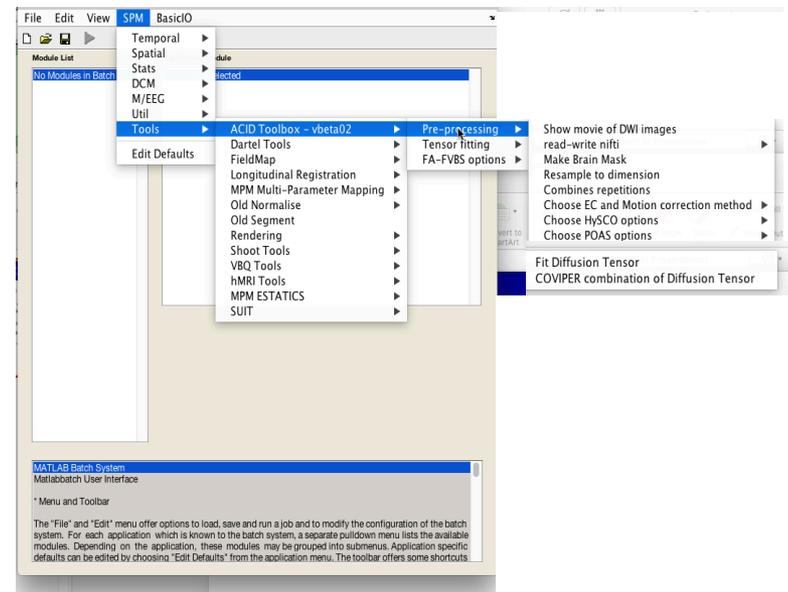


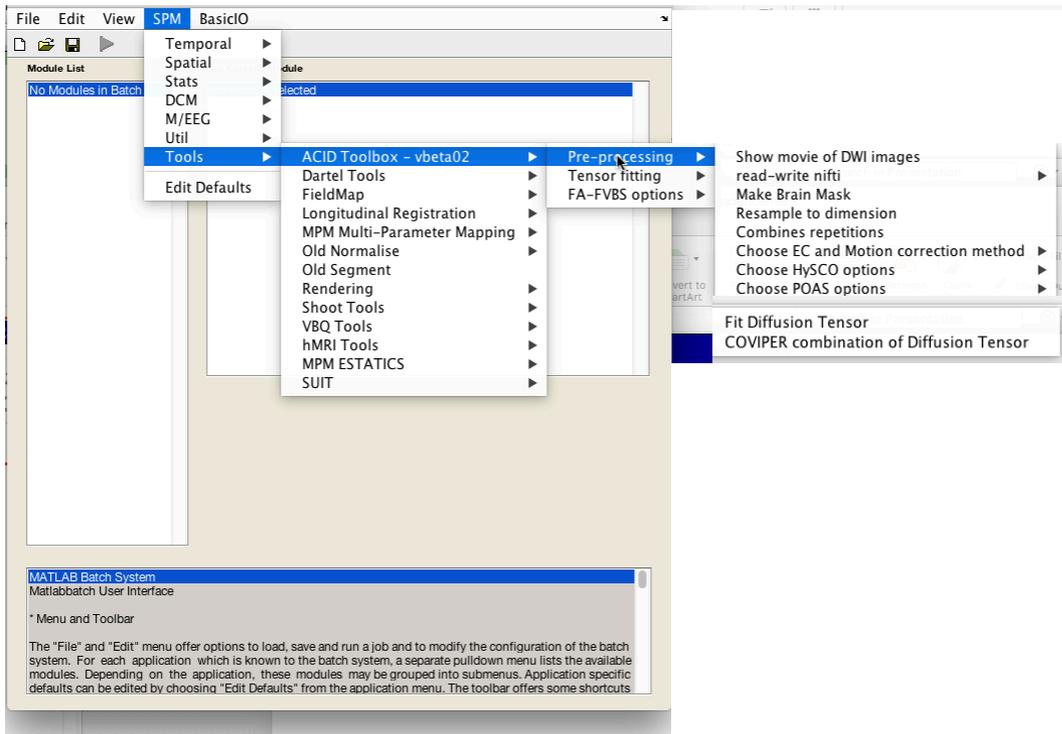
Artefact Correction In Diffusion MRI

ACID SPM toolbox

Siawoosh Mohammadi

Department of Systems Neuroscience
University Medical Center Eppendorf
Hamburg, Germany
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

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



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Artefact Correction In Diffusion MRI

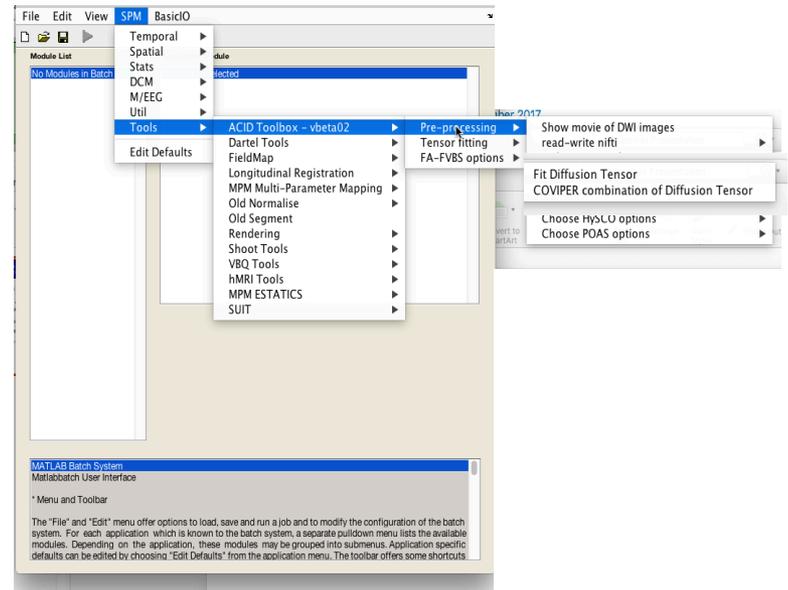
ACID SPM toolbox



NODDI-DTI

Siawoosh Mohammadi

Department of Systems Neuroscience
University Medical Center Eppendorf
Hamburg, Germany
s.mohammadi@uke.de





- 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



- Diffusion MRI: why, how, and what does it mean?
- Pre-processing steps
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Why is diffusion more interesting than standard structural imaging?



Histology



T1w image



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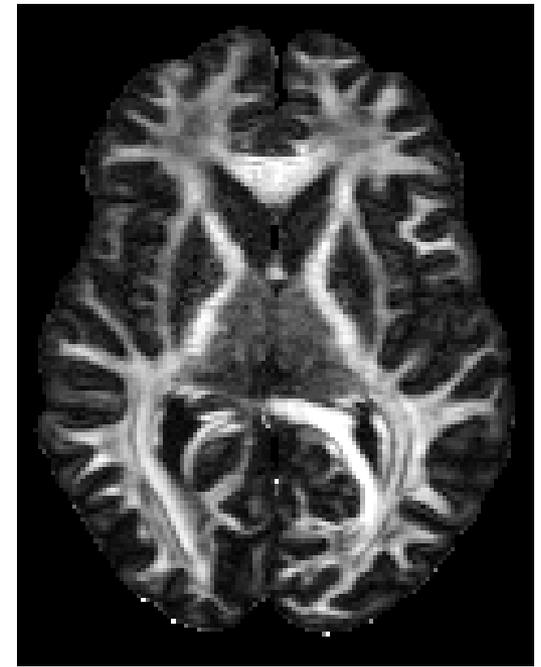
Diffusion MRI reveals microstructural information



Histology

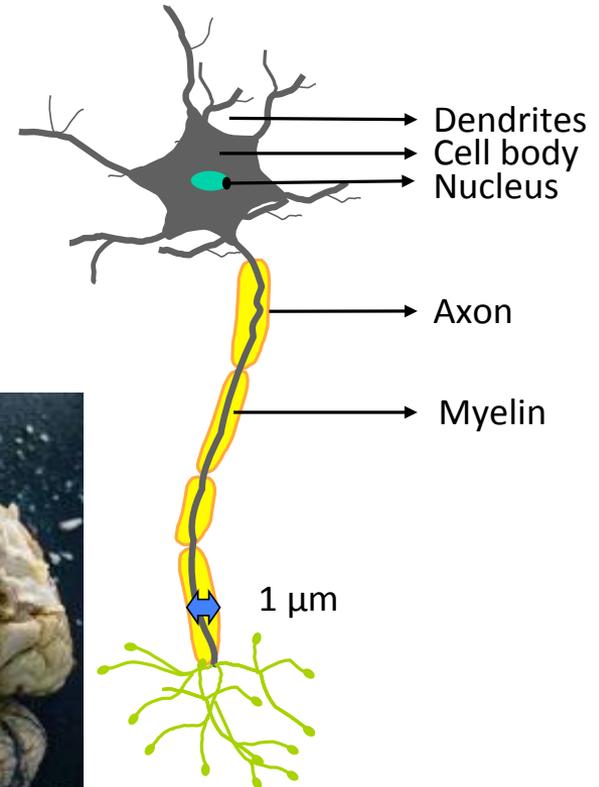


T1w image

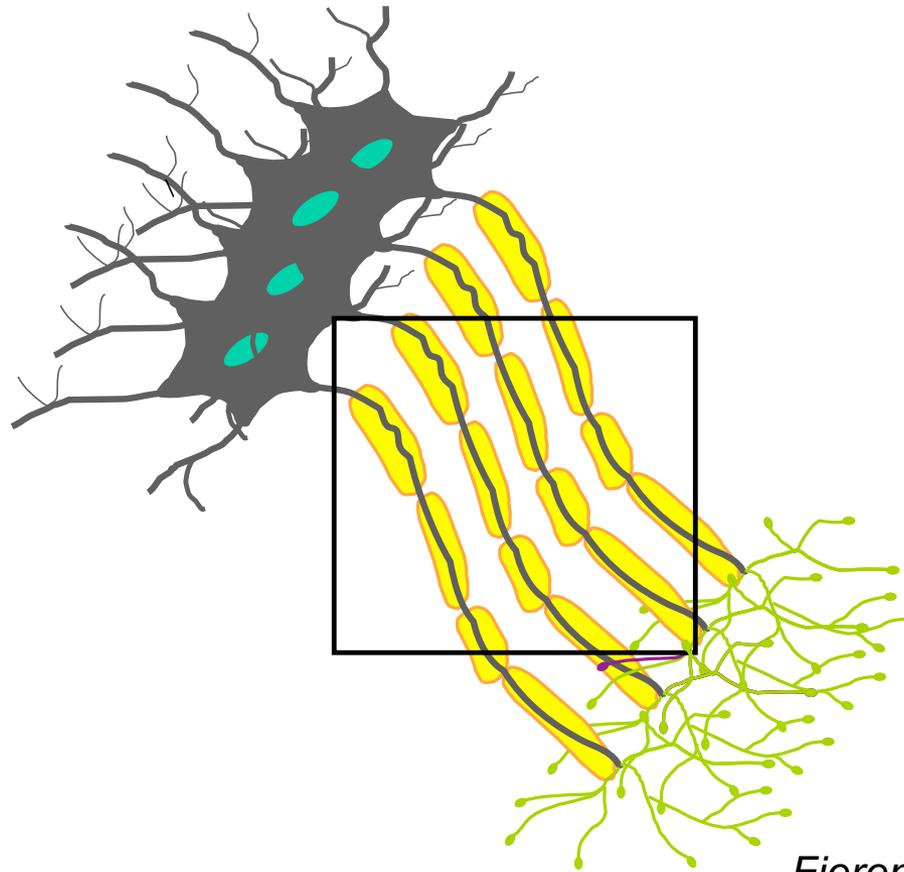


DTI index map

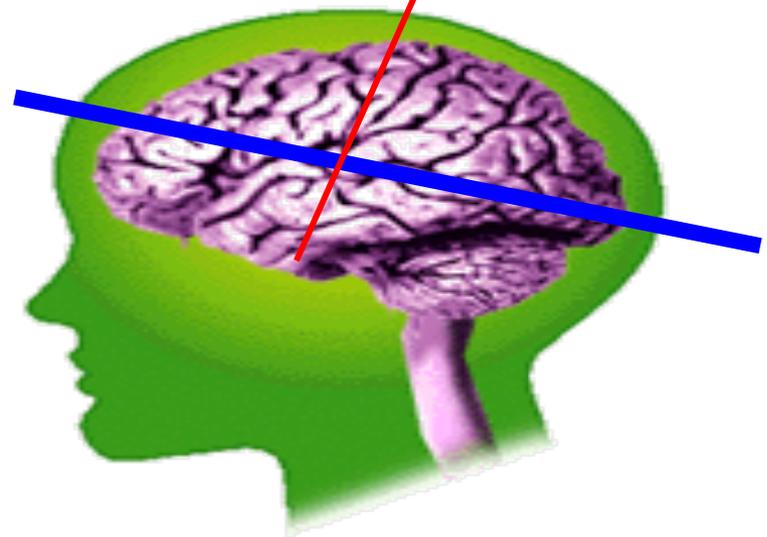
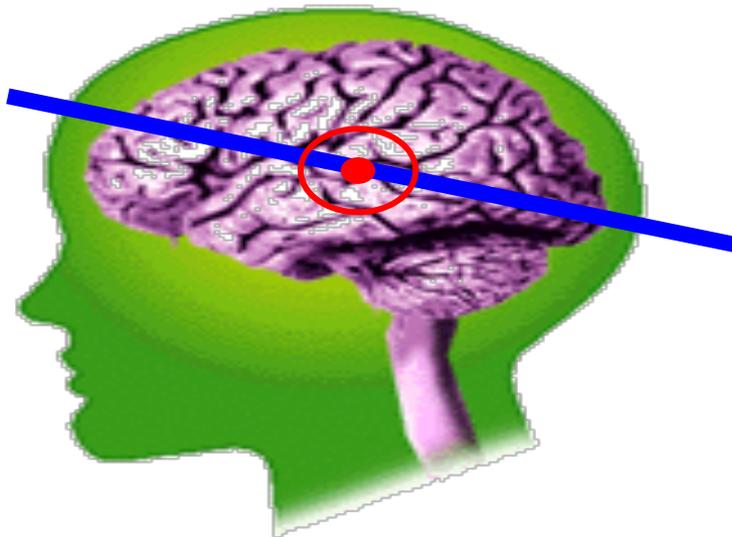
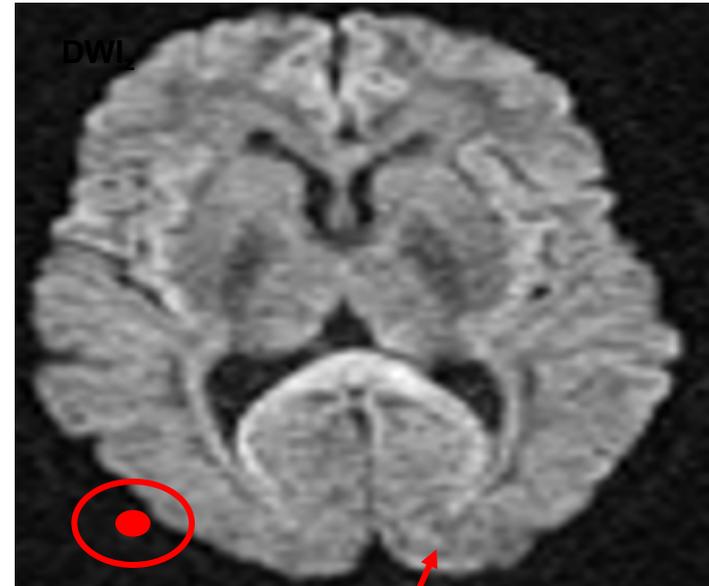
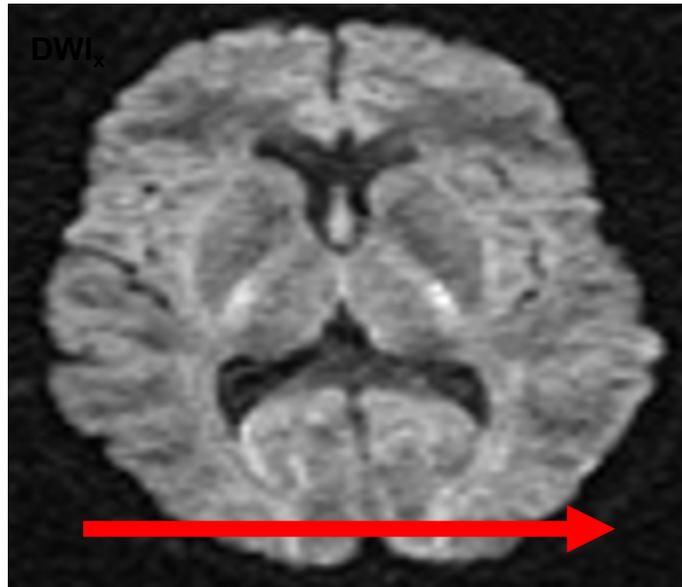
Main features of fibers in the white matter



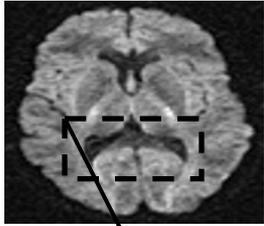
Fieremans, *ESMRMB*, 2015



Fieremans, ESMRMB, 2015



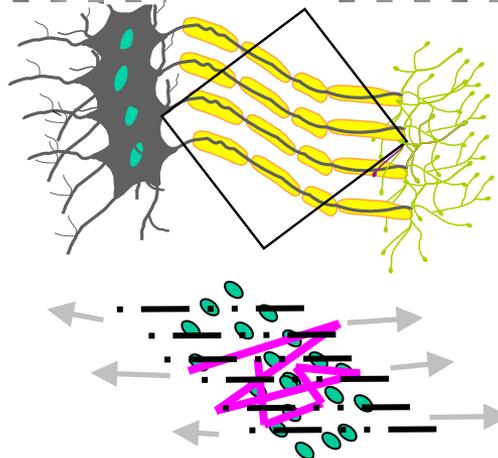
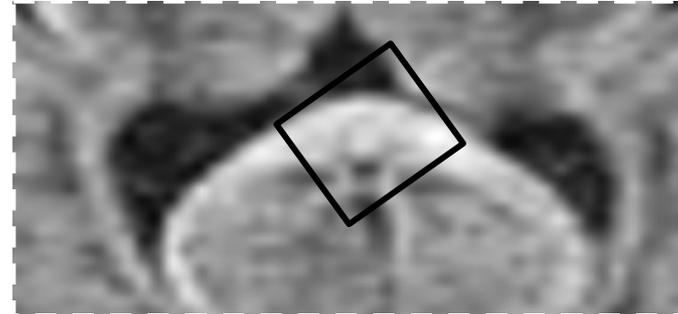
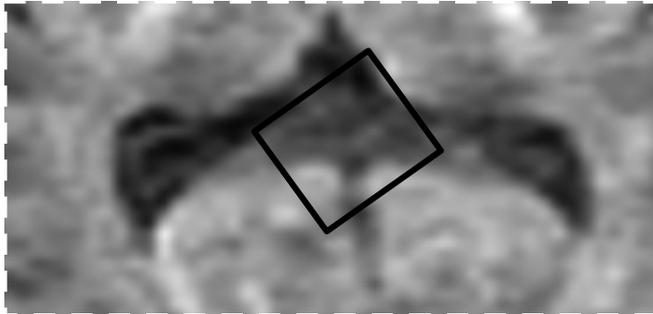
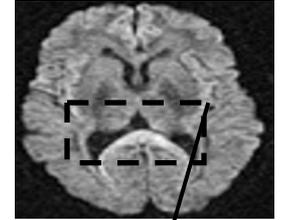
Diffusion weighted images



$$\vec{G}^D = (G_x \ 0 \ 0)$$



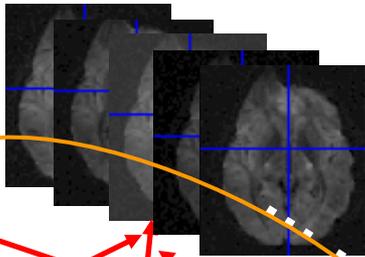
$$\vec{G}^D = (0 \ 0 \ G_z)$$



What do we need for diffusion MRI?

Shell 1
(b-value e.g 1000 s/mm²)

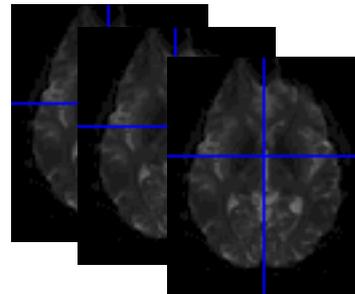
n DW images



b-vectors

Shell 0
(b-value e.g 0 or 100 s/mm²)

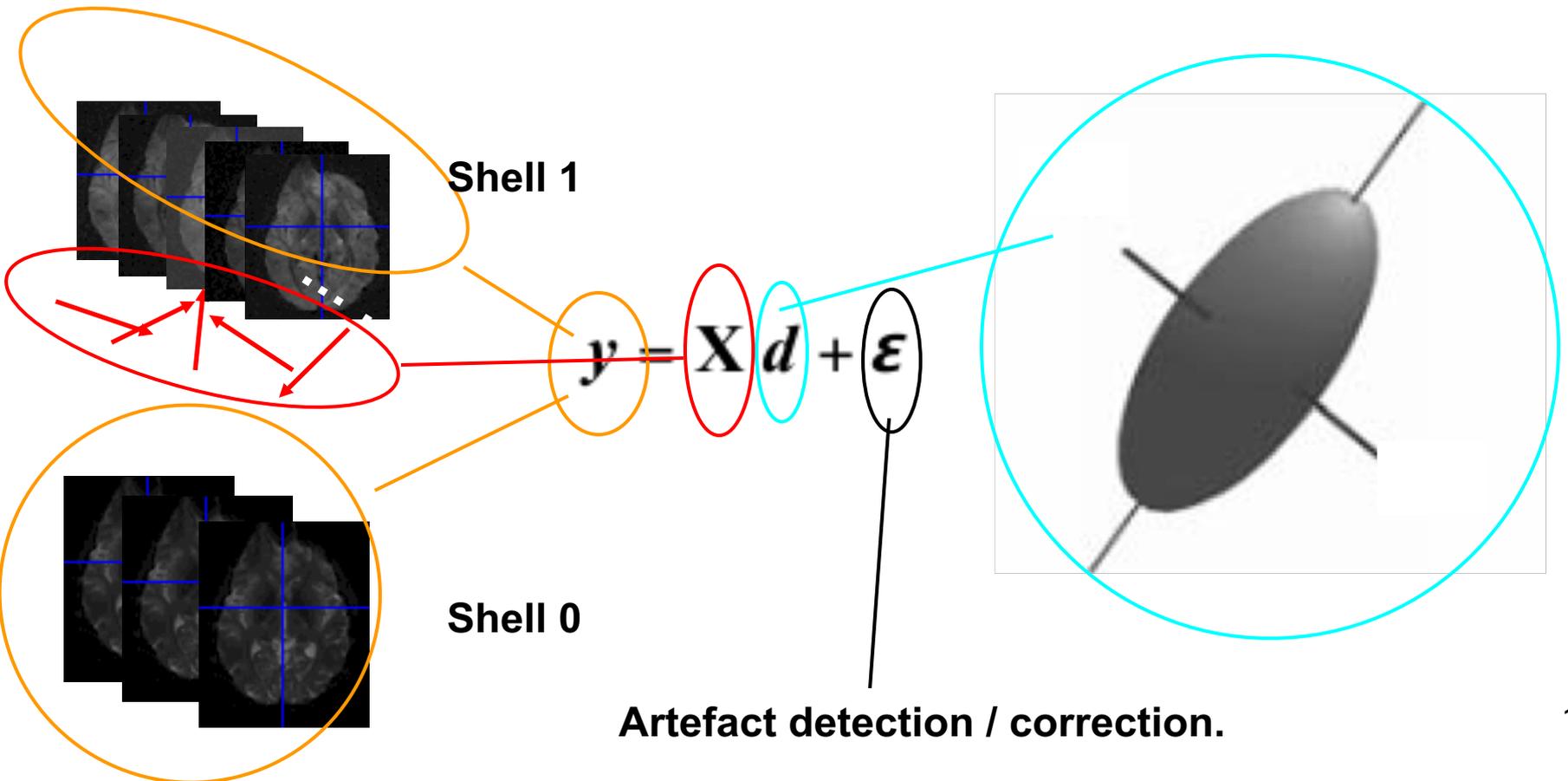
m reference images



+

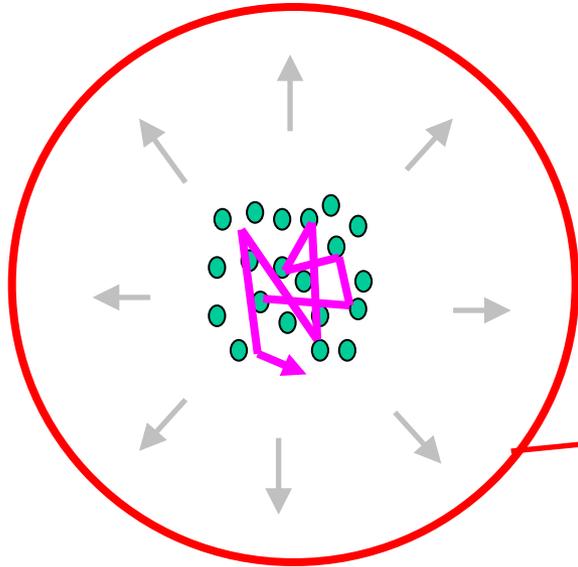
Model

The general linear model framework for diffusion MRI

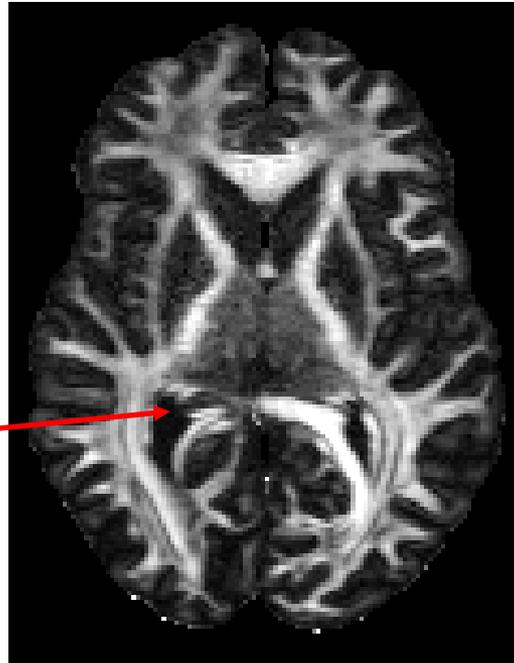


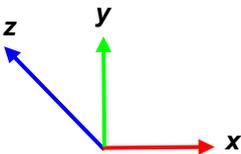
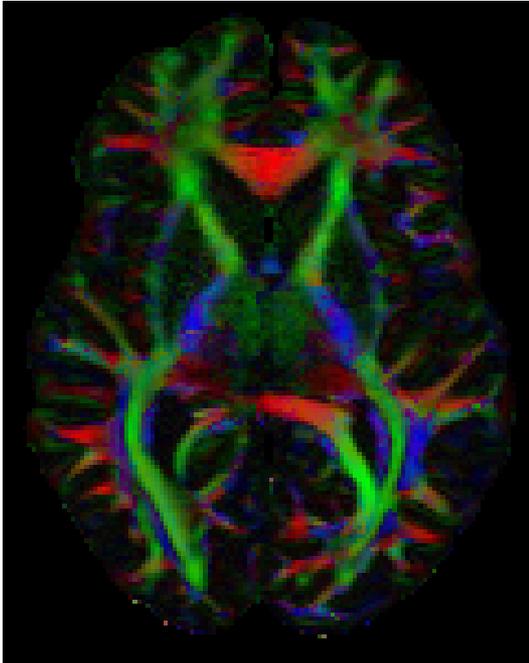


Fractional anisotropy - FA



**CSF: Isotropic
diffusion**

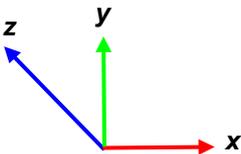
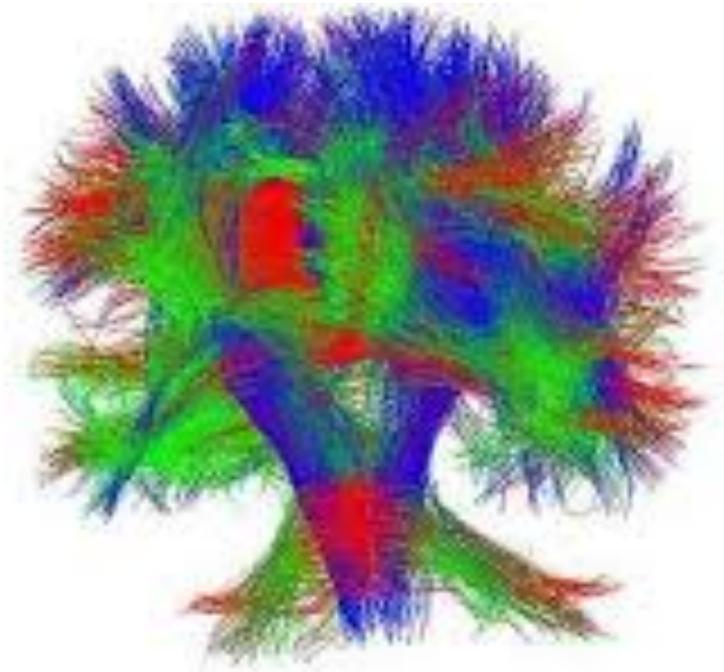
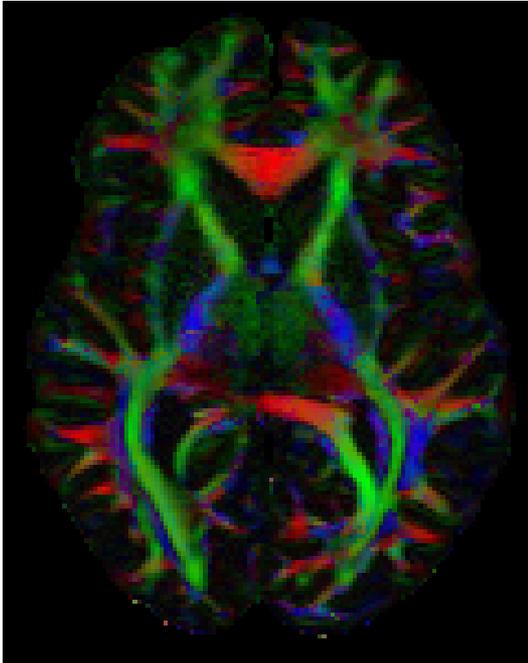






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Diffusion MRI reveals orientation information



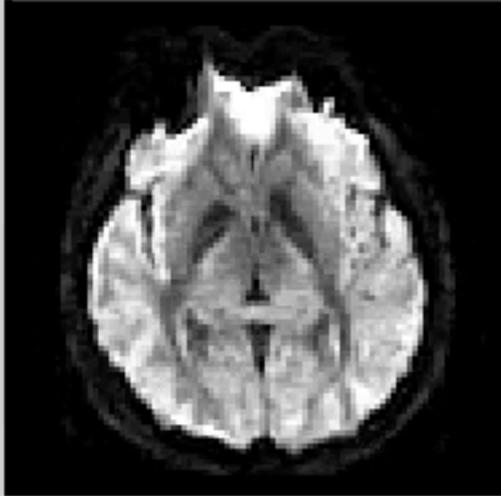
For tractography in SPM contact Marco Reisert:

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



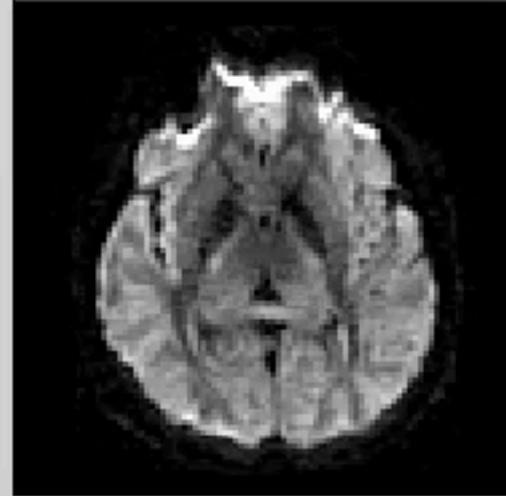
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Single spin echo

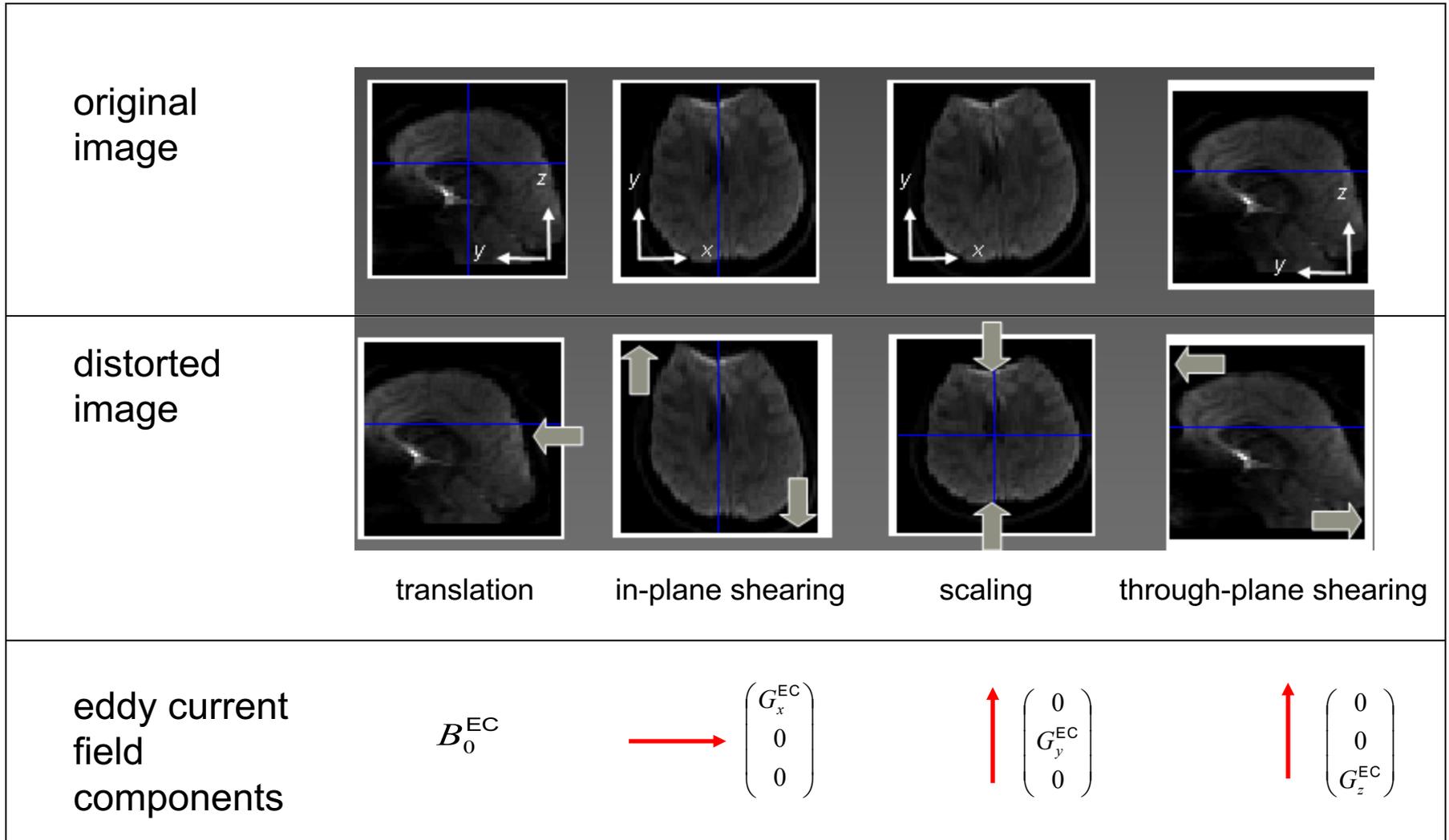


Stejskal & Tanner, JCP, 1965

Double spin echo



Reese et al., MRM, 2003





The screenshot shows the SPM Batch Editor interface. The 'Tools' menu is open, and the path 'Tools > ACID Toolbox - vbeta02 > Pre-processing > Tensor fitting > FA-FVBS options > Choose EC and Motion correction method > Choose EC and Motion correction multi targets' is highlighted. The 'Write EC and Motion corrected Images' option is also visible. The background shows a 'Batch Editor' window with a 'Module List' containing 'No Modules in Batch'. A 'MATLAB Batch System' window is open at the bottom, displaying the 'Matlabbatch User Interface' and a message about the 'File' and 'Edit' menus. A terminal window in the background shows the date '18:04:08 - 26/09/2017' and the text '.....done'. A code editor window on the right shows MATLAB code for processing DWI images, including commands like 'PMSK=spm_se', 'AMSK=ACID_r', and 'spm12 mispl'.



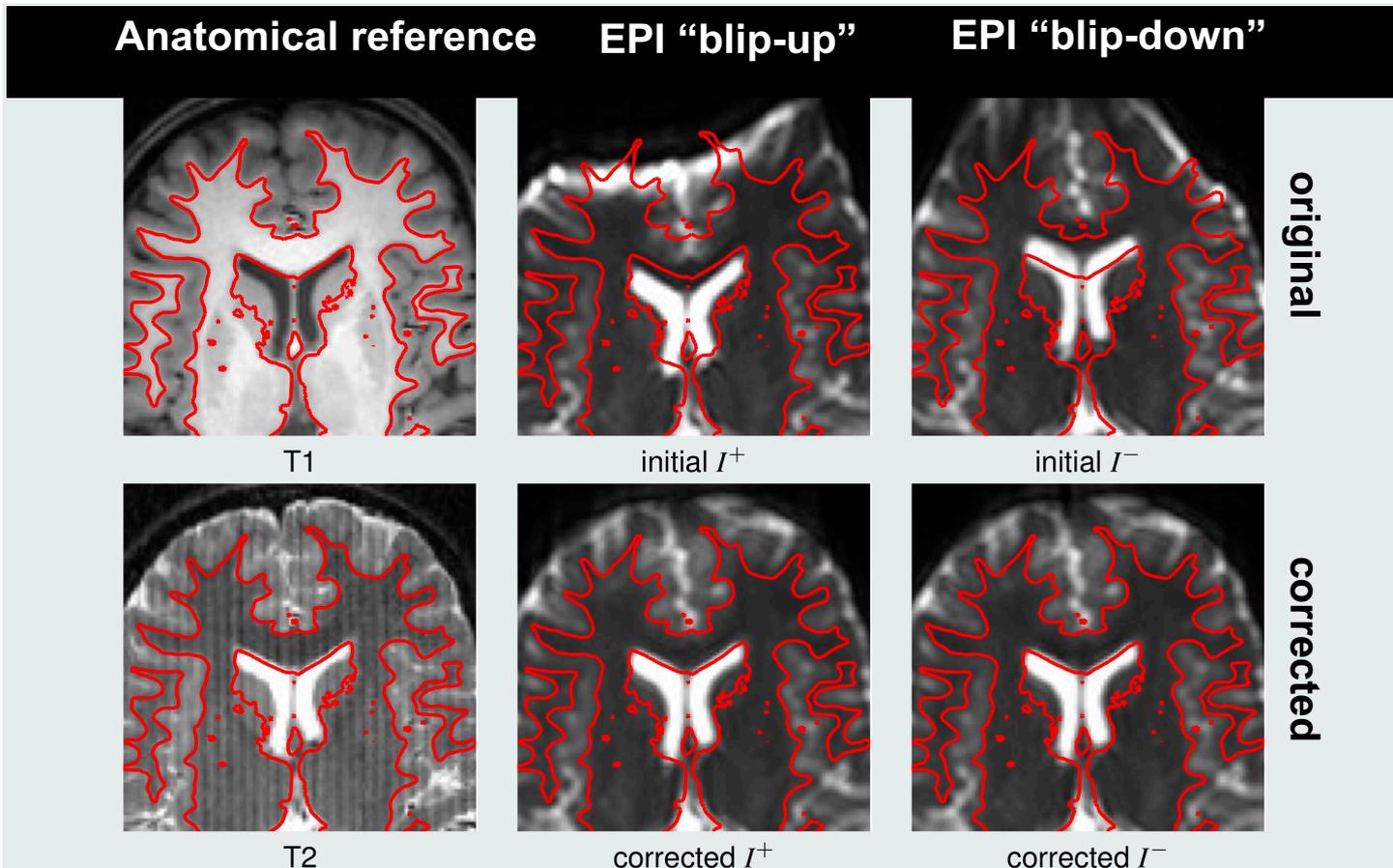
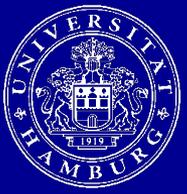
The screenshot displays the MATLAB Batch Editor interface. The main window is titled "Batch Editor" and has a menu bar with "File", "Edit", "View", "SPM", and "BasicIO". The "Module List" on the left contains "EC and Motion Correction". The "Current Module" is "EC and Motion Correction multi targets". The configuration parameters are as follows:

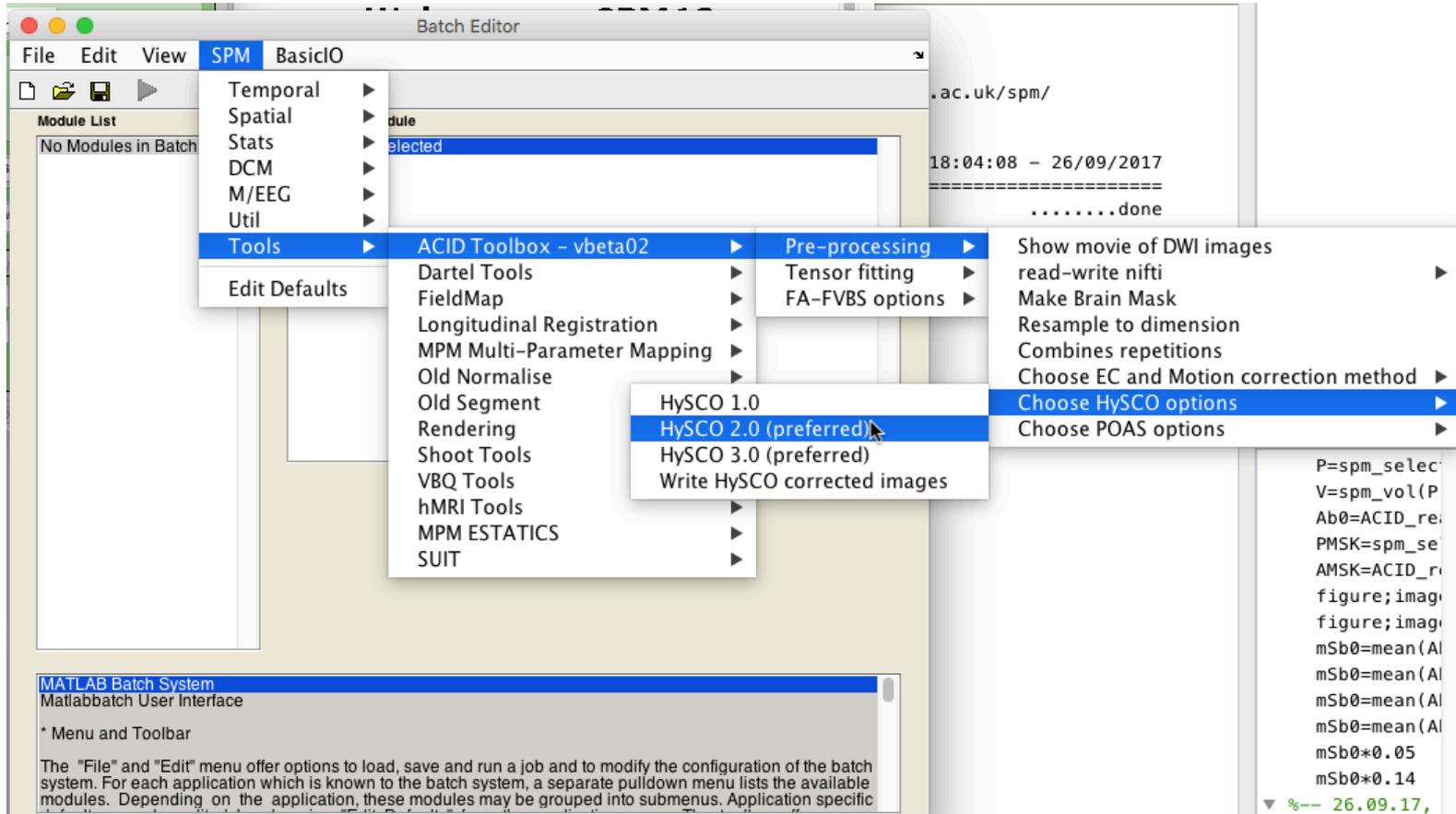
Parameter	Value
Source Images	<-X
Biasfield Image (or done for none)	<-X
b-values source images	[5 1000 1000 2000]
Defaults	
. Enter 12 binaries	1x12 double
. Choose write option	ON
. Choose display option	ON
. Dimension of phase-encoding	y
. Output format	3d output
. Registration scheme	Volume-wise
. Are b=0 images interspersed?	ON

The "Current Item: Source Images" section is currently empty. A "Specify..." button is located below this section. At the bottom of the window, a text box provides instructions: "Source Images: Select source images. These images will be registered to the sources image."



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The screenshot displays the MATLAB Batch Editor interface for the HySCO 2.0 module. The main window is titled "Batch Editor" and shows a "Module List" on the left with "HySCO 2.0 (preferred)<-X" selected. The right pane shows the configuration for the "Current Module: HySCO 2.0 (preferred)".

Parameter	Value
Help on: HySCO 2.0 (preferred)	
Blip-up image	<-X
Blip-down image	<-X
Other blip-up images	
Other blip-down images	
EC and MO Parameters (up)	<-X
EC and MO Parameters (dw)	<-X
Dimension of phase-encoding	y
Maximal data resolution	full
Apply to other images	yes
Weight for "diffusion" regularizer.	50
Weight for "Jacobian" regularizer.	10
Output format	3d output
Choose dimensions for multilevel coarsening.	[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.

The screenshot displays the SPM Batch Editor interface. The main window shows the configuration for the 'HySCO 2.0 (preferred)' module. The 'Blip-up image' parameter is selected, and its help text is visible: 'Select one image volume acquired with blip-up. The reference field inhomogeneity is estimated from this image.'

Other parameters in the configuration include:

- 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: y
- Maximal data resolution: full
- Apply to other images: yes
- Weight for "diffusion" regularizer: 50
- Weight for "Jacobian" regularizer: 10
- Output format: 3d output
- Choose dimensions for multilevel coarsening: [1 1 1]

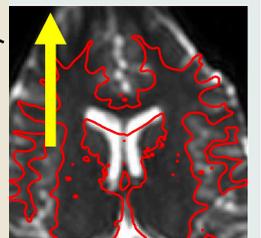
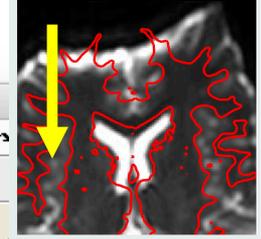
A yellow arrow points from the 'Blip-up image' parameter to a brain scan image on the right, which shows red contours indicating the estimated field inhomogeneity.

The screenshot shows the SPM Batch Editor interface. The 'Tools' menu is open, and the 'HySCO 2.0 (preferred)' module is selected in the 'Module List'. The configuration parameters for the current module are as follows:

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

The 'Current Item: Blip-up image' section is currently empty. Below the configuration area, there is a 'Specify...' button. At the bottom of the window, a help text for the 'Blip-up image' parameter is visible:

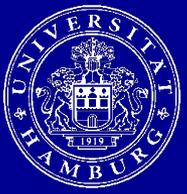
Blip-up image
Select one image volume acquired with blip-up. The reference field inhomogeneity is estimated from this image.



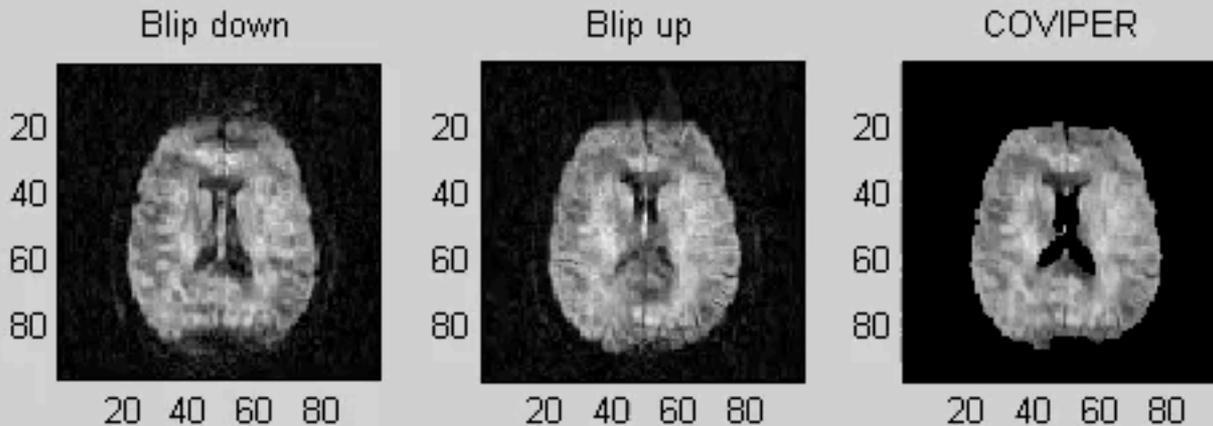
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```



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

Mohammadi et al., MRM, 2012

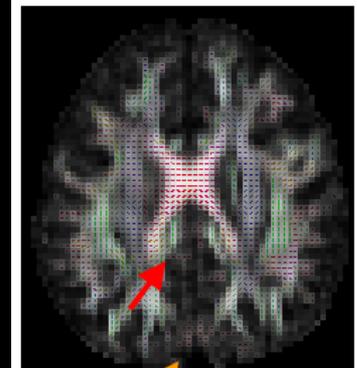
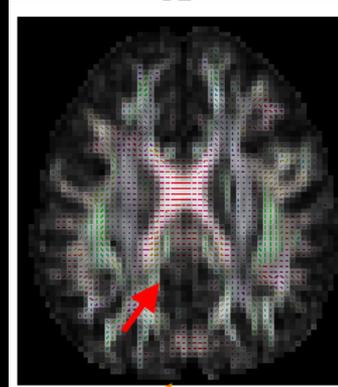
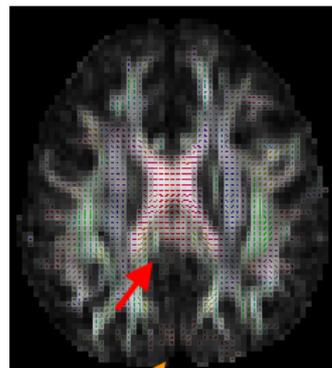
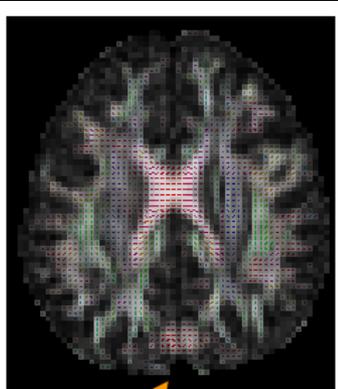
blip-up

blip-down

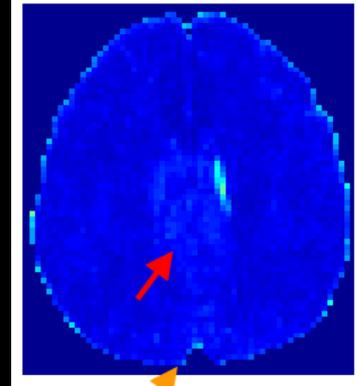
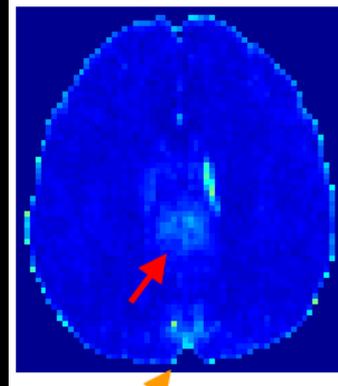
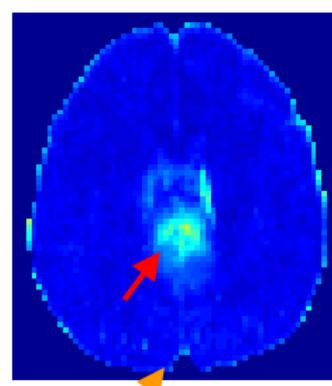
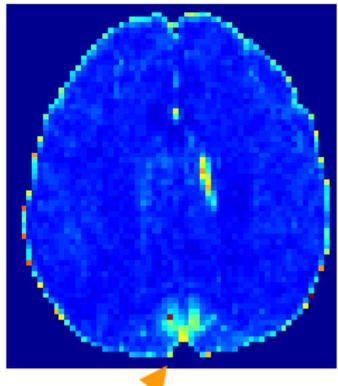
arithmetic mean

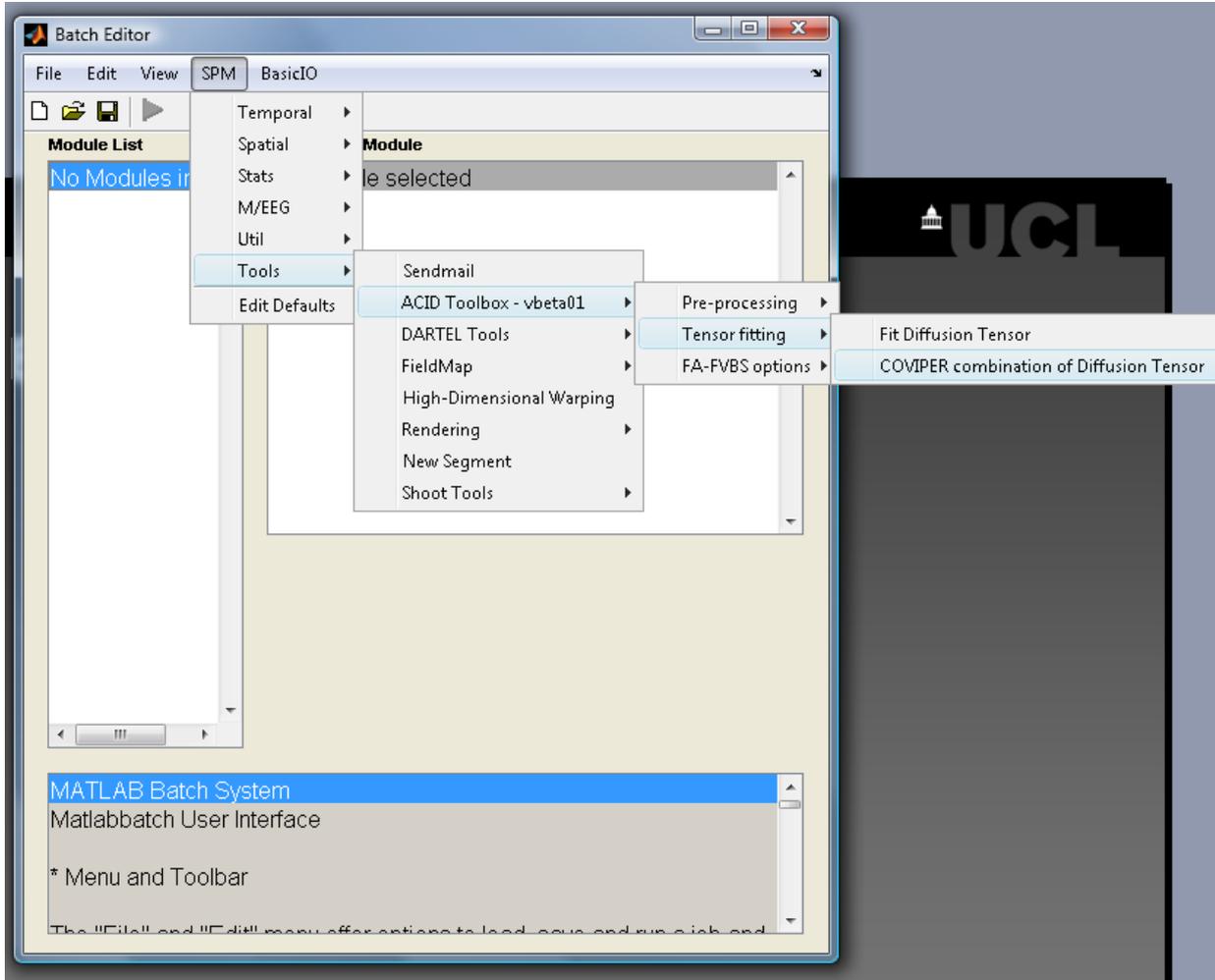
COVIPER

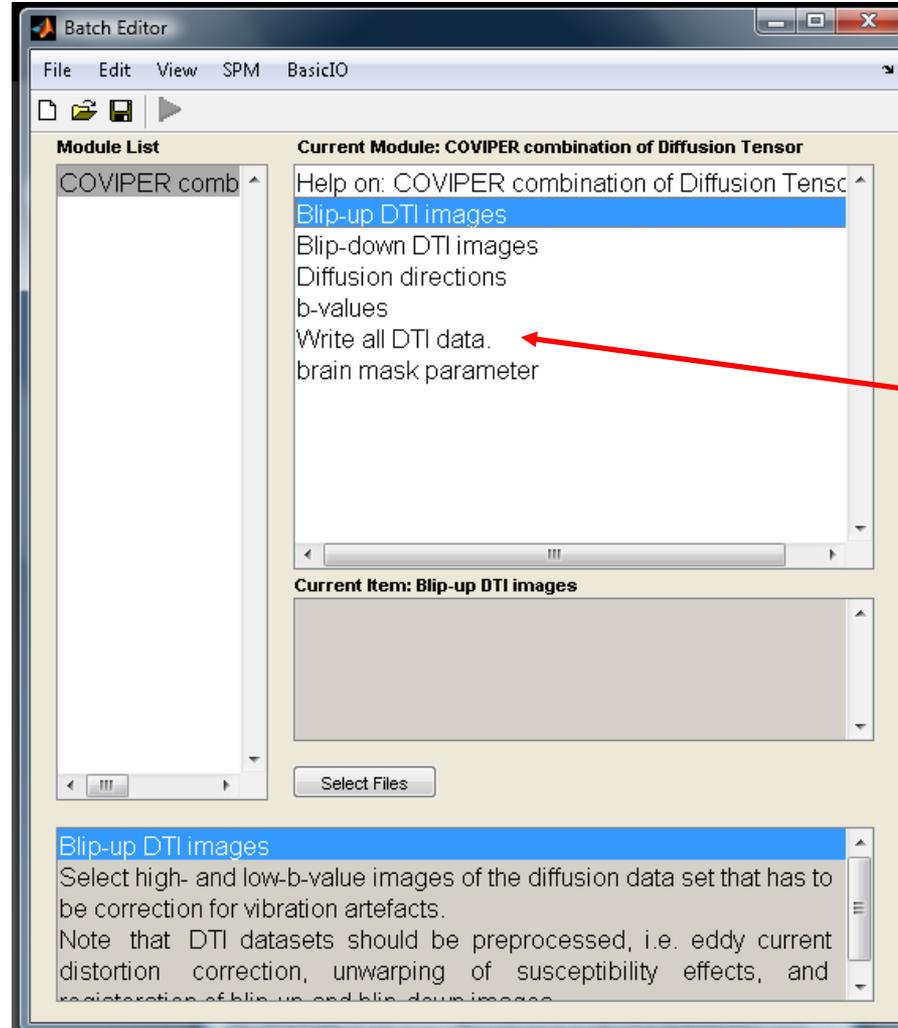
FA



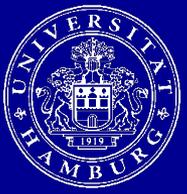
rms(ϵ)





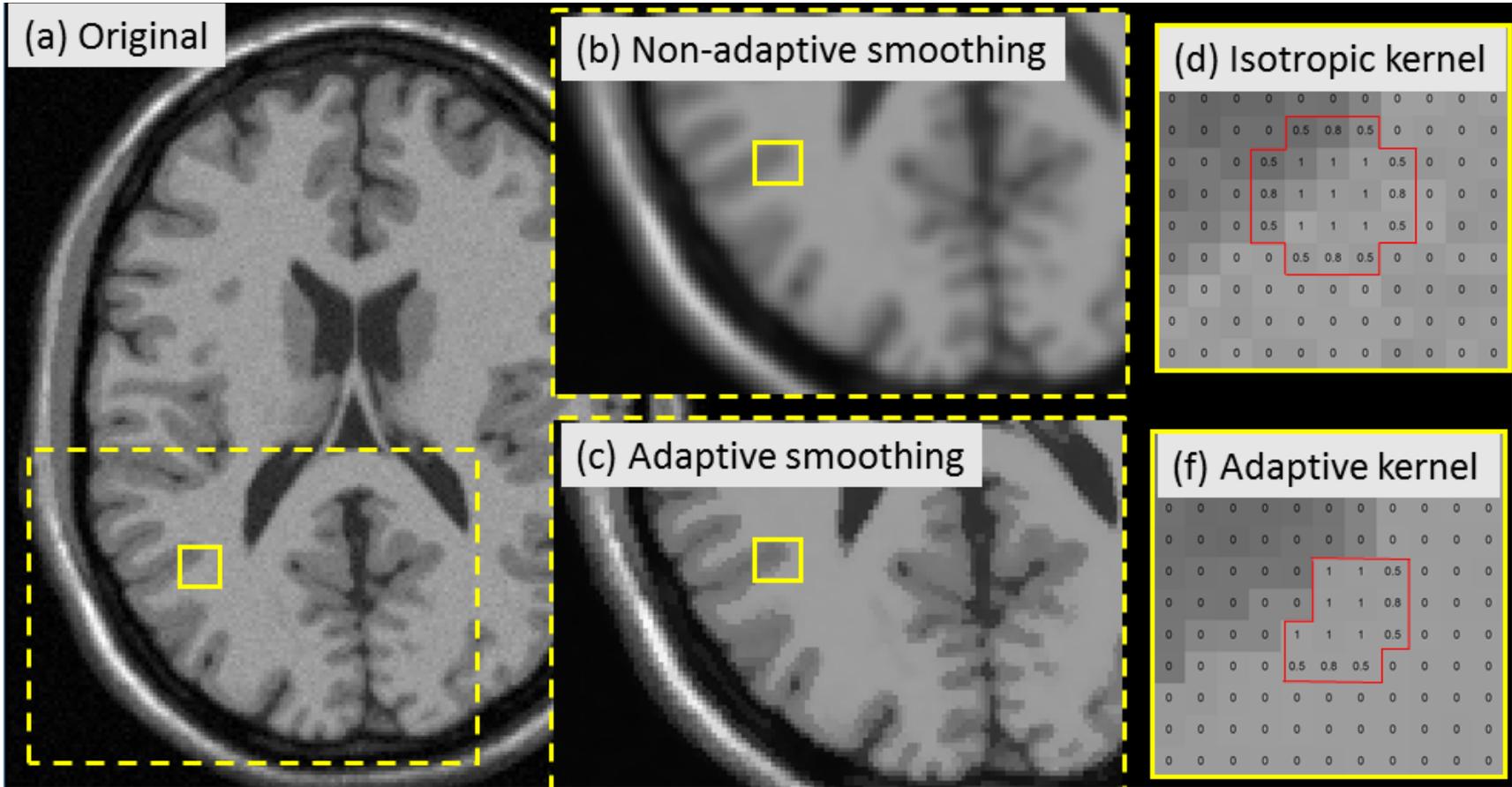


**Corrected DTI
dataset**

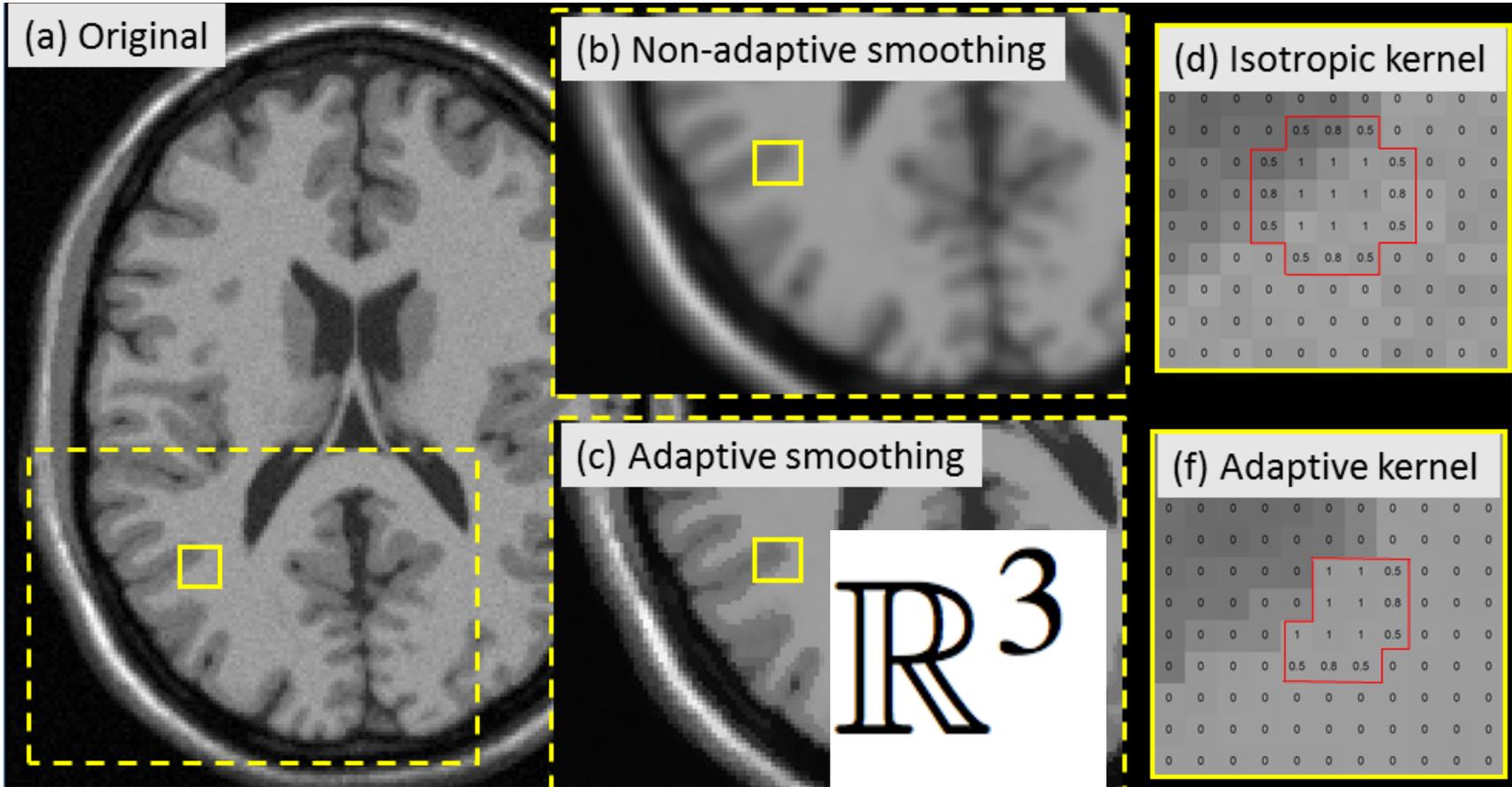


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What is adaptive denoising?

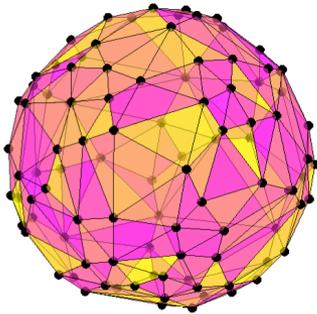


What is adaptive denoising?



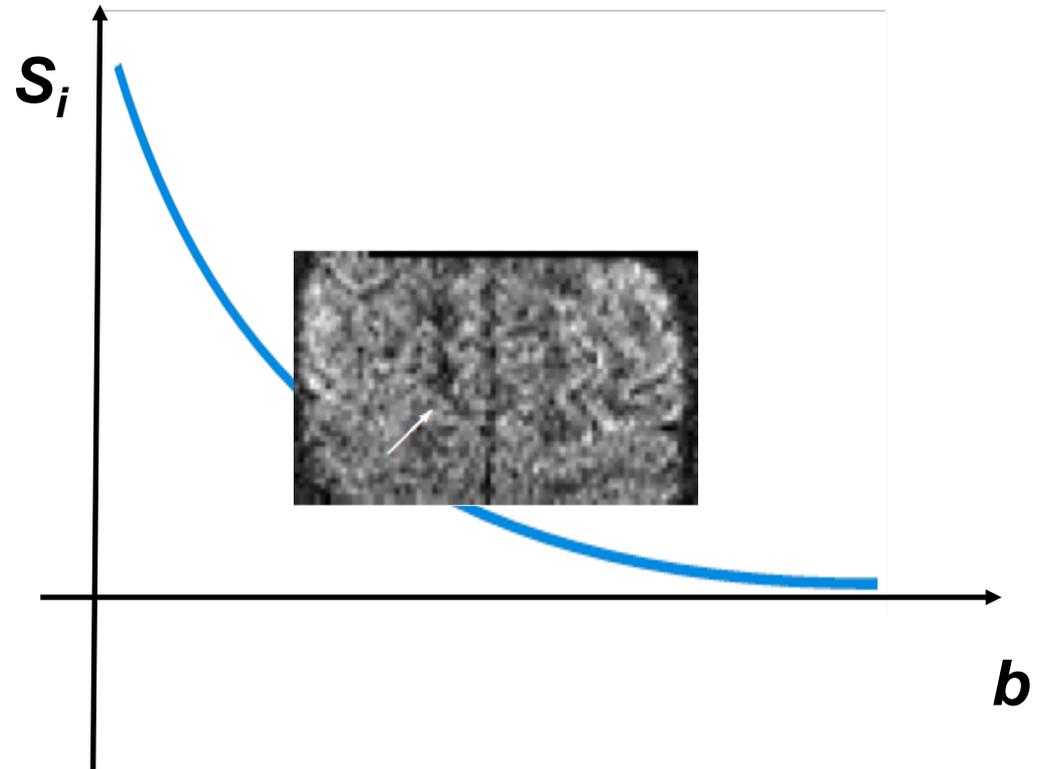
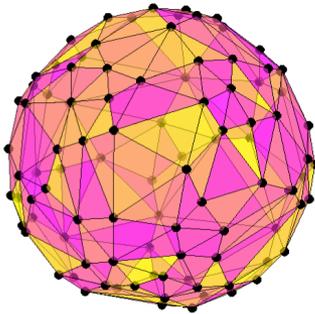
\mathbb{R}^3

S^2



\mathbb{R}^3

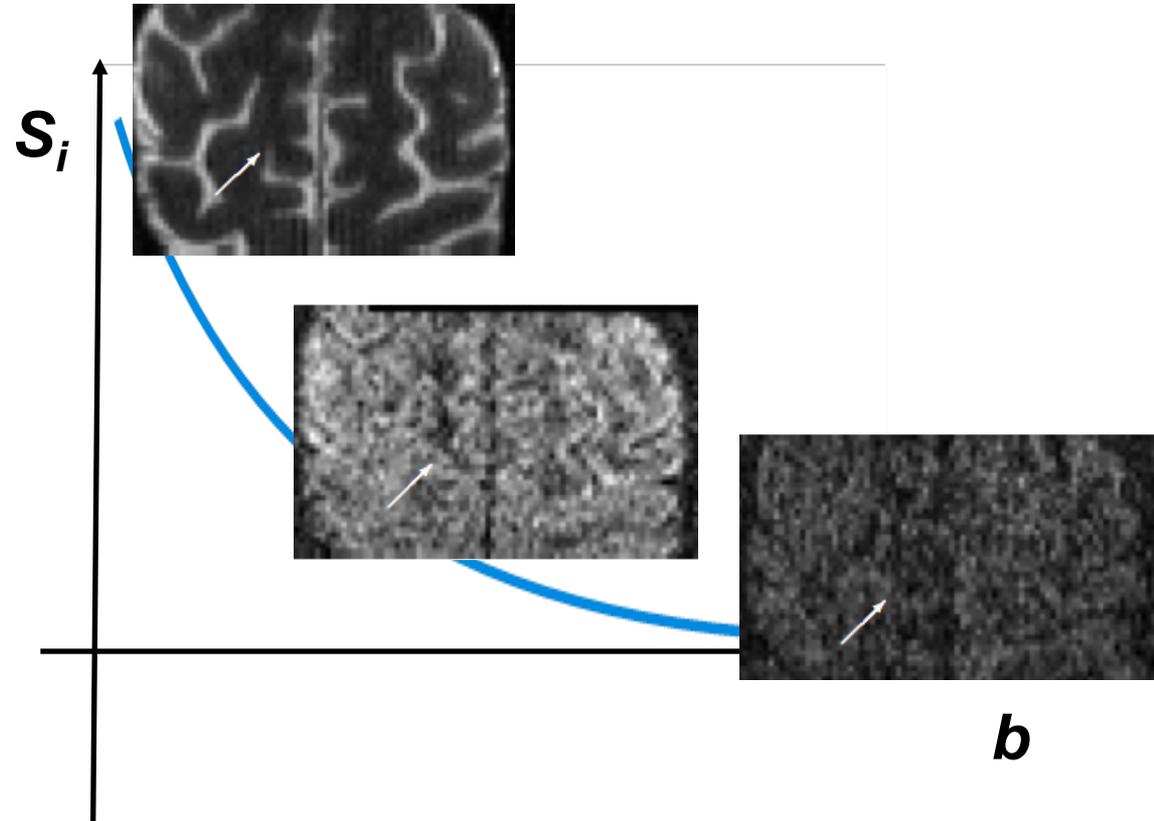
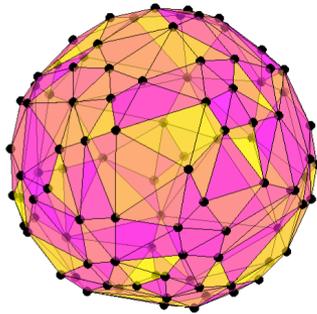
S^2



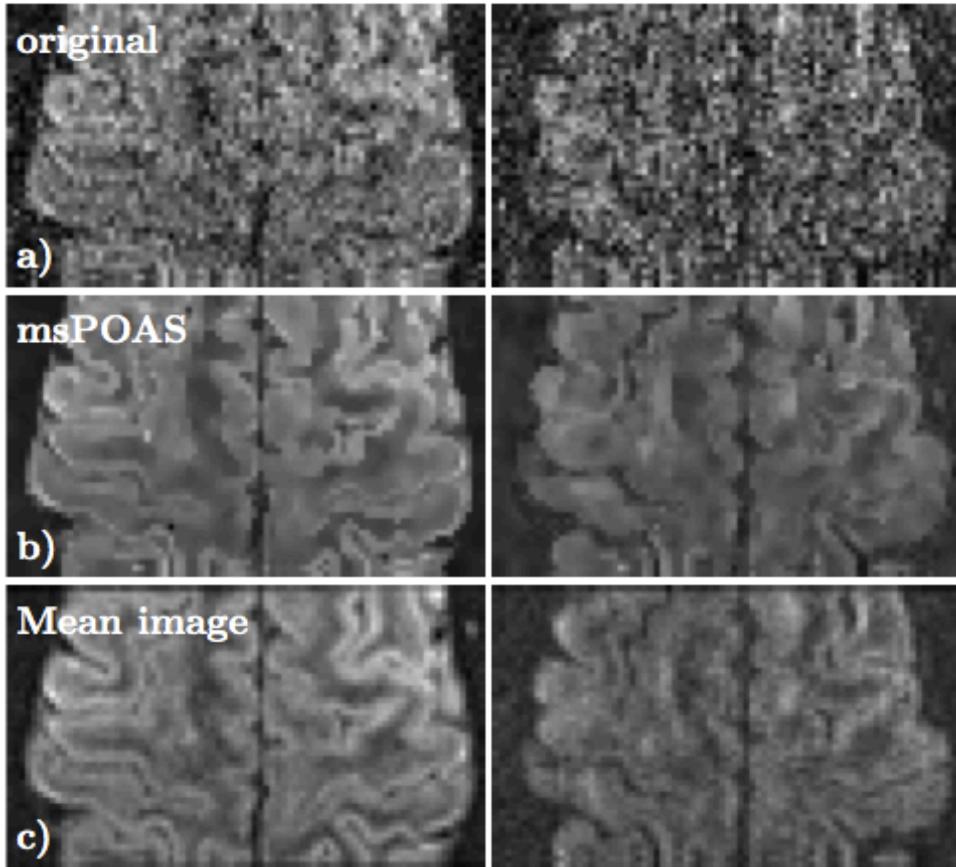
Multiple shells

\mathbb{R}^3

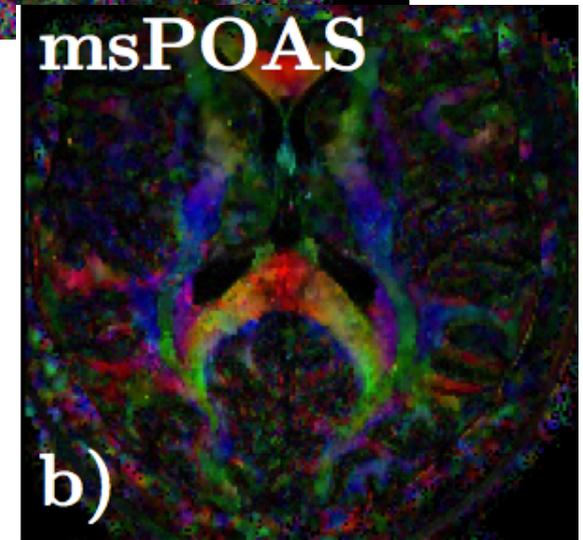
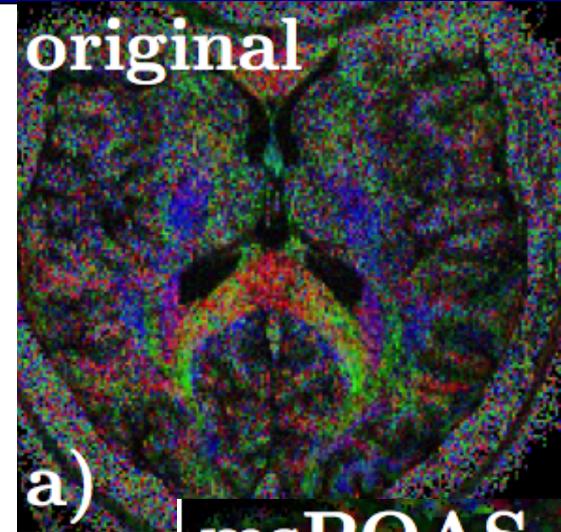
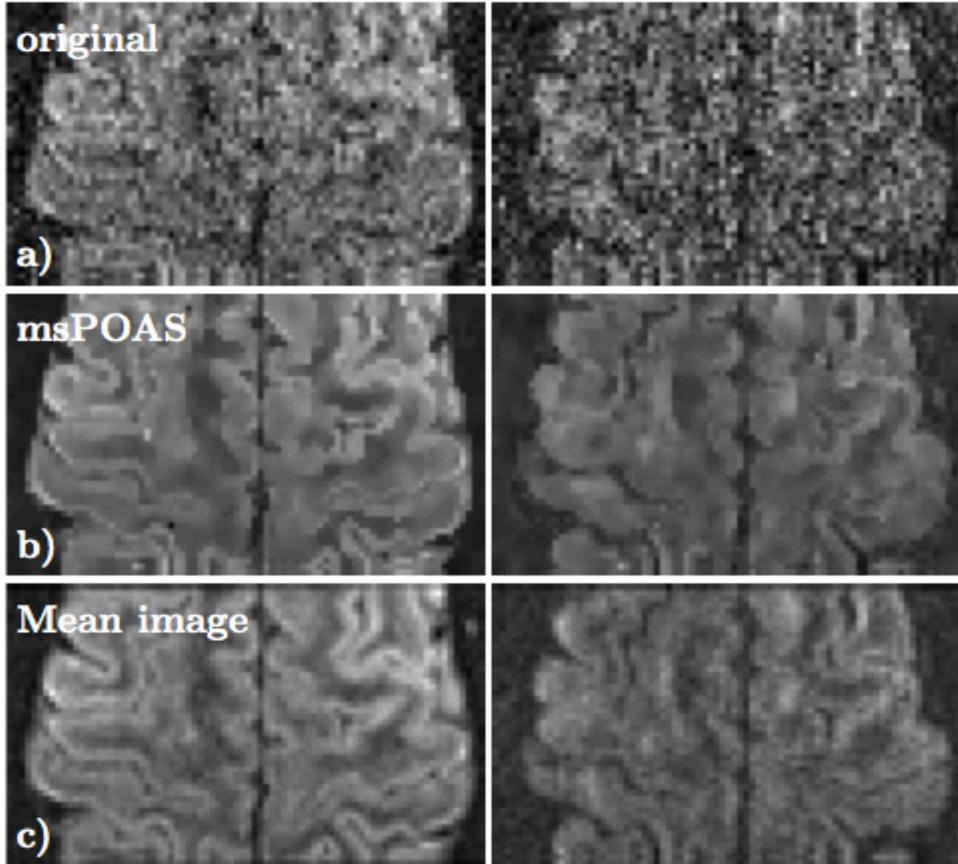
S^2



Multiple shells

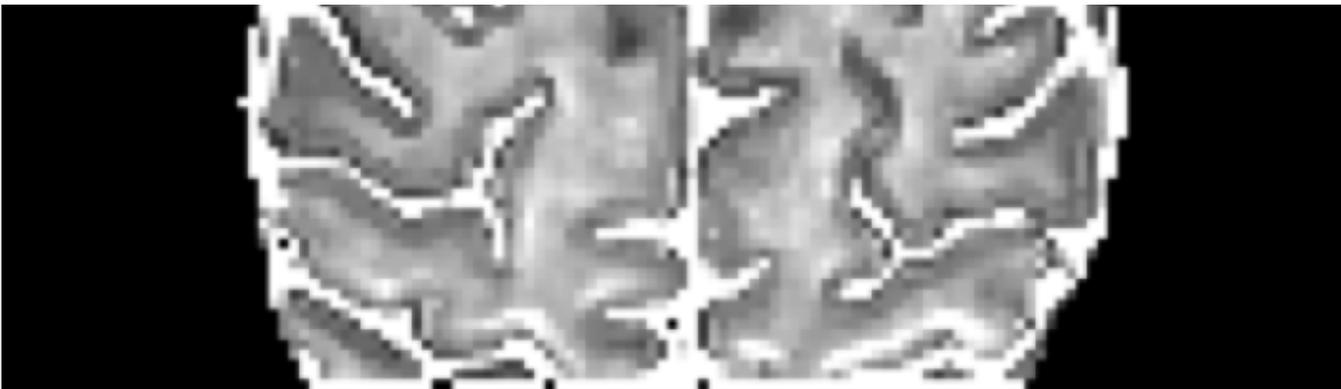


- **Multi-shell dMRI**
- **@1.2 x 1.2 x 1.2 mm³**
- **@ 3T clinical scanner**



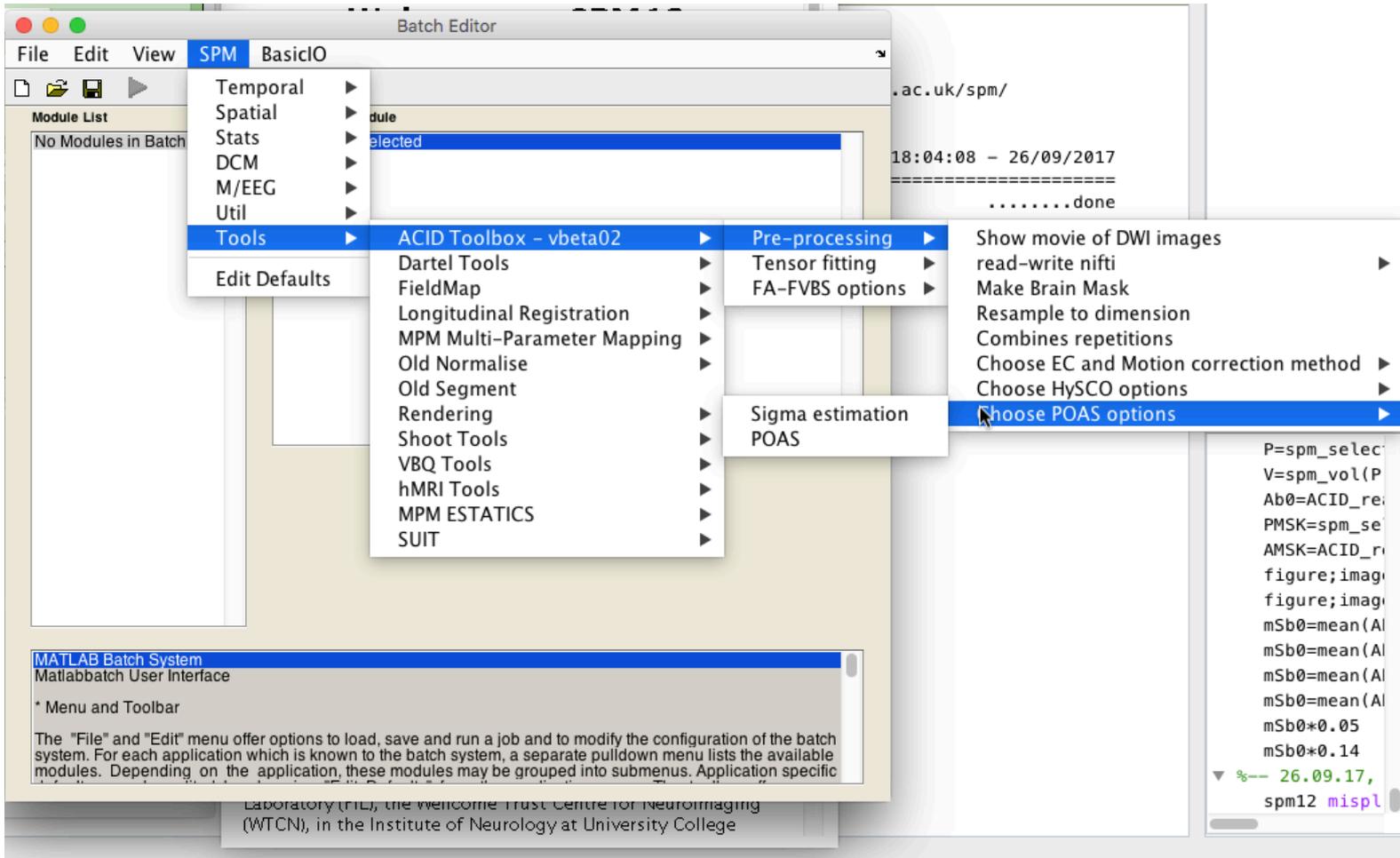


Original

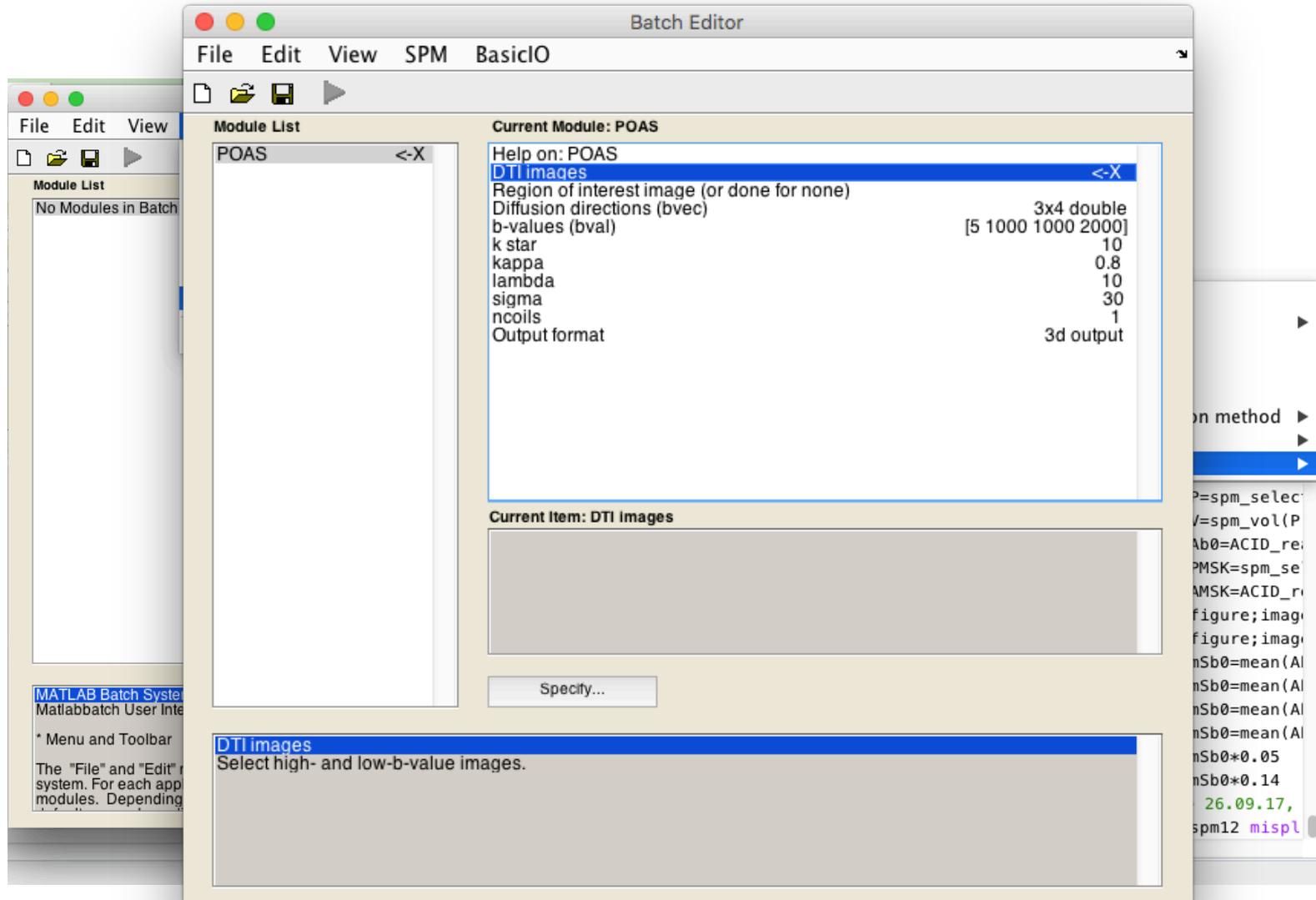


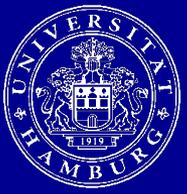
msPOAS

Denoising: multi-shell orientation- position adaptive smoothing (msPOAS)

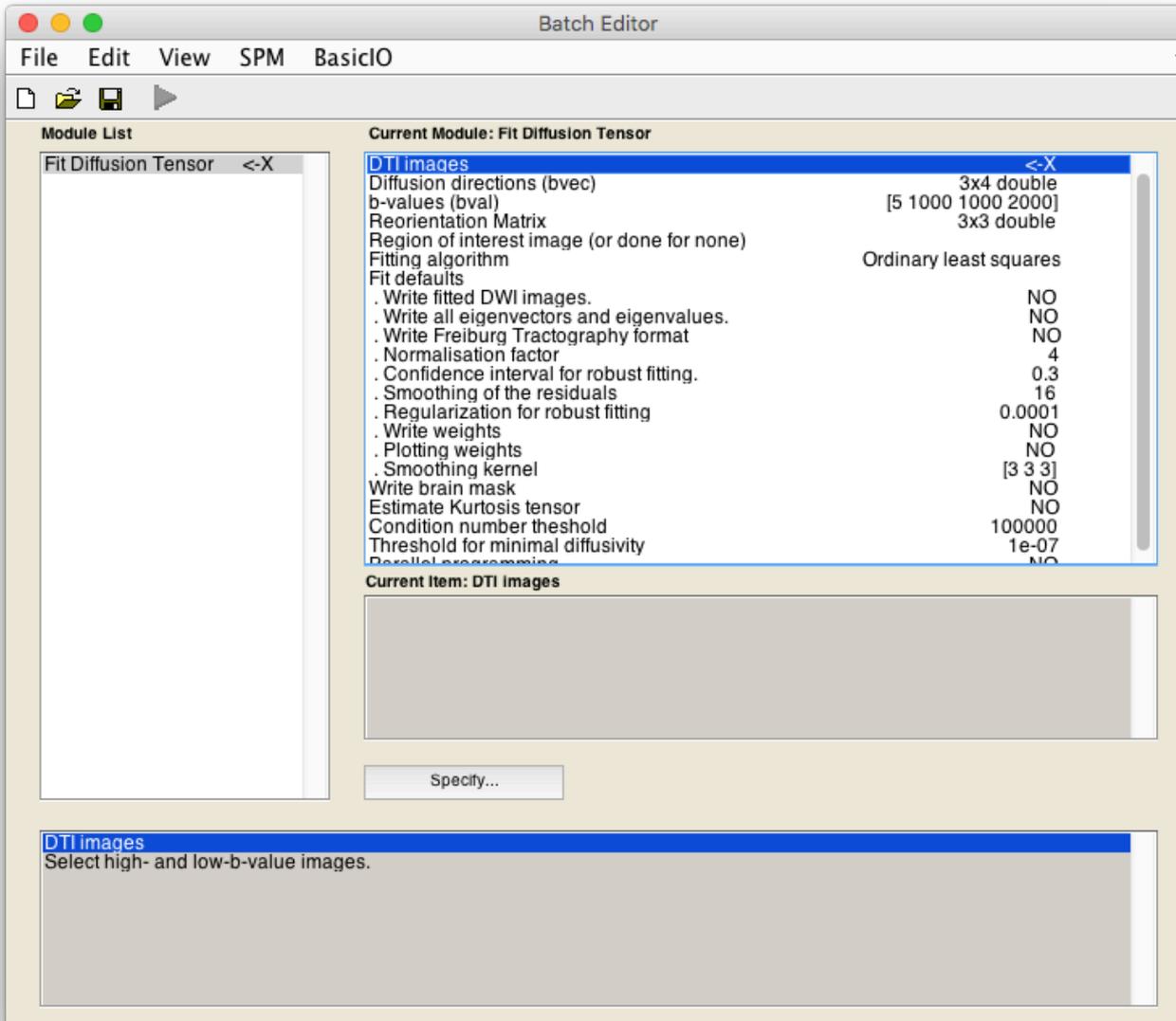


Denoising: multi-shell orientation- position adaptive smoothing (msPOAS)



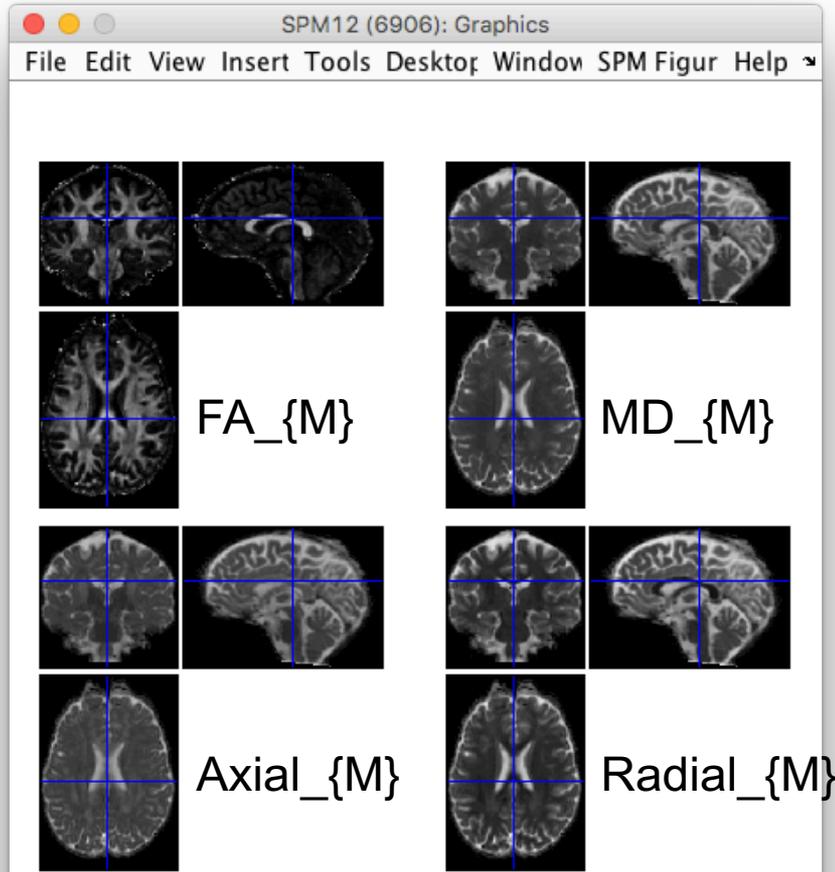


- Diffusion MRI: why, how, and what does it mean?
- Pre-processing steps
 - Eddy current and motion correction
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Most important

- Diffusion Data
- b-values
- b-vectors



{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)

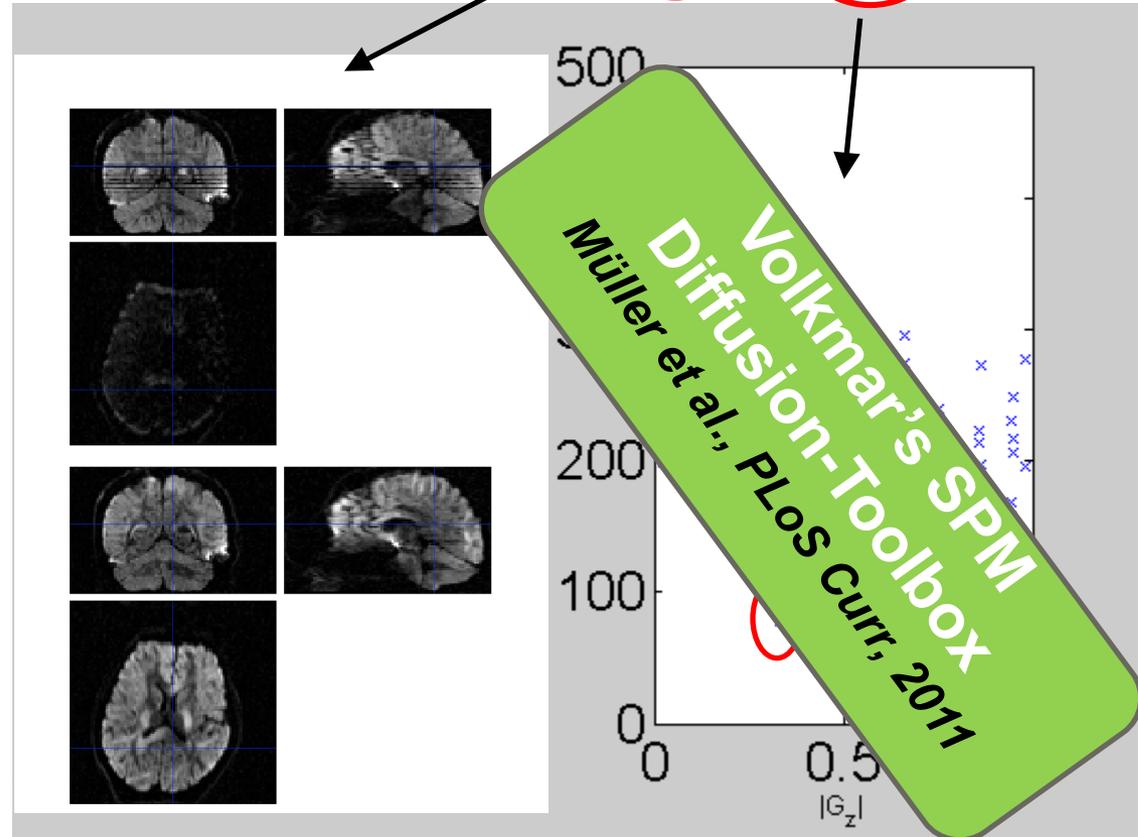
Learn more about the DTI metrics:

Basser et al. 1996; Diffusion MRI..., Ed: H Johansen-Berg & TEJ Behrens, 200?

Based on Zwiers,
NI, 2010

$$y = Xd + \varepsilon$$

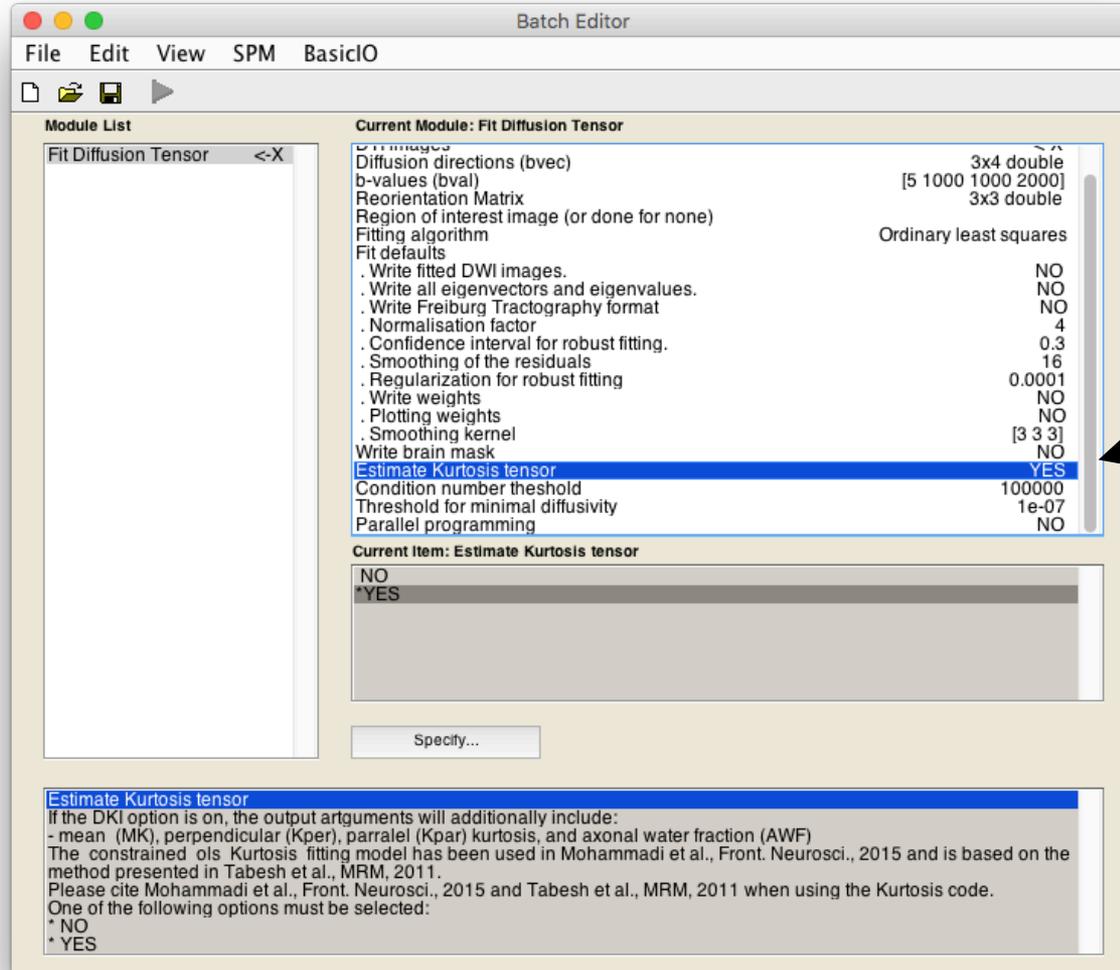
$$\omega = \omega_{\text{DWI}} \times \omega_s \times \omega_v$$





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What is the DKI switch?



Most important

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

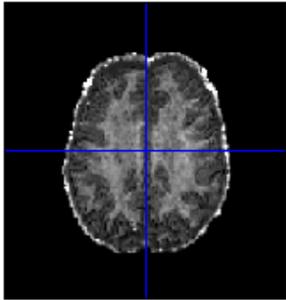
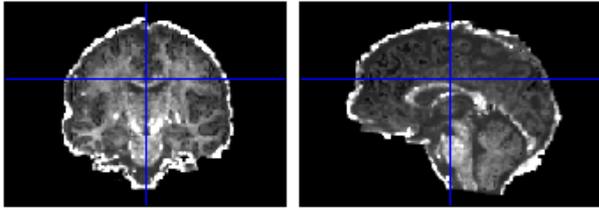
DKI switch



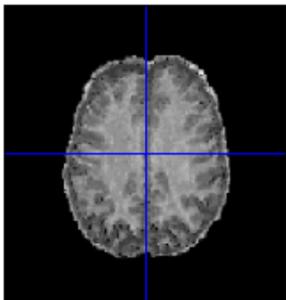
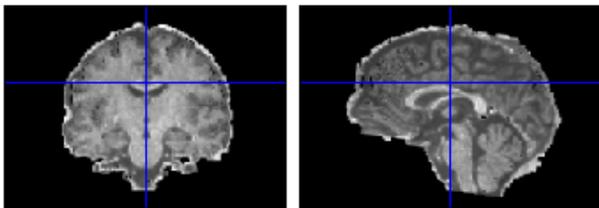
$$\ln \left[\frac{S(\mathbf{n}, b)}{S_0} \right] = -b \sum_{i=1}^3 \sum_{j=1}^3 n_i n_j D_{ij} \text{ — diffusion tensor}$$
$$+ \frac{1}{6} b^2 \overline{D}^2 \sum_{i=1}^3 \sum_{j=1}^3 \sum_{k=1}^3 \sum_{l=1}^3 n_i n_j n_k n_l W_{ijkl},$$

/ 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



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)*

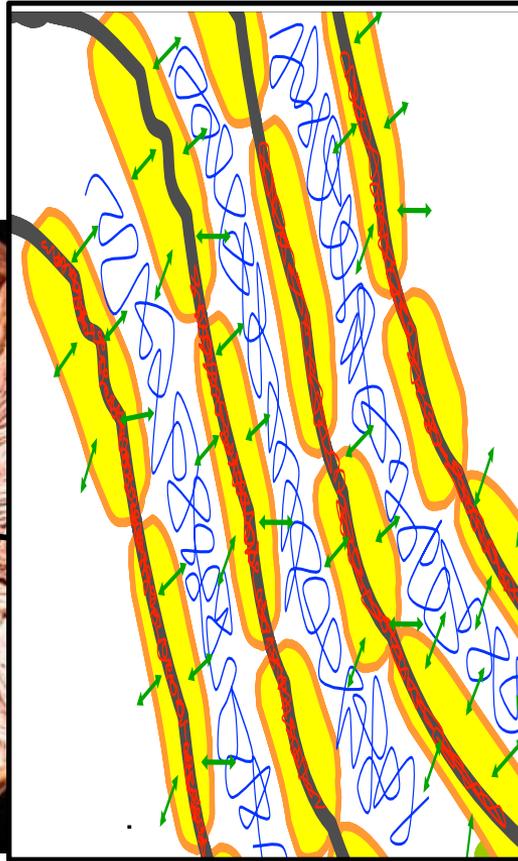
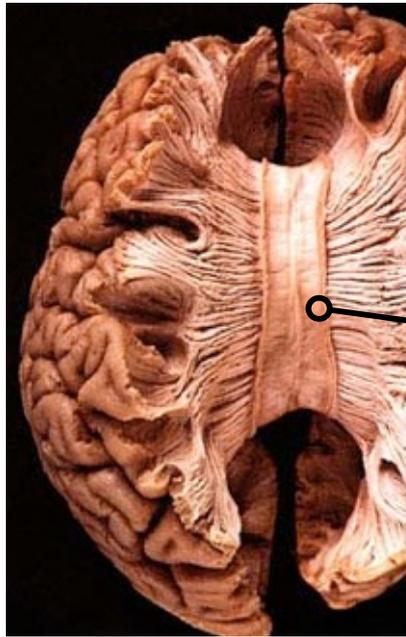
Learn more about these DKI metrics:
Fieremans et al., NI, 2011



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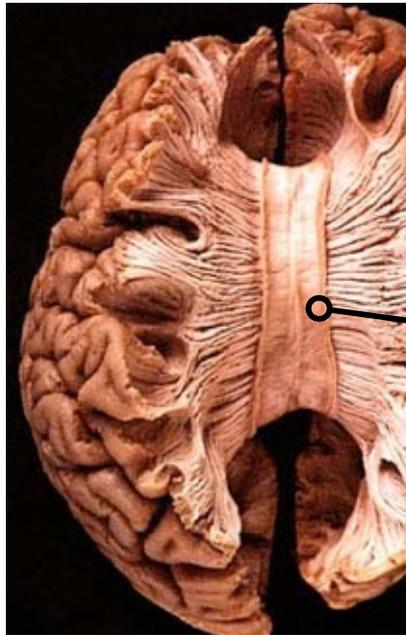
Biophysical model of the diffusion signal



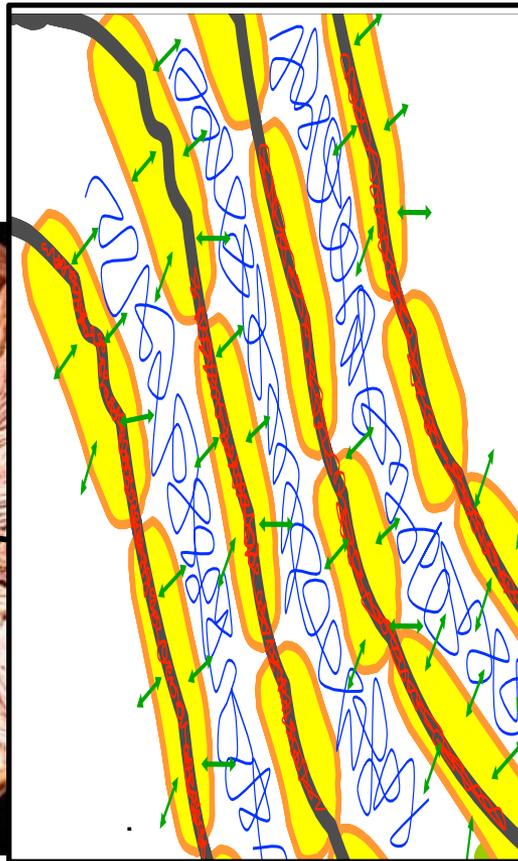
Zhang, OHBM, 2014 Fieremans, ESMRMB, 2015



Biophysical model of the diffusion signal



Zhang, OHBM, 2014



Fieremans, ESMRMB, 2015



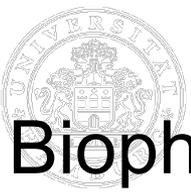
Intra-cellular diffusion
=
restricted diffusion



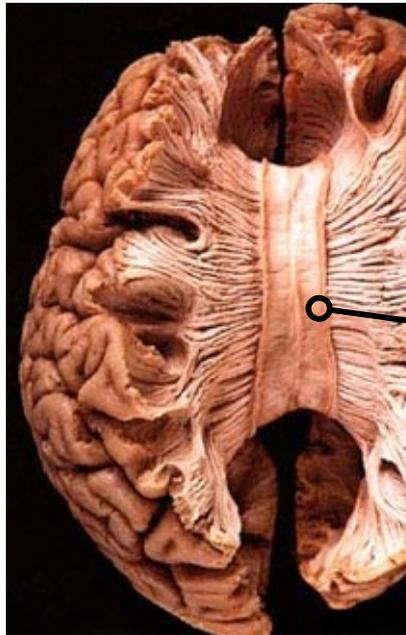
Extra-cellular diffusion
-
restricted diffusion



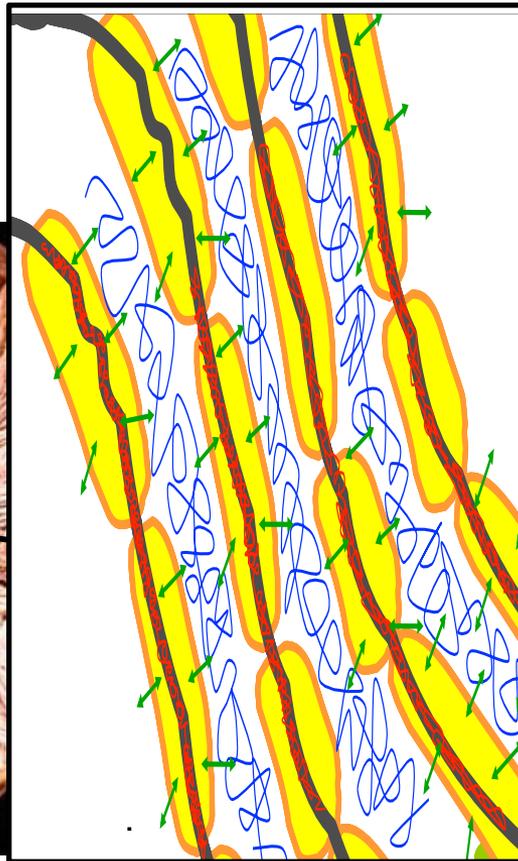
Exchange



Biophysical model of the diffusion signal



Zhang, OHBM, 2014



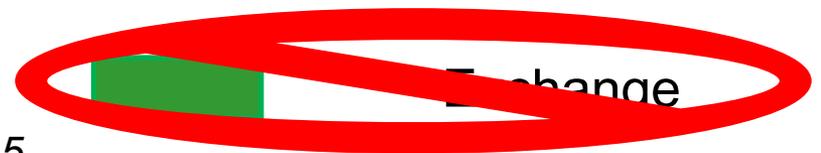
Fieremans, ESMRMB, 2015



Intra-cellular diffusion
=
restricted diffusion

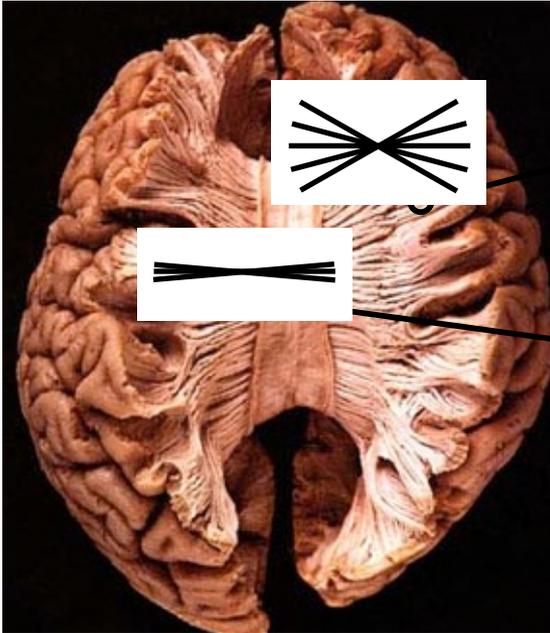


Extra-cellular diffusion
-
restricted diffusion

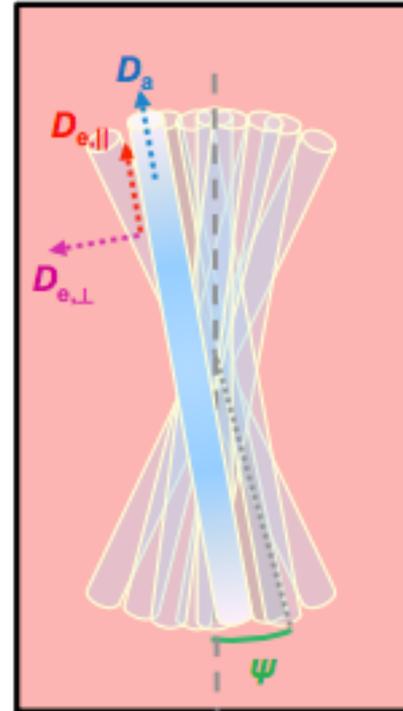




Biophysical model of the diffusion signal



Zhang, OHBM, 2014



Axonal volume fraction

$$\frac{\text{blue box}}{\text{blue box} + \text{red box}} = f$$

Intra axonal space

blue box D_a

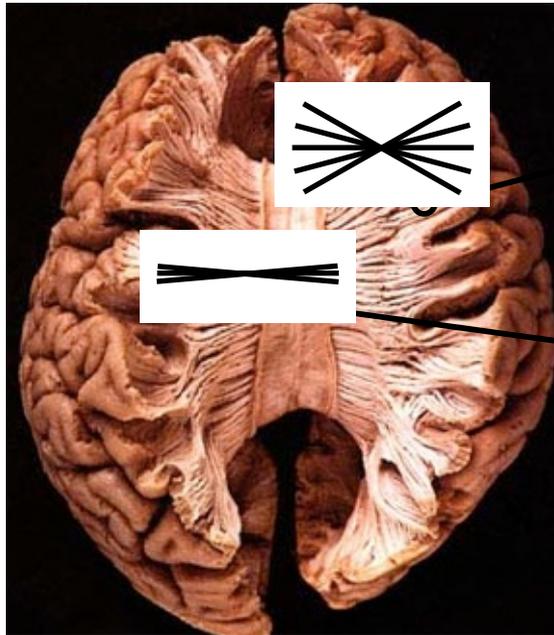
Extra axonal space

red box $D_{e,||}, D_{e,⊥}$

Fieremans, ESMRMB, 2015

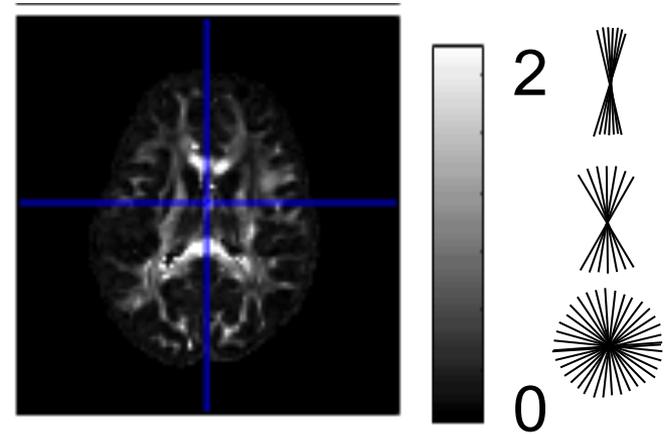


Biophysical model of the diffusion signal

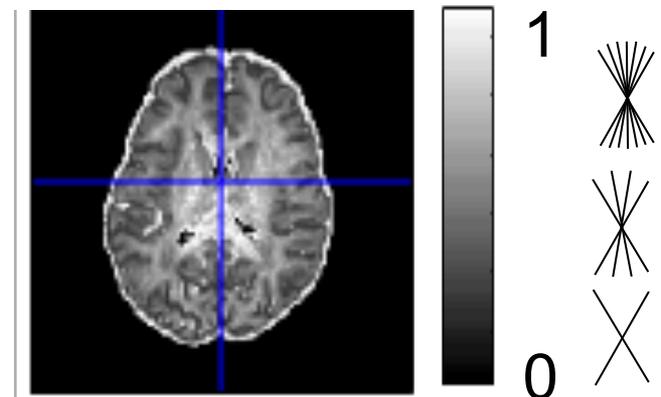


Zhang, OHBM, 2014

Fiber dispersion " σ " [a. u.]



Fiber density " τ " [a. u.]





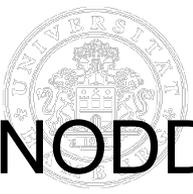
NODDI-DTI:

fiber density “ ν ”

~

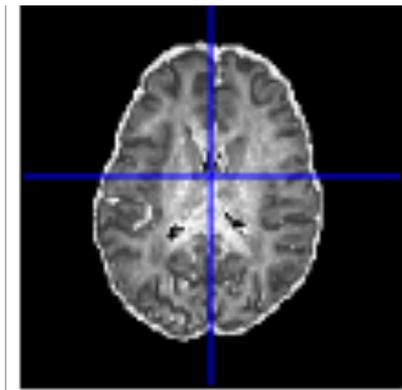
mean diffusivity “MD”

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



NODDI-DTI: fiber density “ ν ” ~ mean diffusivity “MD”

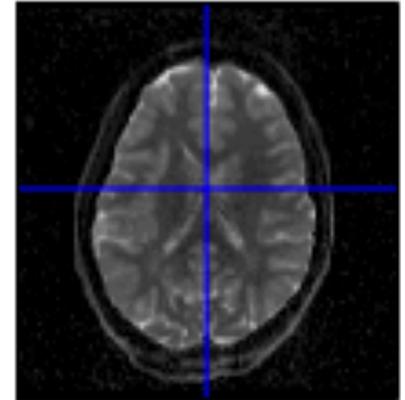
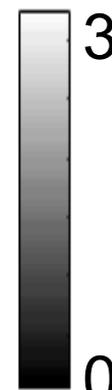
Fiber density [a. u.]



1
0



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



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



NODDI-DTI:

fiber dispersion “ τ ”

~

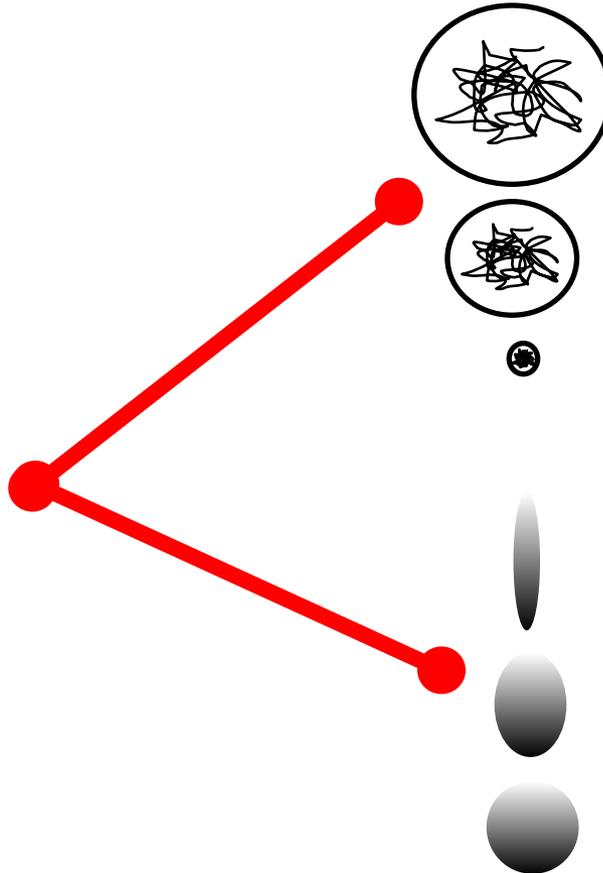
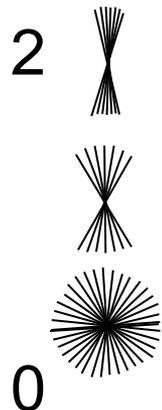
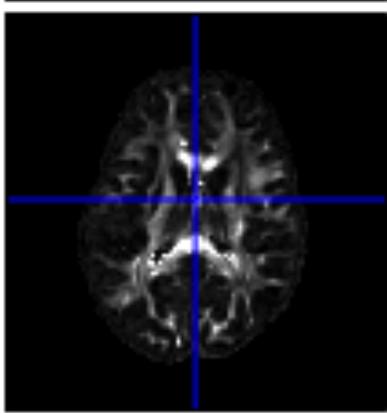
mean diffusivity “MD” & fractional anisotropy “FA”

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



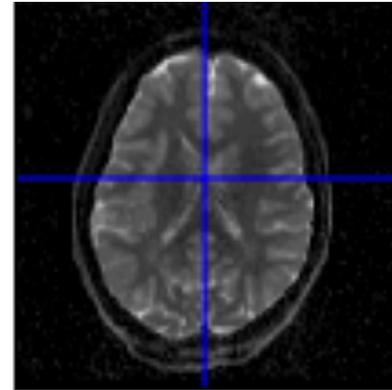
NODDI-DTI: fiber dispersion “ τ ” ~ mean diffusivity “MD” & fractional anisotropy “FA”

Fiber Dispersion [a. u.]

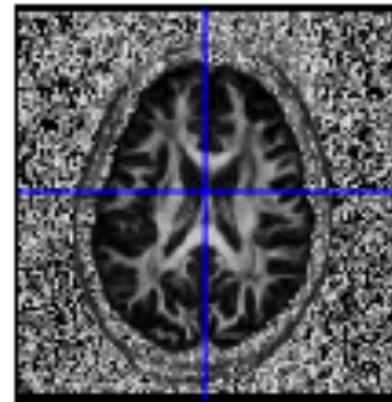


Mean Diffusivity

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



1



Fractional Anisotropy [a. u.]

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



- 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.*)