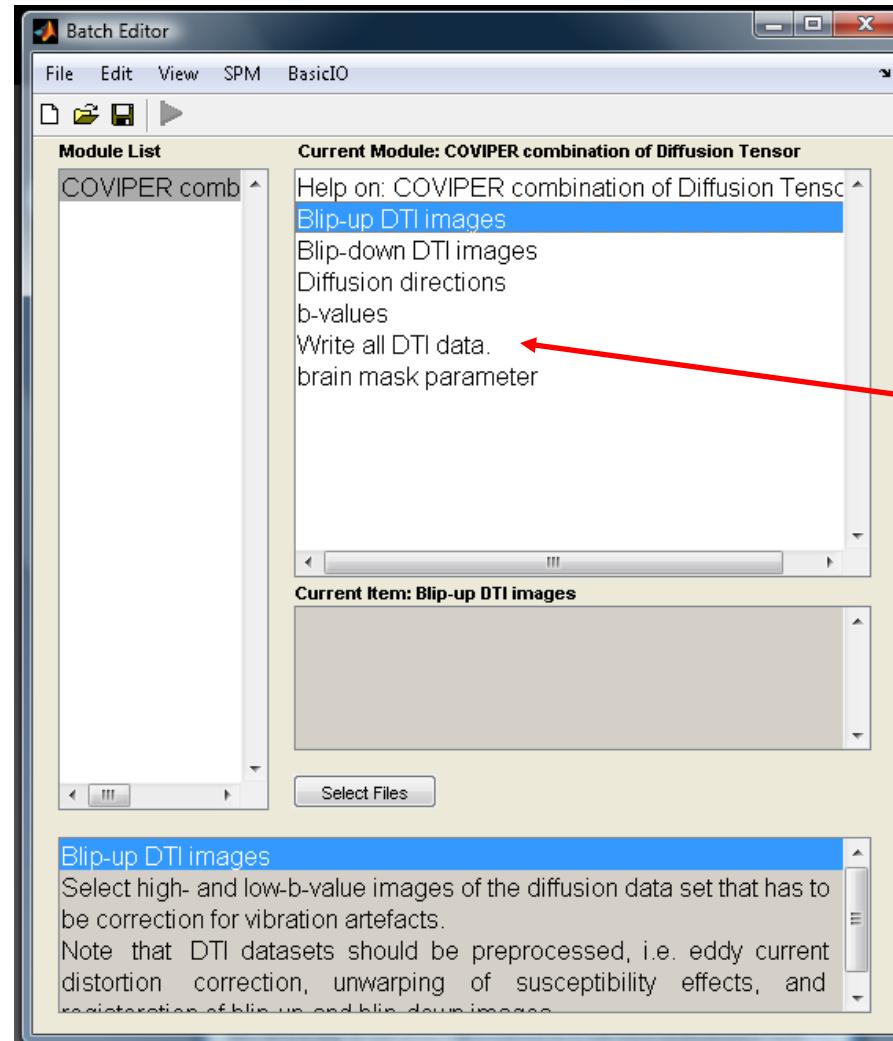
*Mohammadi et al., MRM, 2012*



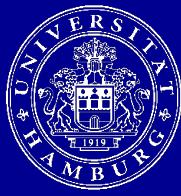




# ACID-COVIPER tool Vibration artefacts

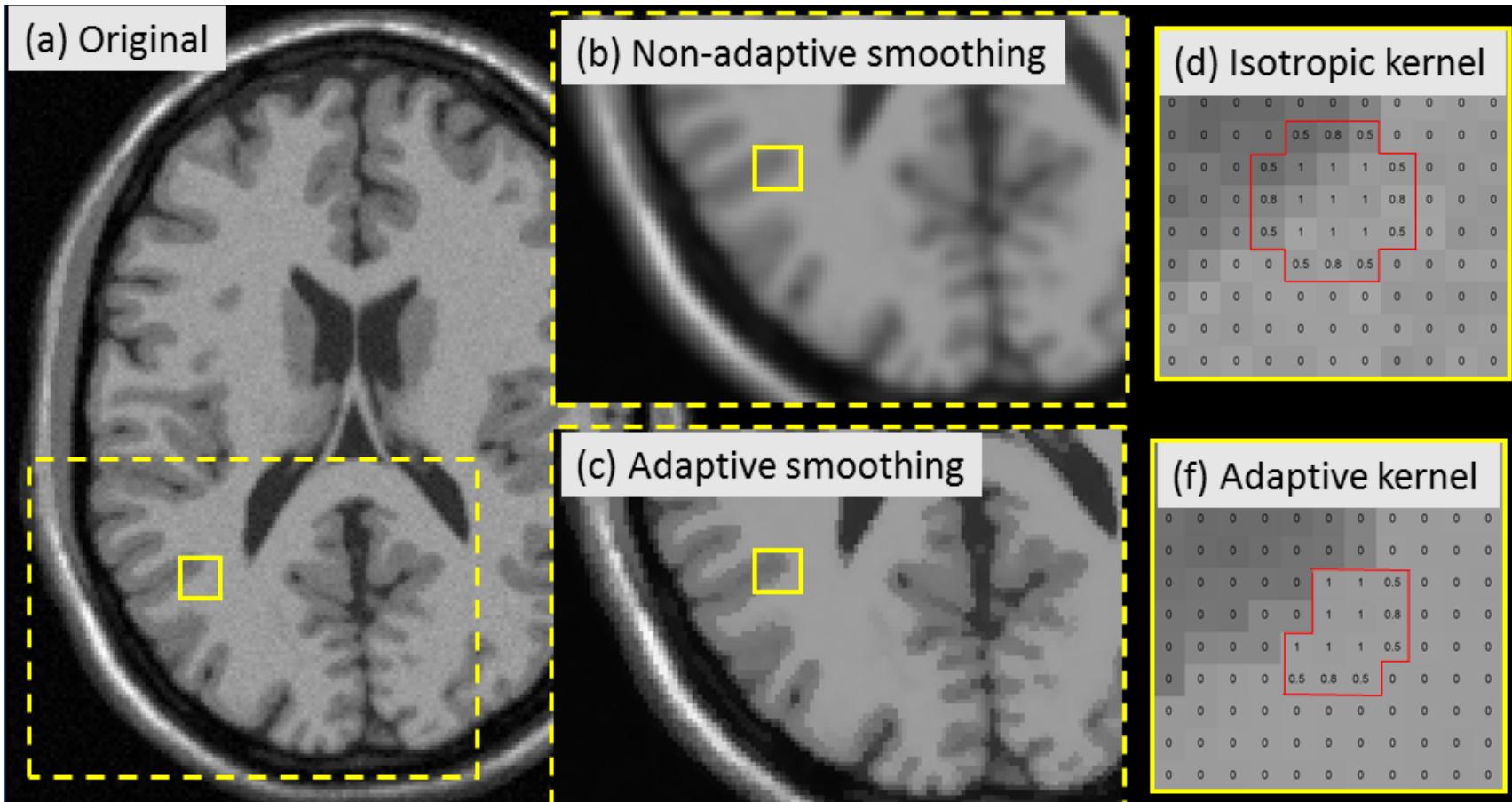


**Corrected DTI  
dataset**

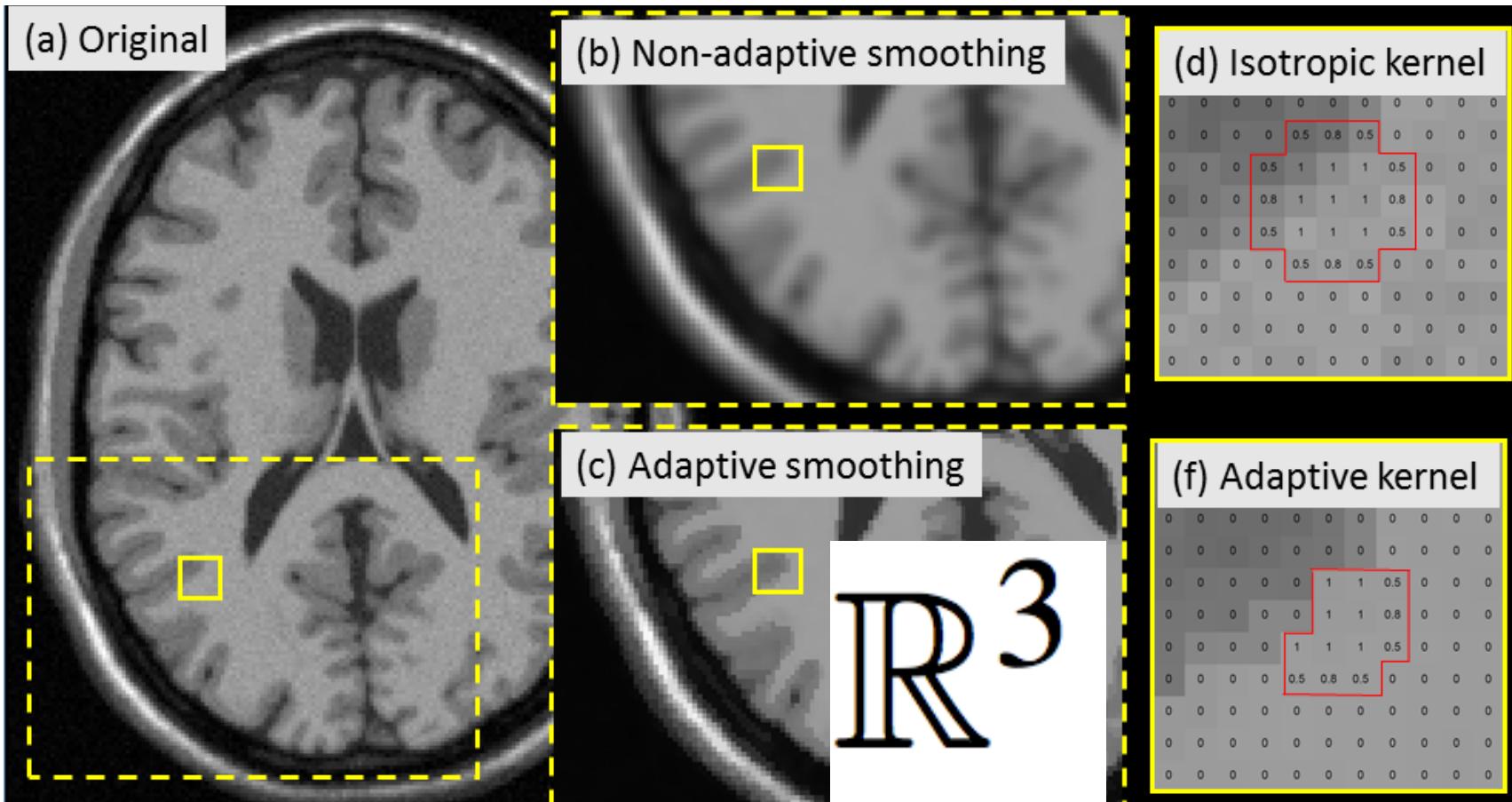


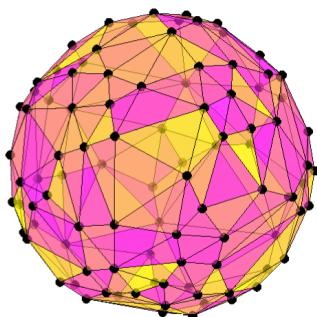
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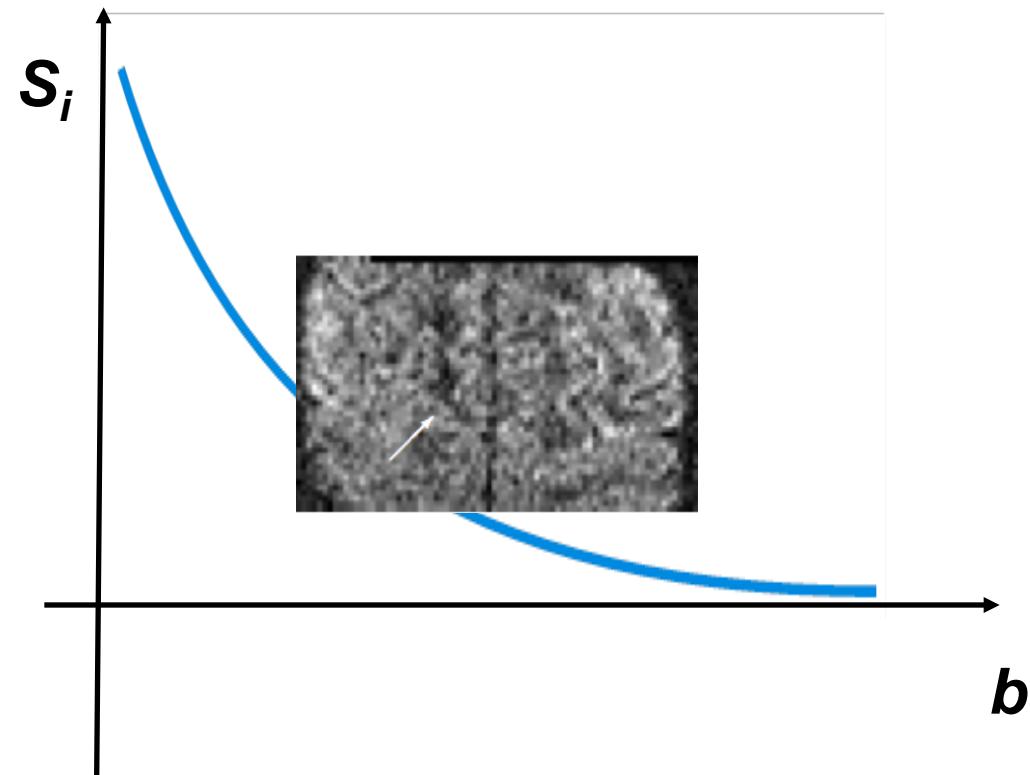
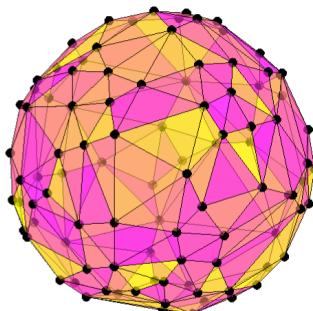
# What is adaptive denoising?

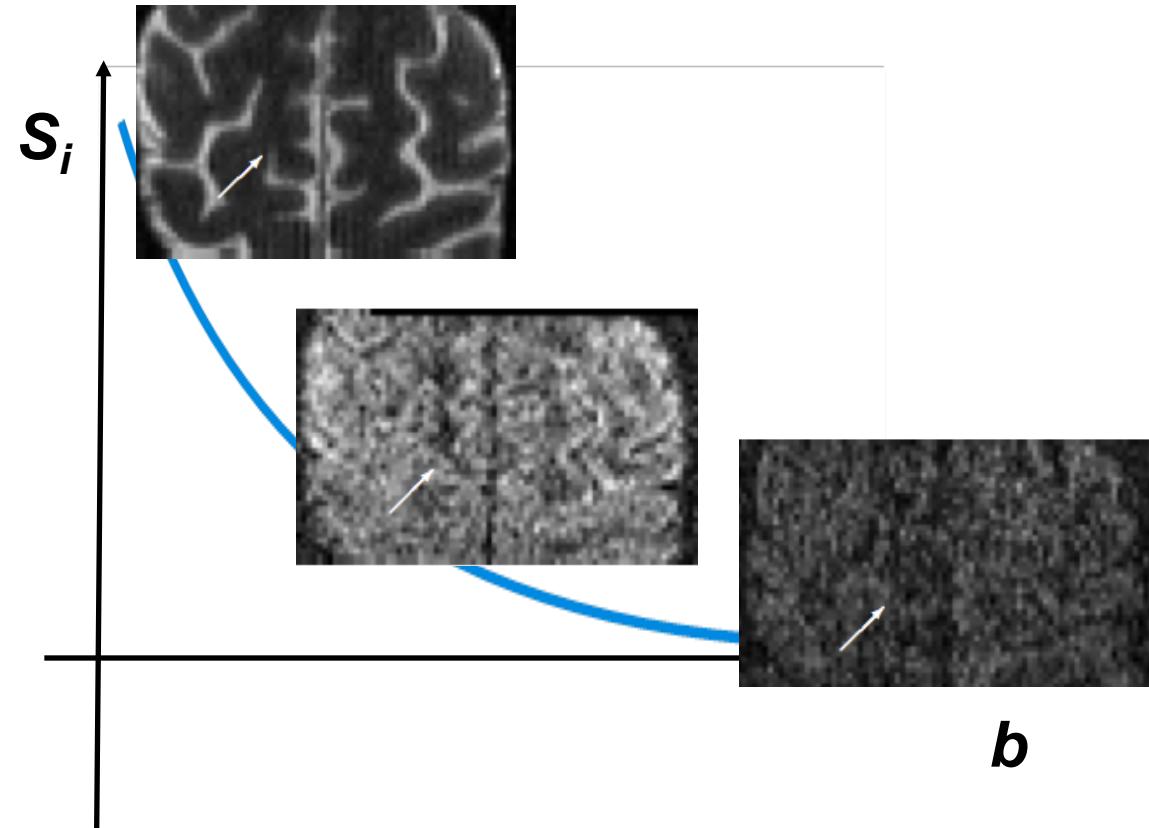
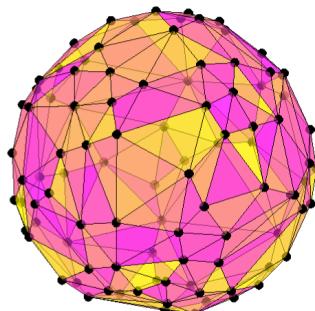


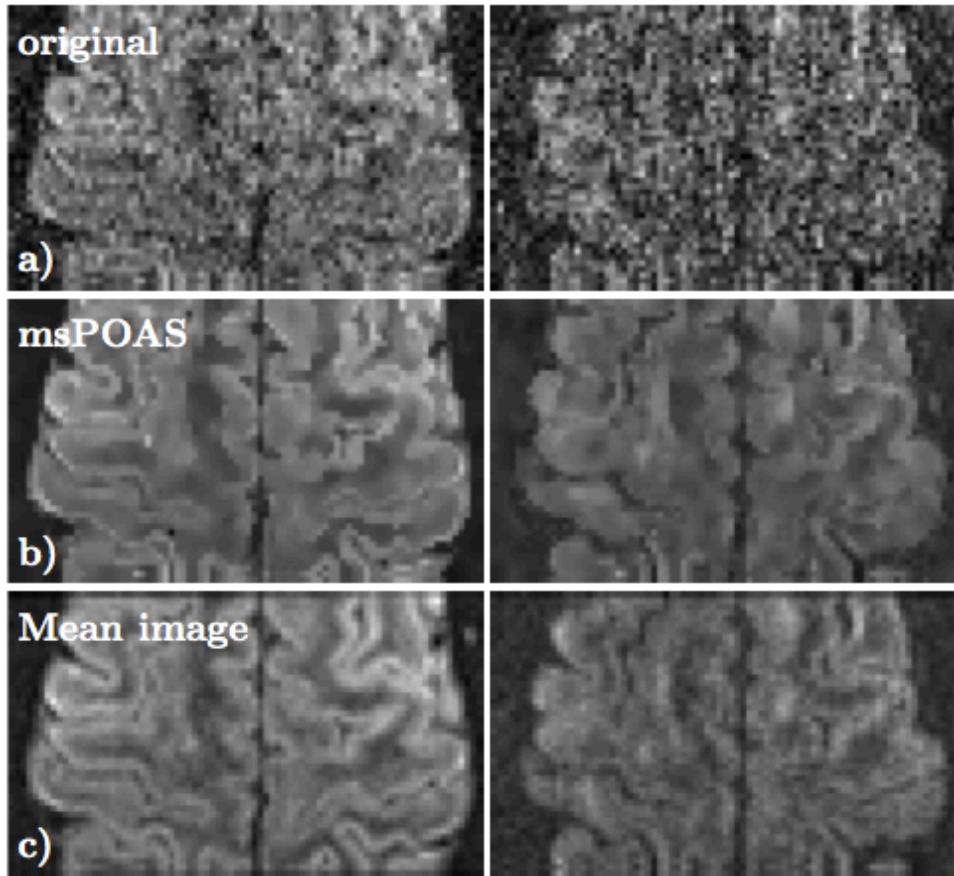
# What is adaptive denoising?



$\mathbb{R}^3$  $S^2$ 

Multi-shell position-orientation  
adaptive smoothing (msPOAS) $\mathbb{R}^3$  $S^2$ **Multiple shells**

Multi-shell position-orientation  
adaptive smoothing (msPOAS) $\mathbb{R}^3$  $S^2$ **Multiple shells**

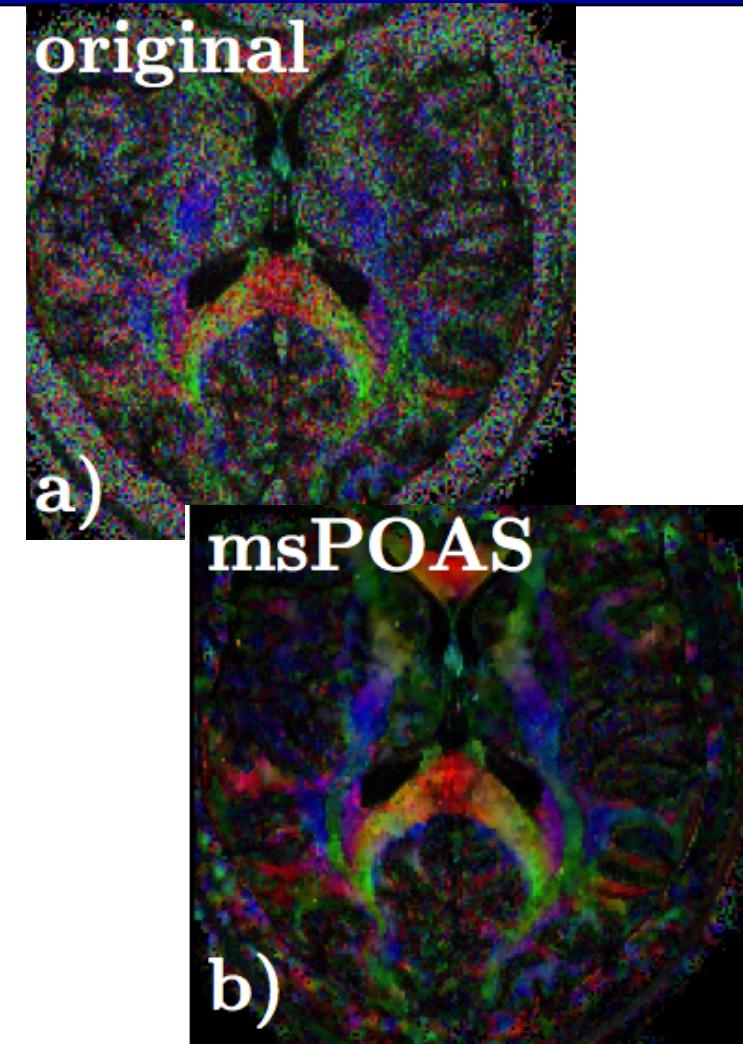
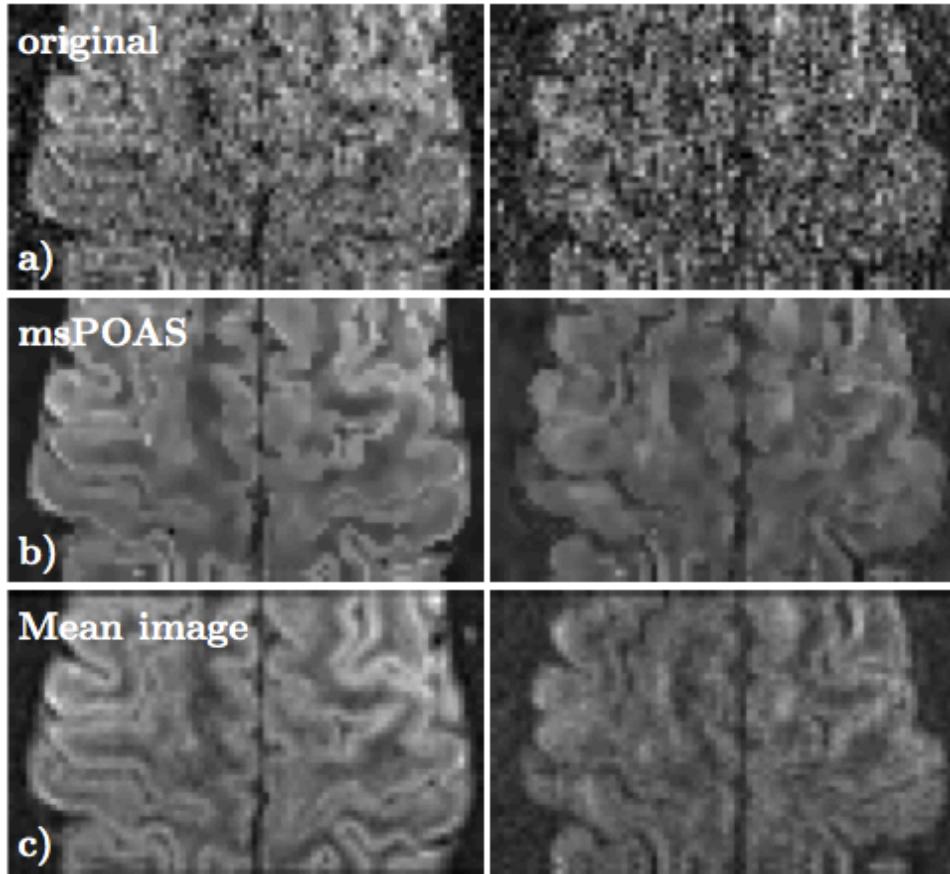


- Multi-shell dMRI
- @ $1.2 \times 1.2 \times 1.2 \text{ mm}^3$
- @ 3T clinical scanner

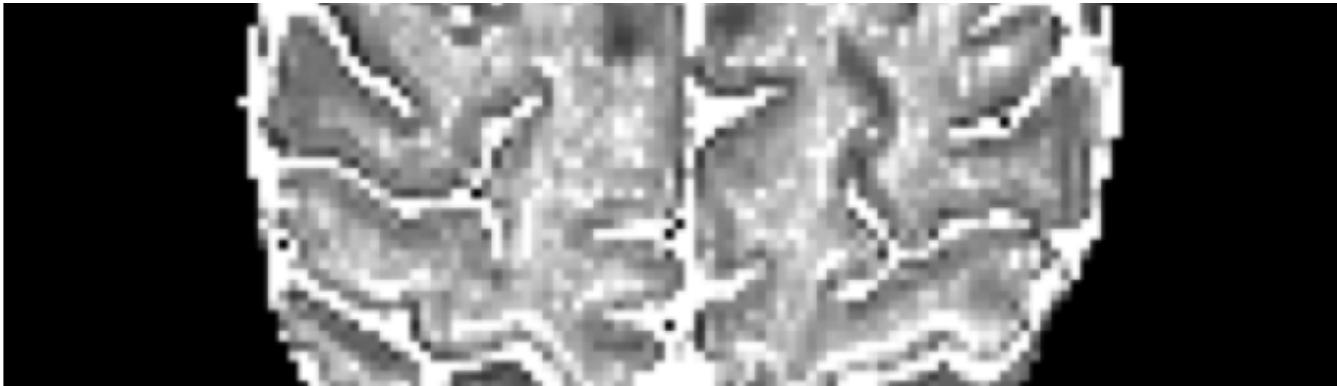


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msPOAS in cortex DWI and across brain



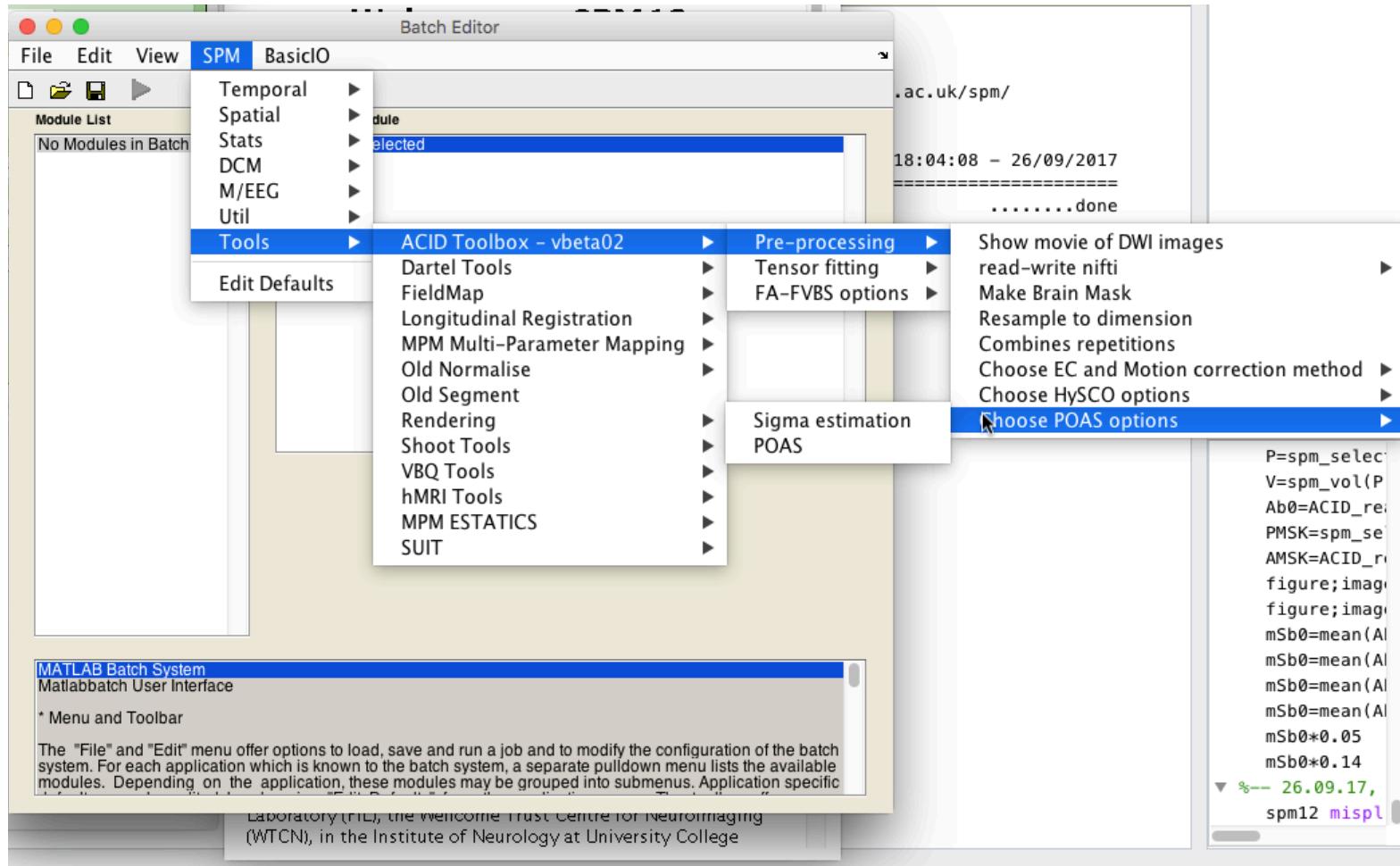
Becker et al., MIA, 2012, Becker et al., 2014

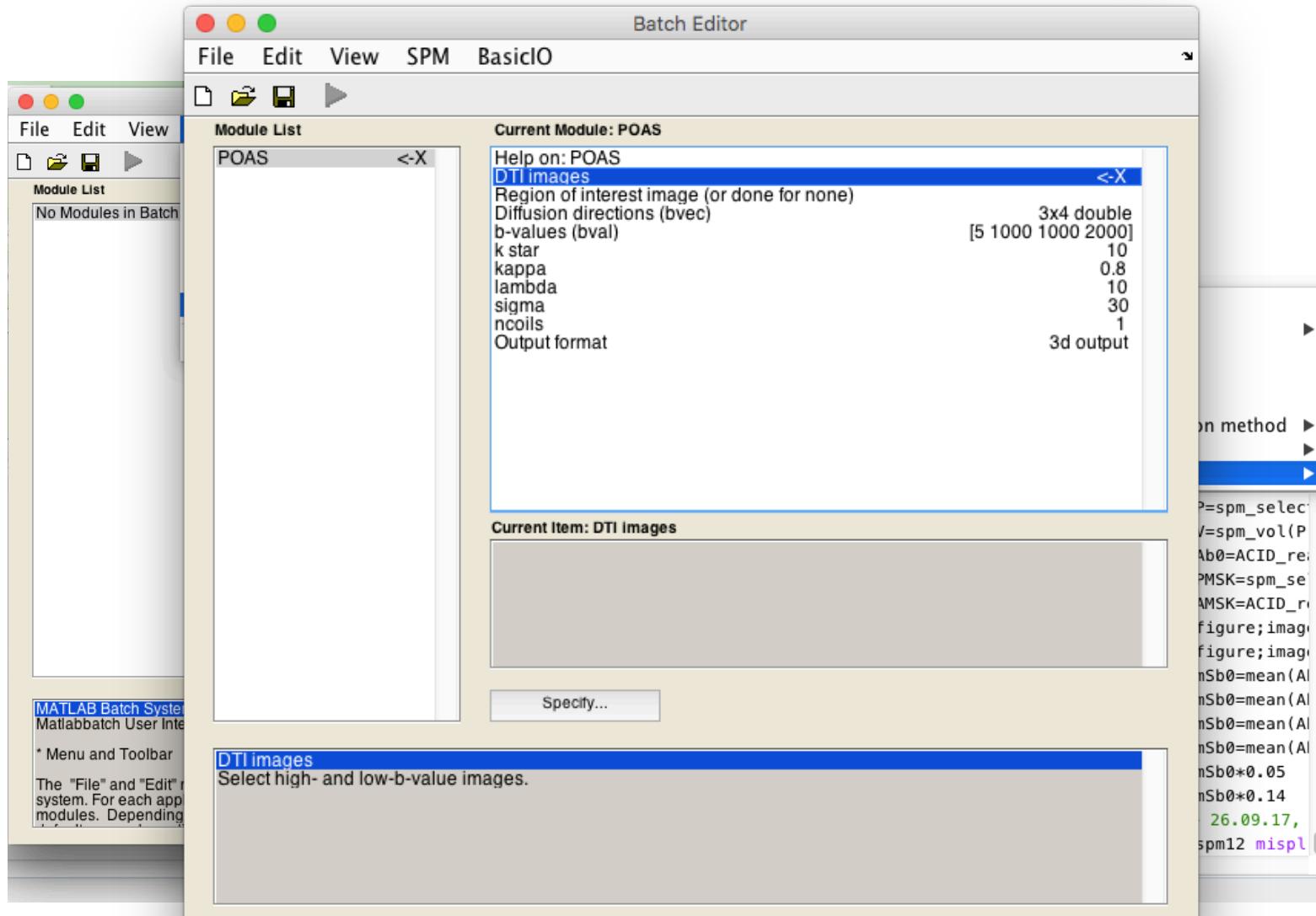


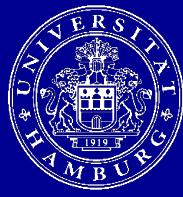
Original



msPOAS







- Diffusion MRI: why, how, and what does it mean?
- Pre-processing steps
  - Eddy current and motion correction
  - Susceptibility artefacts correction
  - Vibration artefact correction
  - Position-orientation adaptive smoothing
- Diffusion models
  - Weighted Ordinary Least Squares, Robust Tensor Fitting
  - Kurtosis Tensor Imaging
  - NODDI-DTI



Batch Editor

File Edit View SPM BasicIO

Module List

Fit Diffusion Tensor <-X

Current Module: Fit Diffusion Tensor

	<-X
DTI images	
Diffusion directions (bvec)	3x4 double
b-values (bval)	[5 1000 1000 2000]
Reorientation Matrix	3x3 double
Region of interest image (or done for none)	
Fitting algorithm	Ordinary least squares
Fit defaults	
. Write fitted DWI images.	NO
. Write all eigenvectors and eigenvalues.	NO
. Write Freiburg Tractography format	NO
. Normalisation factor	4
. Confidence interval for robust fitting.	0.3
. Smoothing of the residuals	16
. Regularization for robust fitting	0.0001
. Write weights	NO
. Plotting weights	NO
. Smoothing kernel	[3 3 3]
Write brain mask	NO
Estimate Kurtosis tensor	NO
Condition number threshold	100000
Threshold for minimal diffusivity	1e-07
Parallel programming	NO

Current Item: DTI Images

Specify...

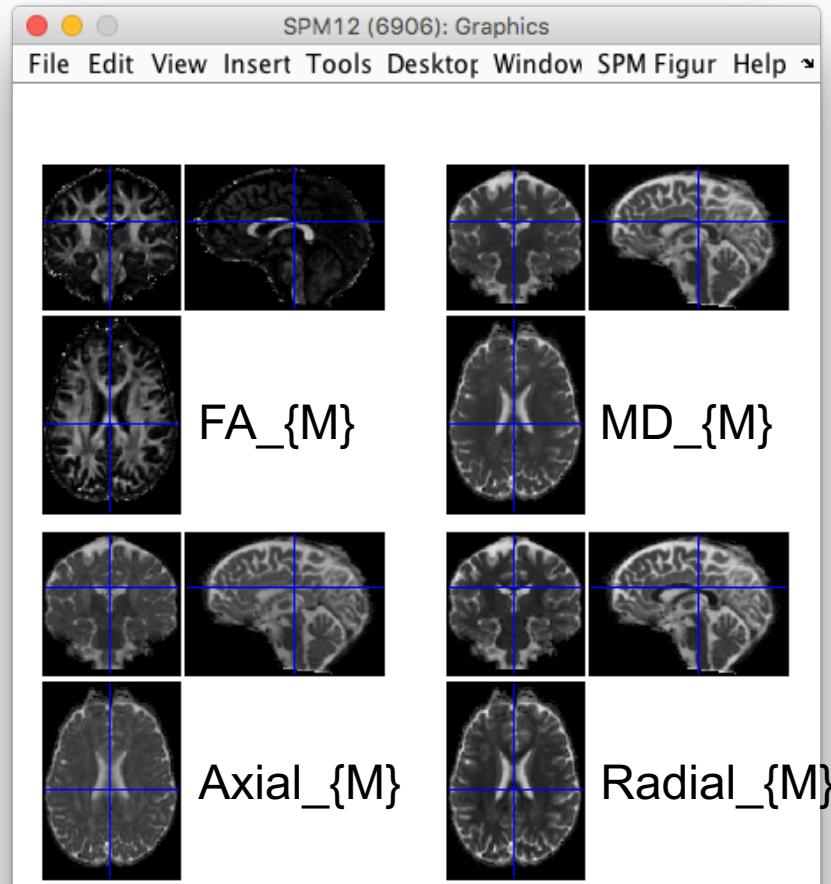
DTI images

Select high- and low-b-value images.

## Most important

- Diffusion Data
- b-values
- b-vectors

# What are the outputs?



**{M} = method:**

- ols: ordinary least square
- wls: weighted ordinary least square
- robust: robust fitting
- *More details here:*
  - Mohammadi et al., MRM, 2012;
  - Mohammadi et al., NI, 2013

**More advanced:**

- Tensor fit error: RES\_{M}
- Eigenvalues and Eigenvectors
- Output for Freiburg Fibertools  
(Tractography – contact Marco Reisert / Volkmar Glauche)

Learn more about the DTI metrics:

Basser et al. 1996; *Diffusion MRI...*, Ed: H Johansen-Berg & TEJ Behrens, 2007

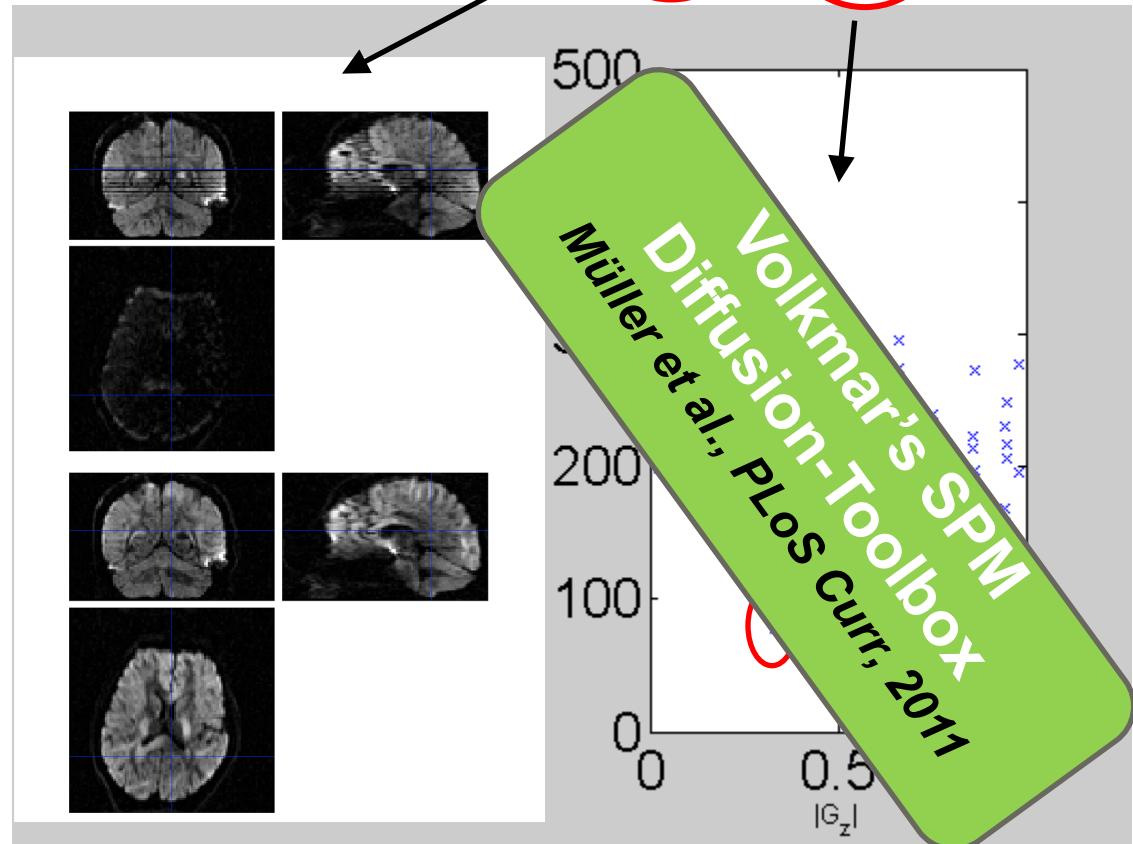


# Robust tensor fitting for spinal cord DTI

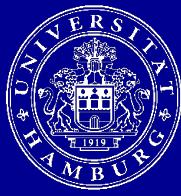
**Based on Zwiers,  
NI, 2010**

$$y = \mathbf{X} d + \boldsymbol{\varepsilon}$$

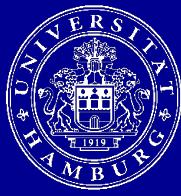
$$\omega = \omega_{\text{DWI}} \times \omega_s \times \omega_v$$



Mohammadi et al., MRM, 2012  
Mohammadi et al., NI, 2013



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Batch Editor

File Edit View SPM BasicIO

Module List

Current Module: Fit Diffusion Tensor

Diffusion directions (bvec)	3x4 double
b-values (bval)	[5 1000 1000 2000]
Reorientation Matrix	3x3 double
Region of interest image (or done for none)	Ordinary least squares
Fitting algorithm	NO
Fit defaults	NO
. Write fitted DWI images.	NO
. Write all eigenvectors and eigenvalues.	NO
. Write Freiburg Tractography format	NO
. Normalisation factor	4
. Confidence interval for robust fitting.	0.3
. Smoothing of the residuals	16
. Regularization for robust fitting	0.0001
. Write weights	NO
. Plotting weights	NO
. Smoothing kernel	[3 3 3]
Write brain mask	NO
Estimate Kurtosis tensor	YES
Condition number threshold	100000
Threshold for minimal diffusivity	1e-07
Parallel programming	NO

Current Item: Estimate Kurtosis tensor

NO
*YES

Specify...

Estimate Kurtosis tensor

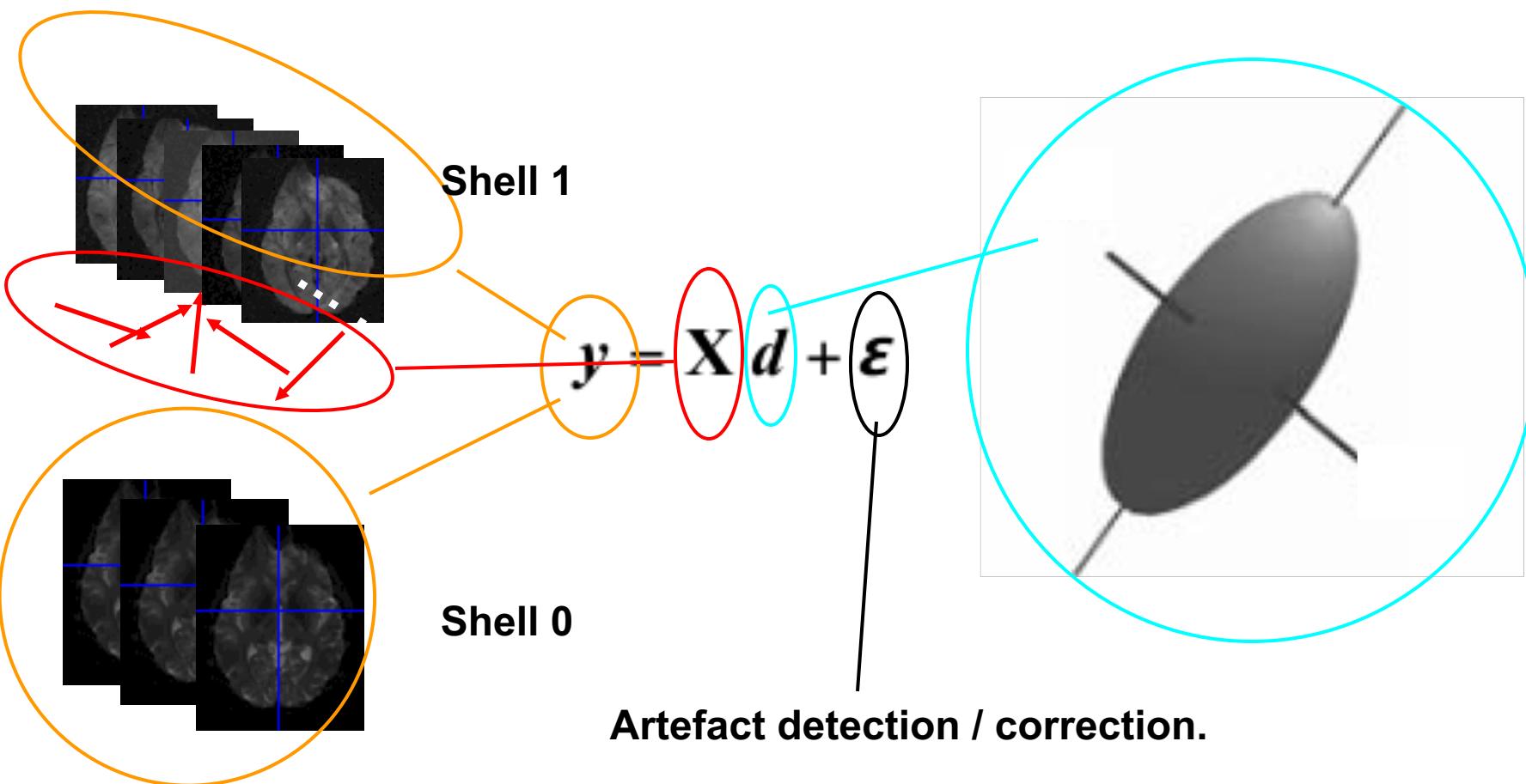
If the DKI option is on, the output arguments will additionally include:  
- mean (MK), perpendicular (Kper), parallel (Kpar) kurtosis, and axonal water fraction (AWF)  
The constrained ols Kurtosis fitting model has been used in Mohammadi et al., Front. Neurosci., 2015 and is based on the method presented in Tabesh et al., MRM, 2011.  
Please cite Mohammadi et al., Front. Neurosci., 2015 and Tabesh et al., MRM, 2011 when using the Kurtosis code.  
One of the following options must be selected:  
\* NO  
\* YES

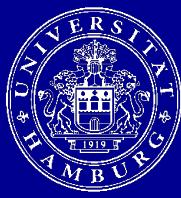
## Most important

- Diffusoin Data
- b-values (multi-shell)
- b-vectors

DKI switch

# The general linear model framework for diffusion MRI



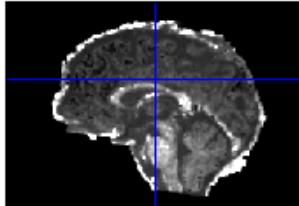
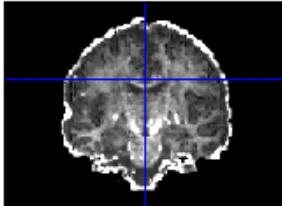


$$\ln \left[ \frac{S(\mathbf{n}, b)}{S_0} \right] = -b \sum_{i=1}^3 \sum_{j=1}^3 n_i n_j D_{ij} \quad \text{— diffusion tensor}$$
$$+ \frac{1}{6} b^2 \bar{D}^2 \sum_{i=1}^3 \sum_{j=1}^3 \sum_{k=1}^3 \sum_{l=1}^3 n_i n_j n_k n_l W_{ijkl},$$

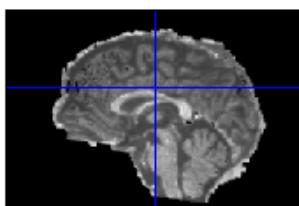
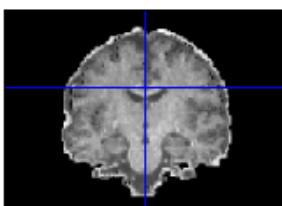
/ kurtosis tensor

The kurtosis tensor is fitted using the constrained least square model suggested by Tabesh et al., 2011. For implementation into ACID, see Mohammadi et al., Frontiers in Neurosci., 2015

# What are the outputs?



MK\_ols



AWF\_ols

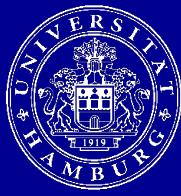
## Maps

- MK – mean kurtosis
- AWF – axonal water fraction

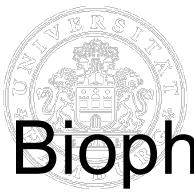
Learn more about MK and AWF:

- *Jensen et al., 2010 (review about DKI);*
- *Fieremans et al., 2011 (biophysical model of AWF)*
- *Jelescu et al., 2015 (comparison to NODDI)*

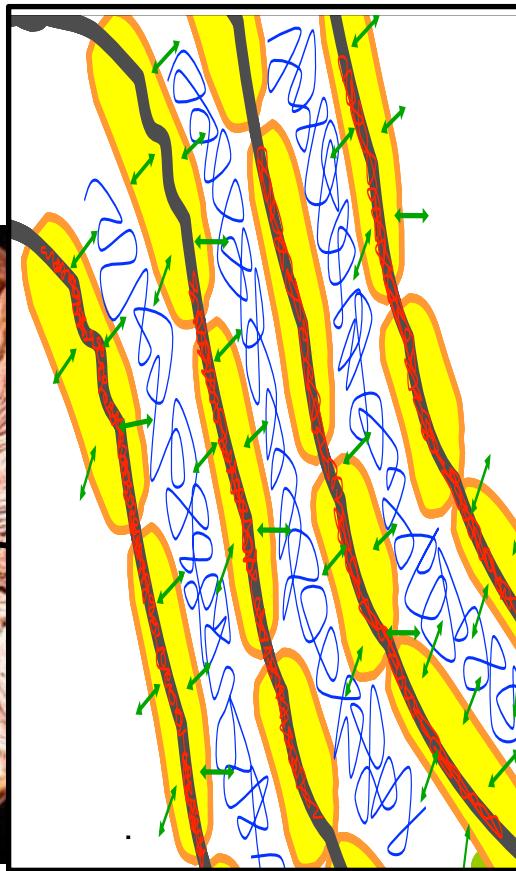
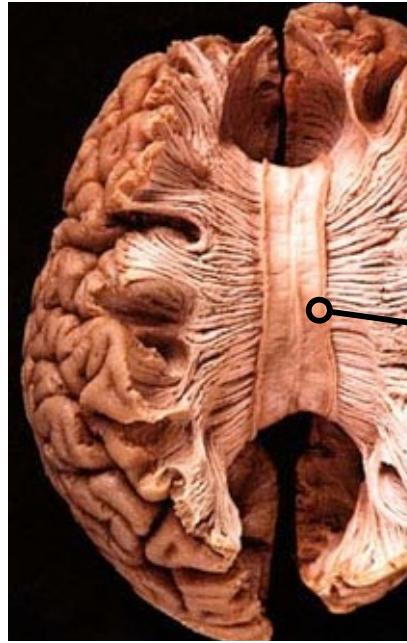
Learn more about these DKI metrics:  
*Fieremans et al., NI, 2011*



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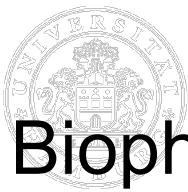


# Biophysical model of the diffusion signal

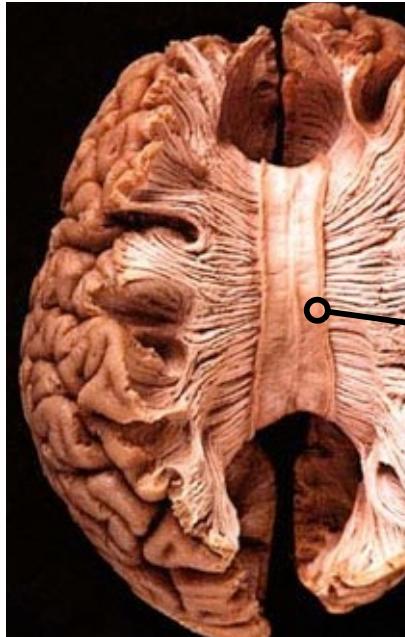


Zhang, OHBM, 2014

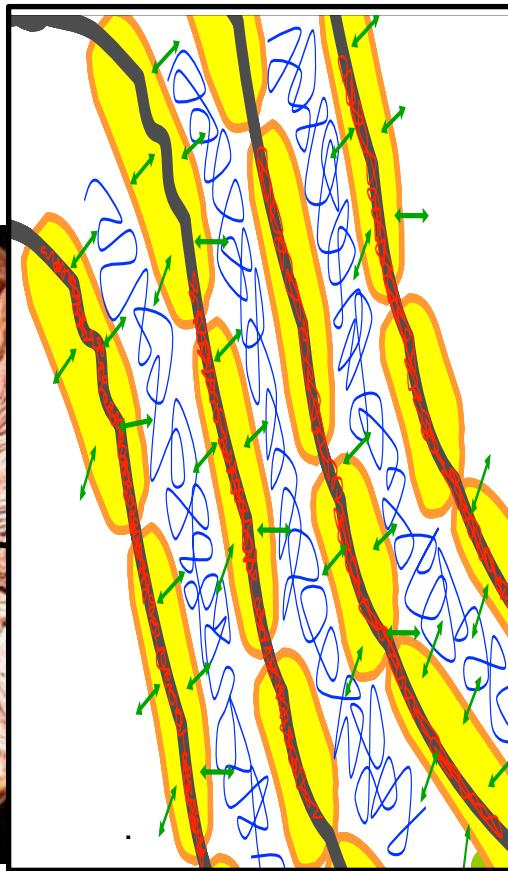
Fieremans, ESMRMB, 2015



# Biophysical model of the diffusion signal



Zhang, OHBM, 2014



Fieremans, ESMRMB, 2015



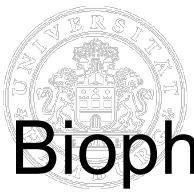
Intra-cellular diffusion  
=  
restricted diffusion



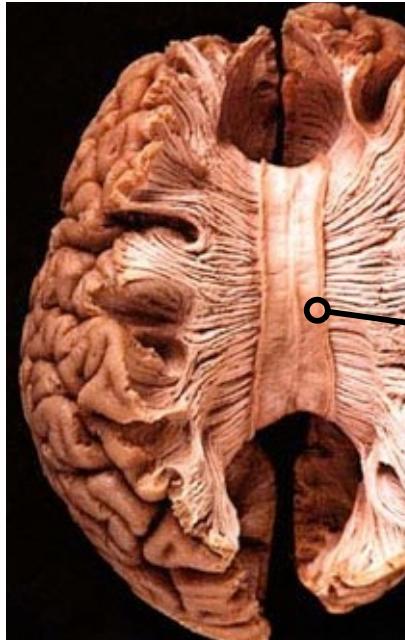
Extra-cellular diffusion  
—  
restricted diffusion



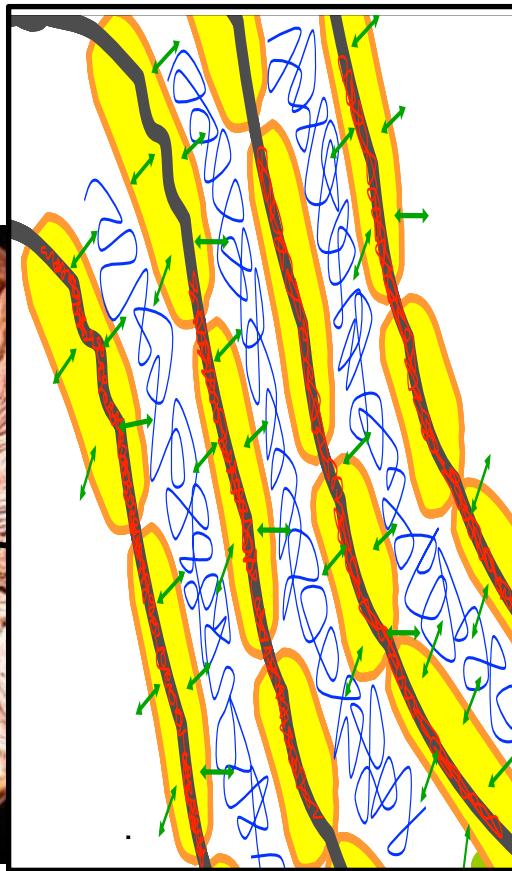
Exchange



# Biophysical model of the diffusion signal



Zhang, OHBM, 2014



Fieremans, ESMRMB, 2015

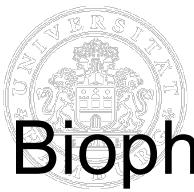


Intra-cellular diffusion  
=  
restricted diffusion

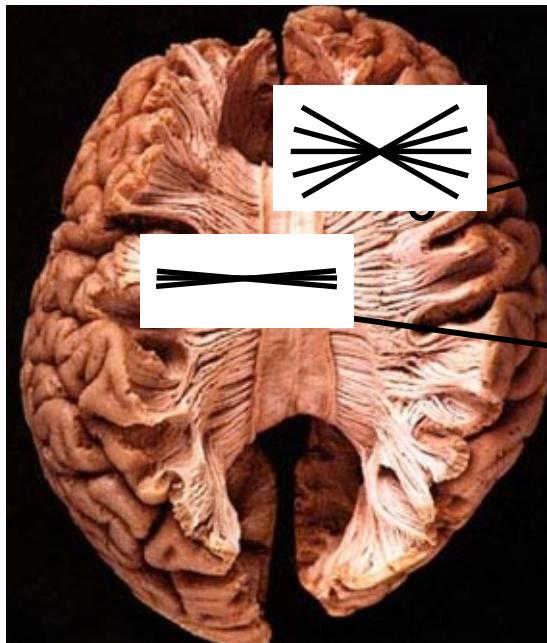


Extra-cellular diffusion  
—  
restricted diffusion

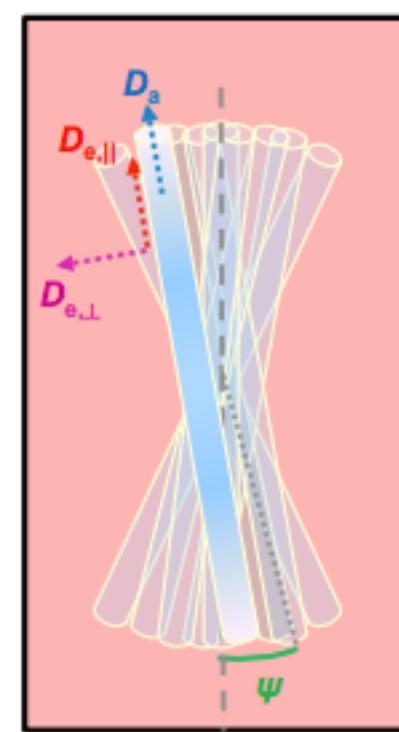




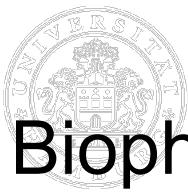
# Biophysical model of the diffusion signal



Zhang, OHBM, 2014

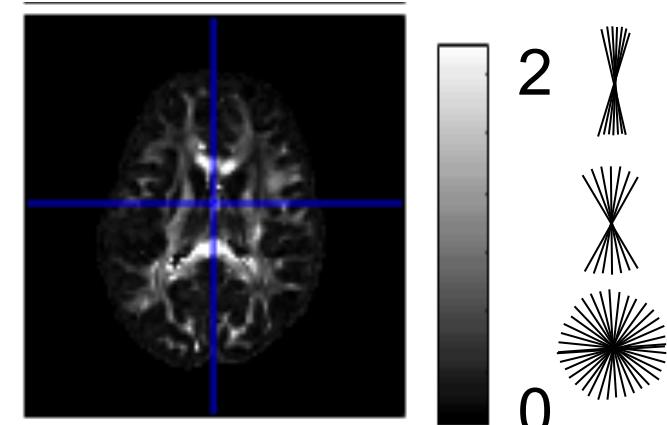
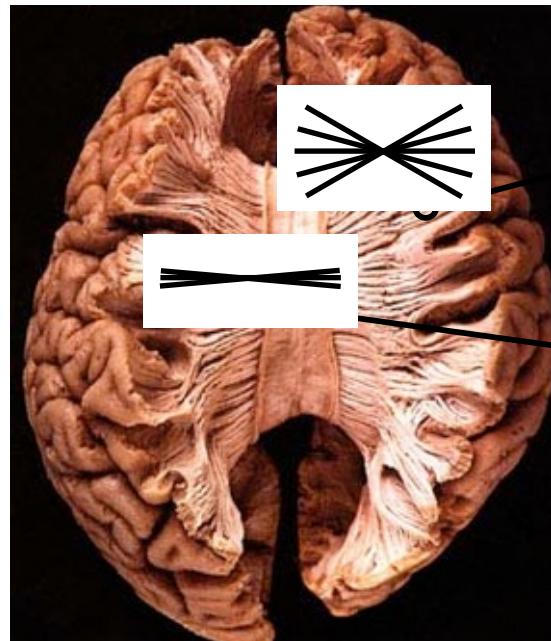


Fieremans, ESMRMB, 2015

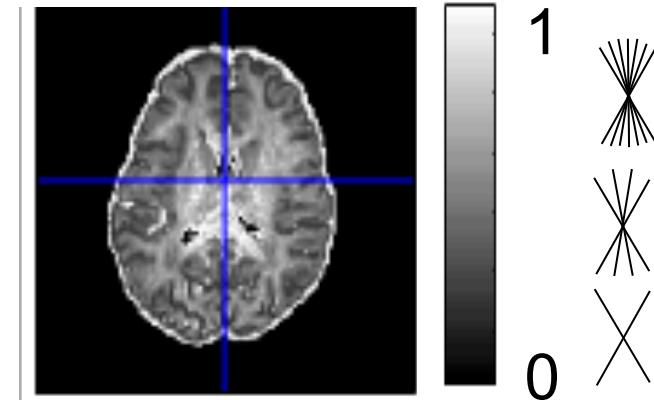


# Biophysical model of the diffusion signal

Fiber dispersion “” [a. u.]



Fiber density “ $\tau$ ” [a. u.]



Zhang, OHBM, 2014



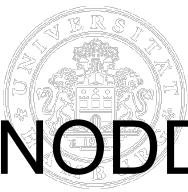
# NODDI-DTI:

fiber density “ $\nu$ ”

~

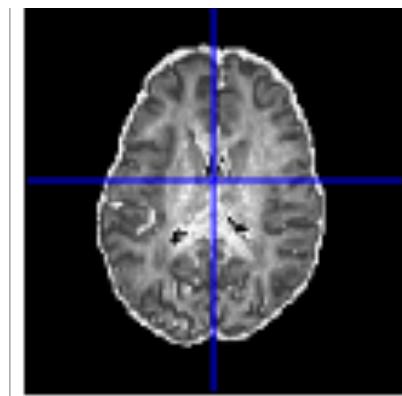
mean diffusivity “MD”

$$\nu = 1 - \sqrt{\frac{1}{2} \left( \frac{3\text{MD}}{d} - 1 \right)}$$

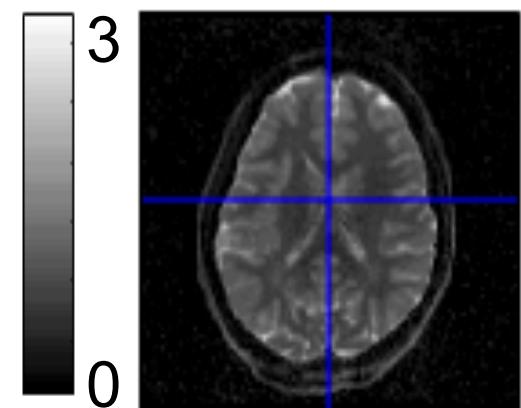


# NODDI-DTI: fiber density “ $\nu$ ”~ mean diffusivity “MD”

Fiber density [a. u.]



Mean diffusivity  $\left[ \frac{\text{mm}^2}{\text{s}} \times 10^{-3} \right]$



$$\nu = 1 - \sqrt{\frac{1}{2} \left( \frac{3MD}{d} - 1 \right)}$$



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# NODDI-DTI:

fiber dispersion “ $\tau$ ”

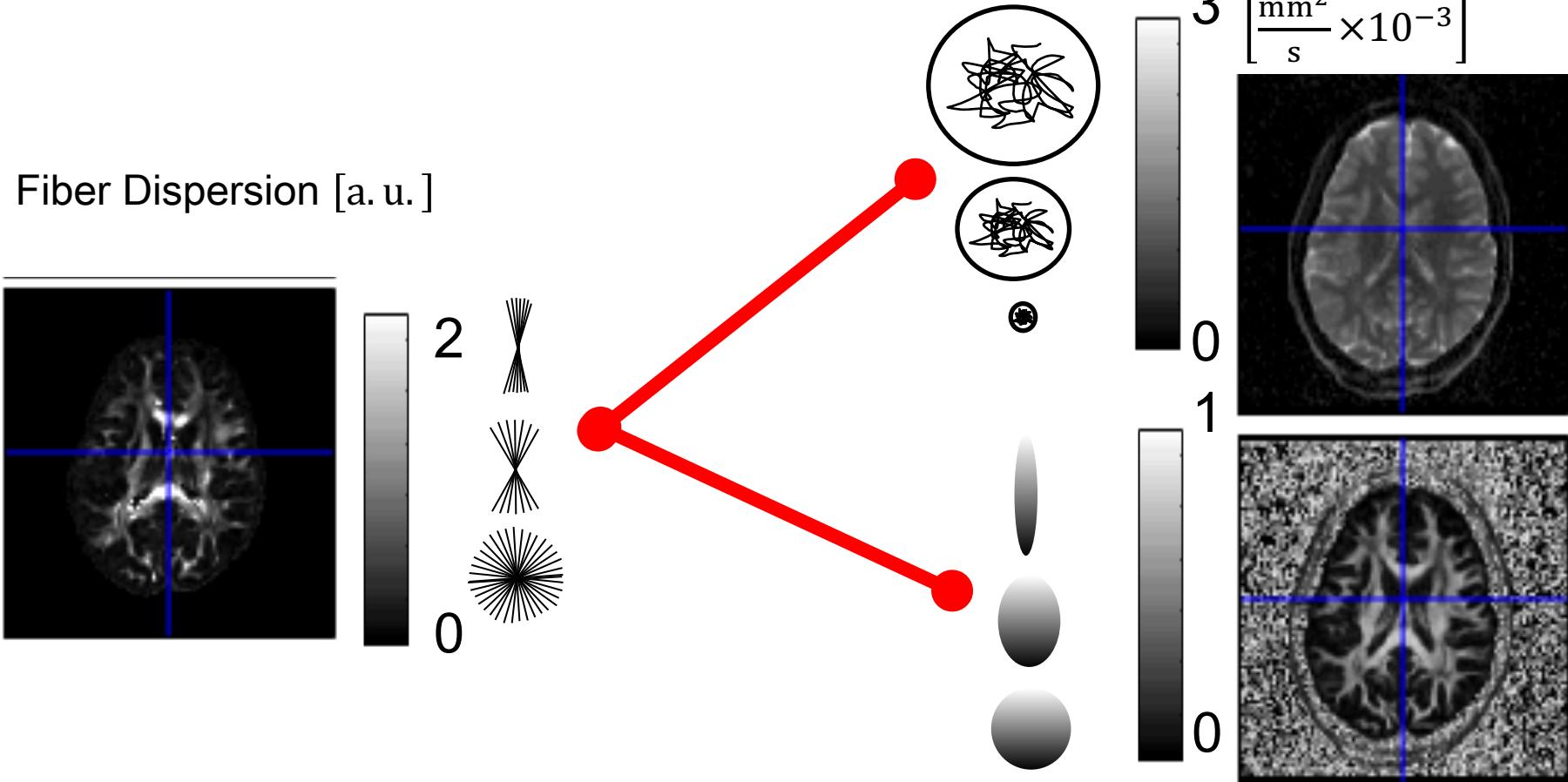
~

mean diffusivity “MD” & fractional anisotropy “FA”

$$\tau = \frac{1}{3} \left( 1 + \frac{4}{|d - MD|} \frac{MD \times FA}{\sqrt{3 - 2FA^2}} \right)$$



# NODDI-DTI: fiber dispersion “ $\tau$ ” ~ mean diffusivity “MD” & fractional anisotropy “FA”



$$\tau = \frac{1}{3} \left( 1 + \frac{4}{|d - MD|} \frac{MD \times FA}{\sqrt{3 - 2FA^2}} \right)$$

Fractional Anisotropy [a. u.]  
Edwards et al., 2017



## Contributors



- Lars Ruthotto, Emroy University (HySCO and DKI)



- Karsten Tabelow & Jörg Polzehl, WIAS, Berlin (msPOAS and DKI)



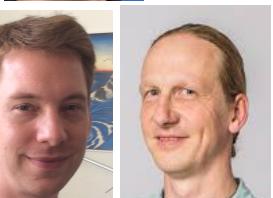
- Volkmar Glauche, Universität Freiburg (FA-VBS)



- Luke Edward, MPI-CBS, Leipzig (NODDI-DTI)



- Gergely David, University Zürich (Spinal Cord branch - *in prep.*)



- Jan-Malte Öschger, UKE (Rician noise bias – *in prep.*)