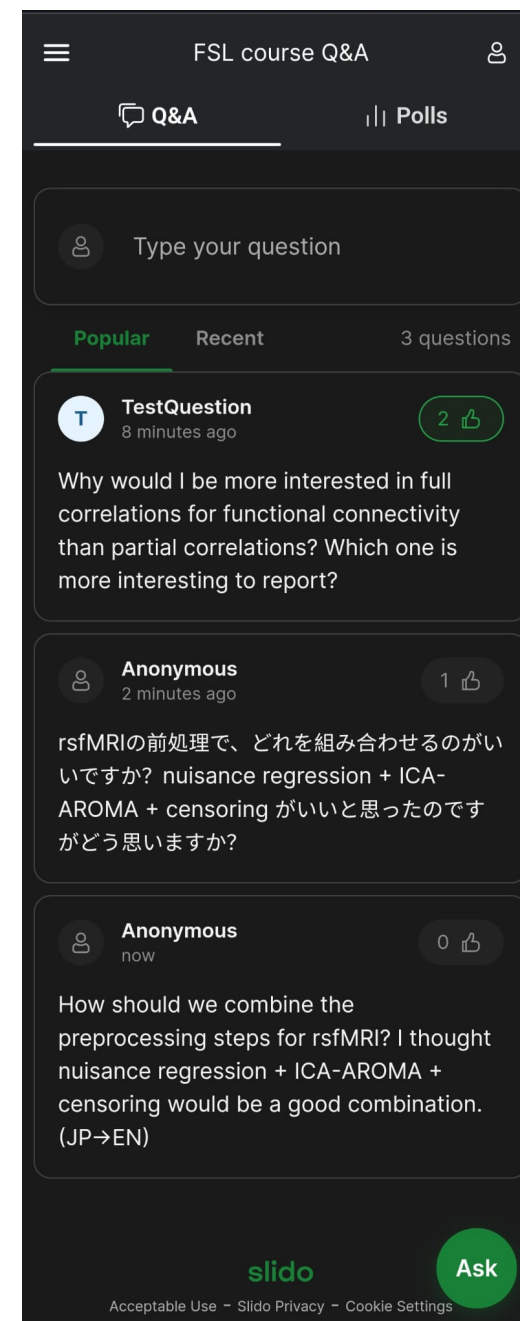
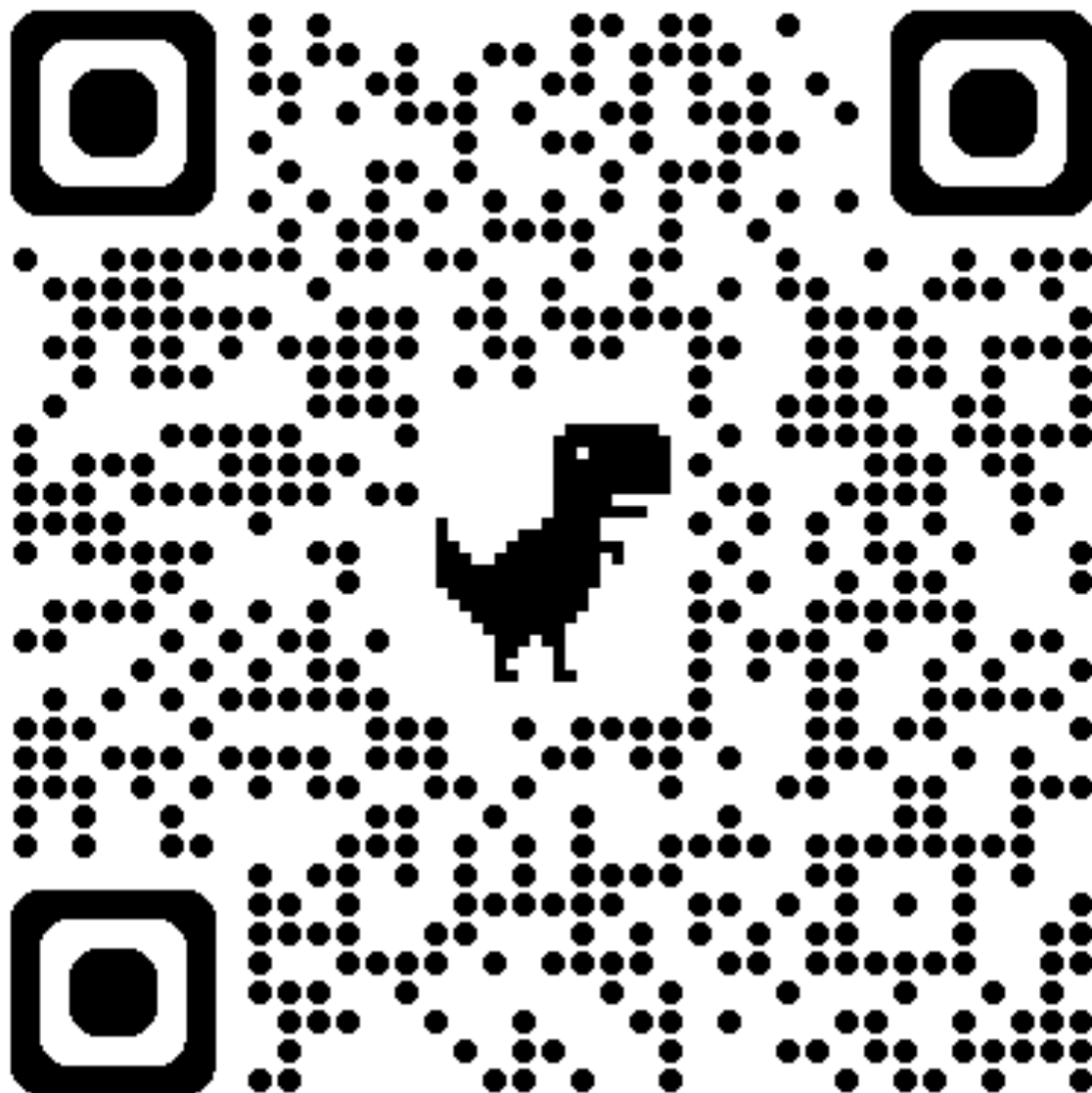
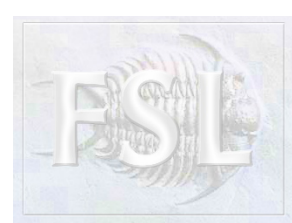


Diffusion MRI Processing and Analysis

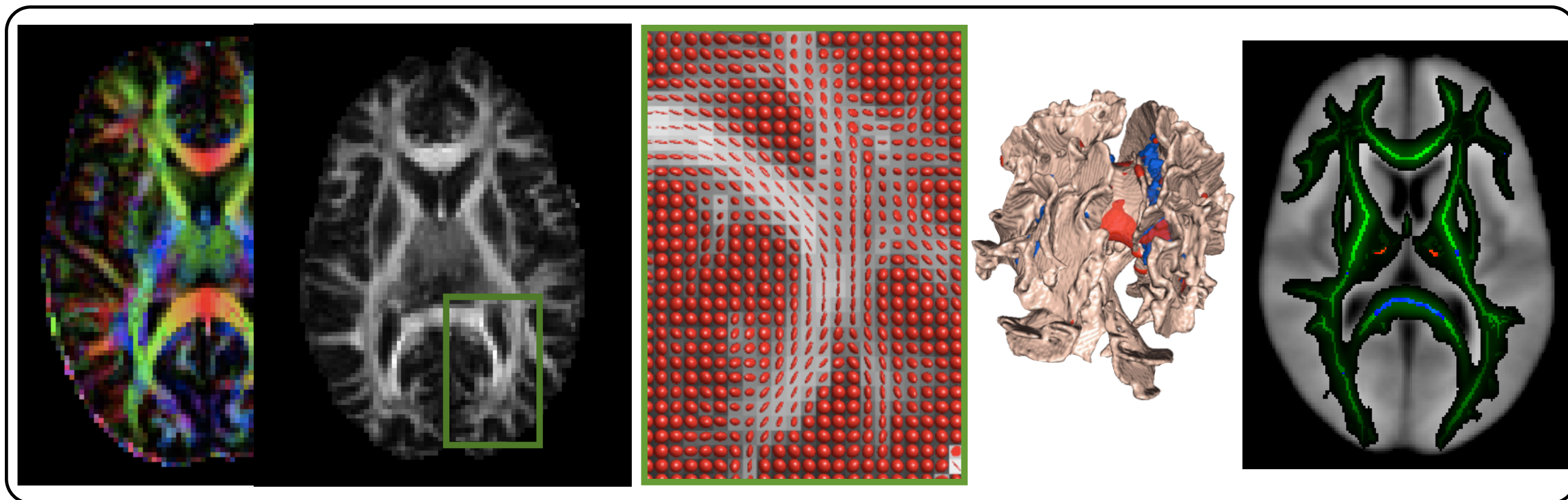
Submit your questions online





Overview

- What is Diffusion? Diffusion-weighting in MRI
- Diffusion Tensor Model and DTI
- Tract-Based Diffusion analysis (TBSS)
- Distortion Correction for Diffusion MRI

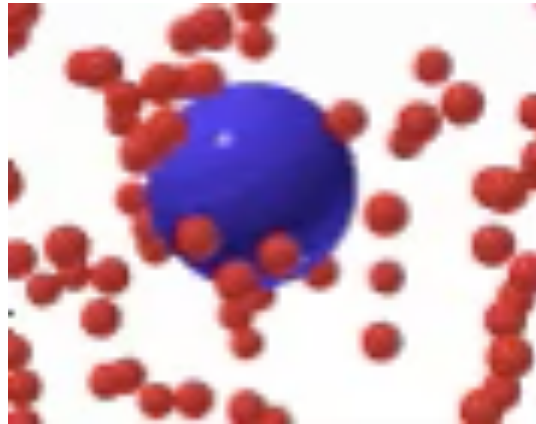




Diffusion - Brownian Motion



Robert Brown (1773-1858)



Molecules are in constant motion at non-zero absolute temperatures ($> -273^{\circ}\text{C}$)

Diffusion = thermally-driven random motion

Diffusion - Brownian Motion



Albert Einstein (1879-1955)

How can we describe this motion?
For an ensemble of molecules, in n -dimensional space:

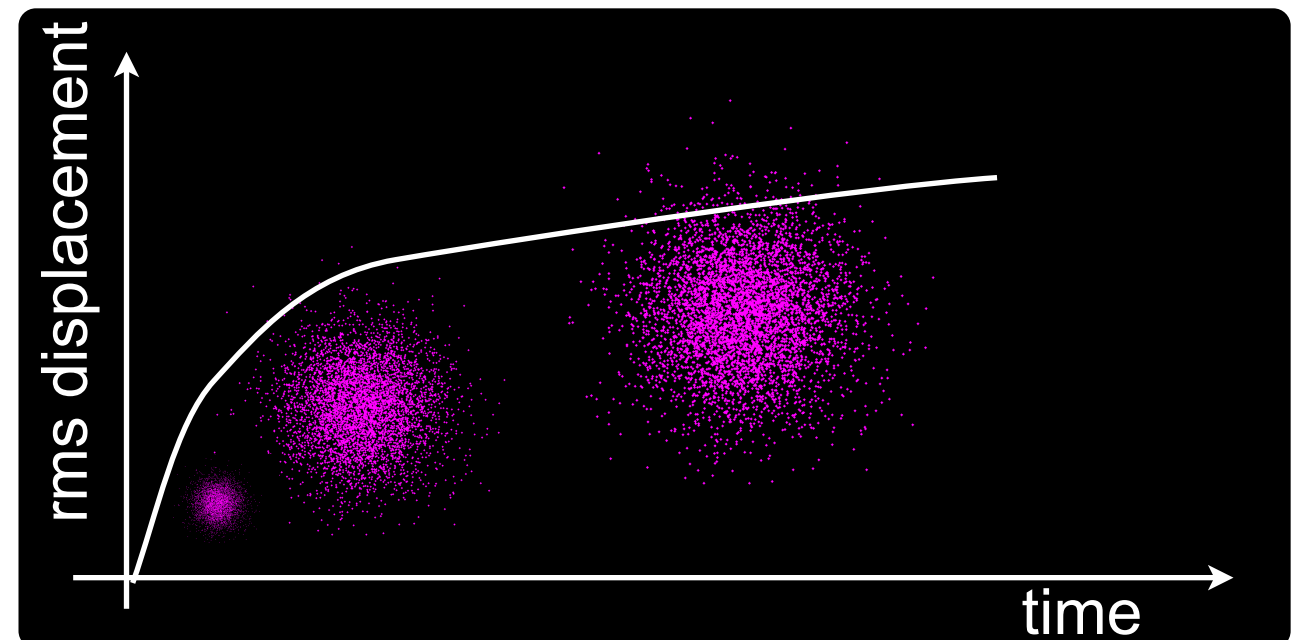
$$\langle x^2 \rangle = 2nDt$$

mean squared displacement

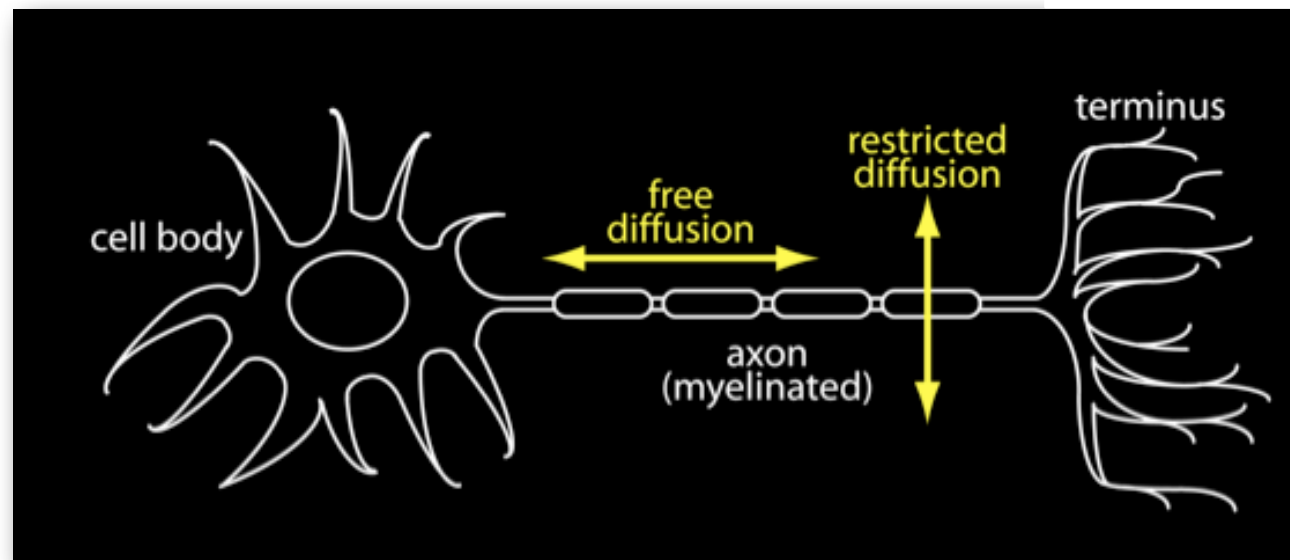
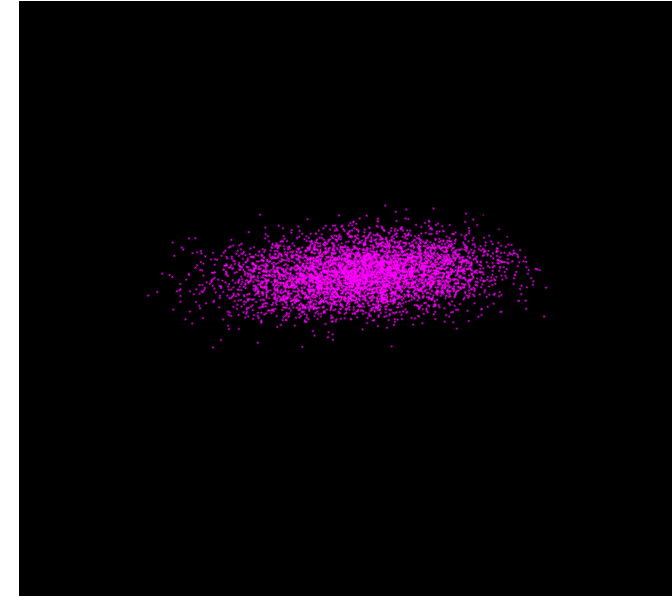
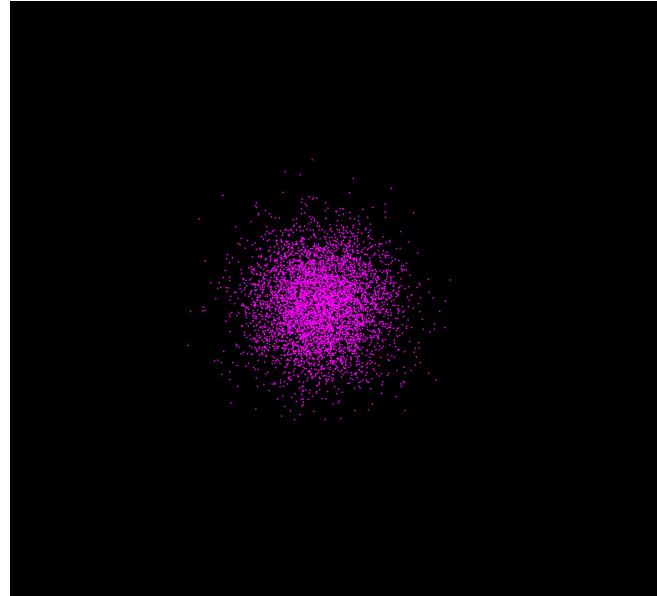
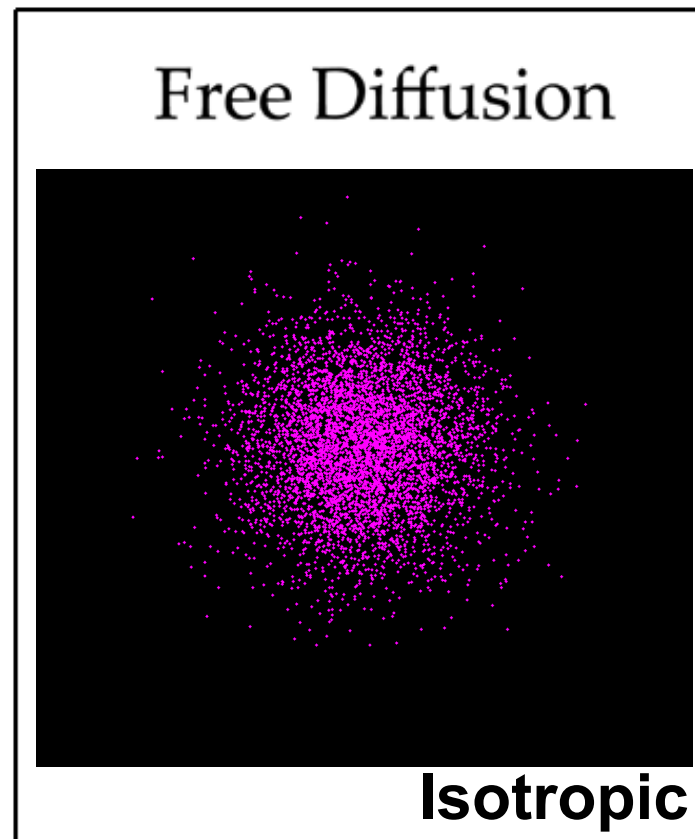
Diffusion coefficient

time

Valid for a homogeneous, barrier-free medium.



Water Diffusion in the Brain. Why is it Interesting?

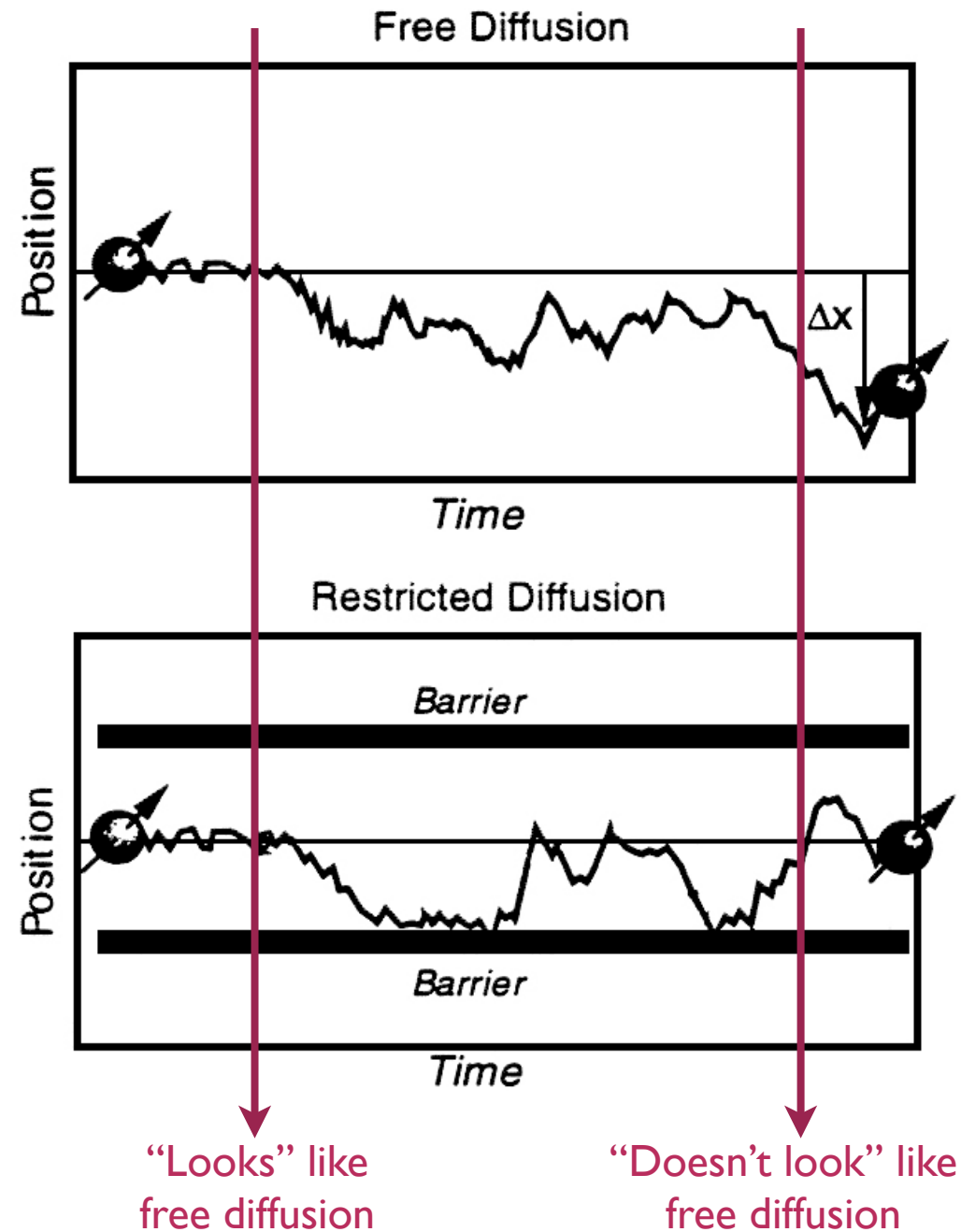


Diffusion is restricted by tissue boundaries, membranes, etc.
Marker for tissue microstructure (healthy and pathology)
Diffusion is **anisotropic** in white matter

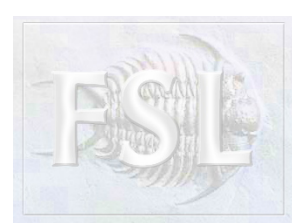
[Beaulieu, NMR Biomed, 2002]



Apparent Diffusion



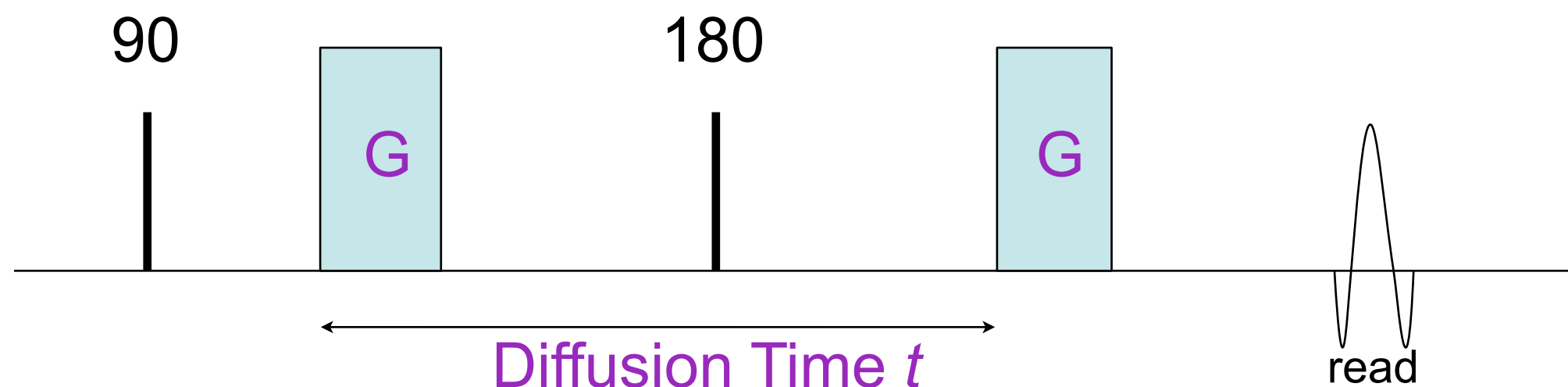
Observed diffusion in tissues depends on the experiment =
“Apparent diffusion” &
“Apparent diffusion coefficient” (ADC)



Measuring Diffusion with MRI: Diffusion MRI (dMRI)

Pulsed-Gradient Spin-Echo Sequence:

To achieve diffusion-weighting along a direction $\mathbf{x}$, apply strong magnetic field gradients along $\mathbf{x}$.



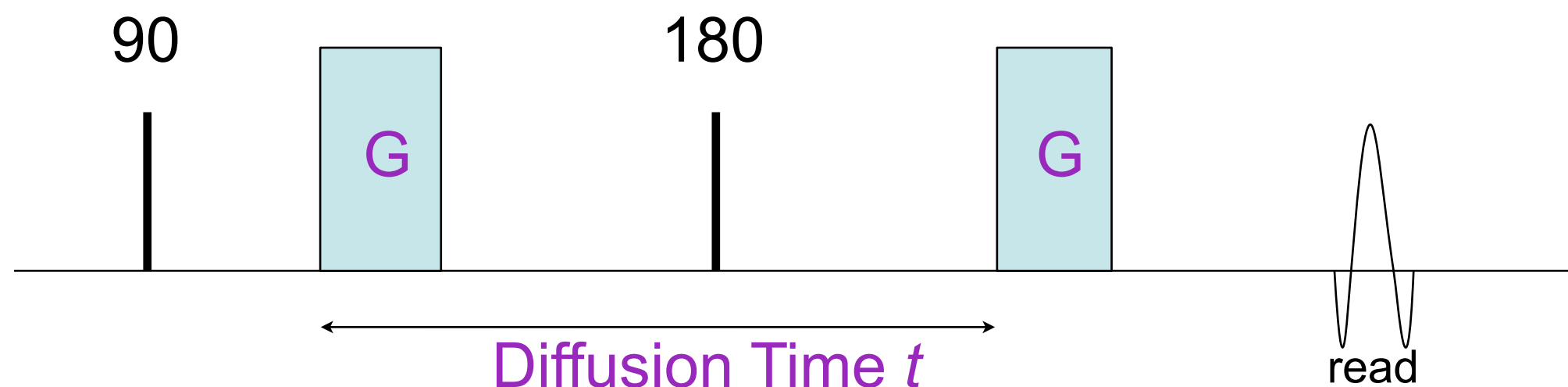
If particles diffuse along $\mathbf{x}$ during the allowed time (DiffTime), a signal attenuation is observed, compared to the signal with $G=0$.



Measuring Diffusion with MRI: Diffusion MRI (dMRI)

Pulsed-Gradient Spin-Echo Sequence:

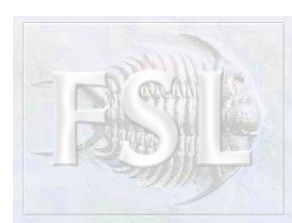
To achieve diffusion-weighting along a direction $\mathbf{x}$, apply strong magnetic field gradients along $\mathbf{x}$.



$$D \sim 2.4 \mu\text{m}^2/\text{ms}$$
$$t \sim 50\text{ms}$$

$$\Rightarrow x = \sqrt{6Dt} \sim 27\mu\text{m}$$

st. deviation of displacements

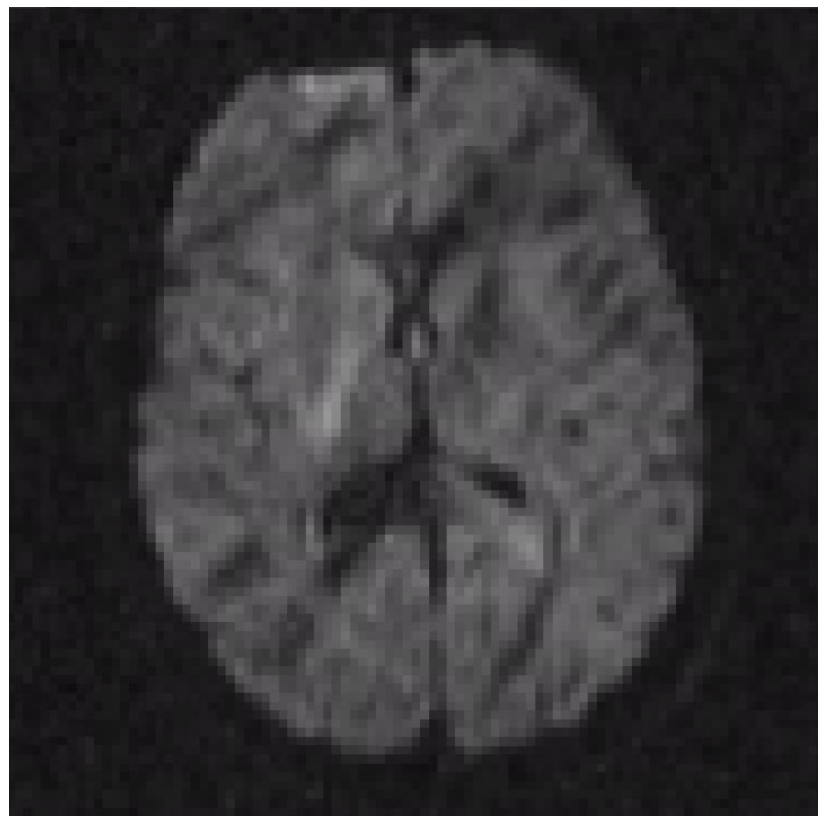


Measuring Diffusion with MRI: Diffusion MRI (dMRI)

T2w Image
No Diffusion-weighting
($G=0$)
 S_0



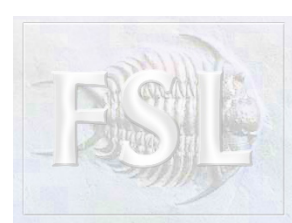
Diffusion-weighted
Image
 S



Ratio
 S/S_0



Removes T2w contrast



Measuring Diffusion with MRI: Diffusion MRI (dMRI)

Diffusion contrast can be modulated by:

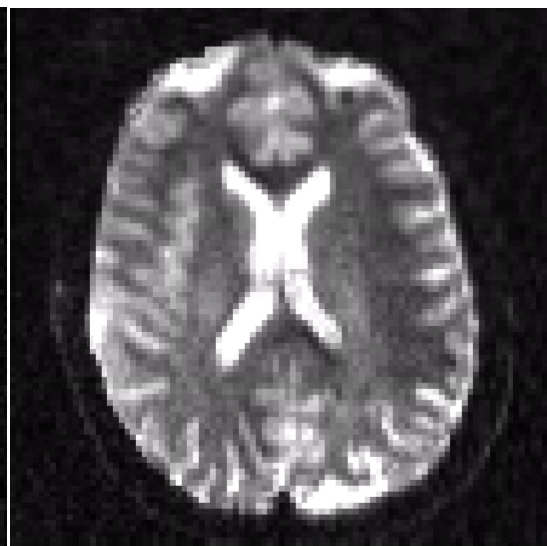
A) Diffusion weighting: Gradient **strength**, Diffusion **time**

$$\mathbf{b\ value} \sim G^2 \cdot \text{DiffTime} \quad (\text{units in s/mm}^2)$$

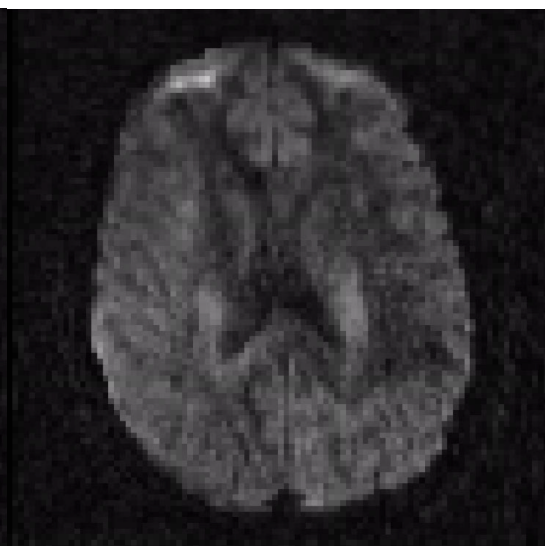
b=0



b=300



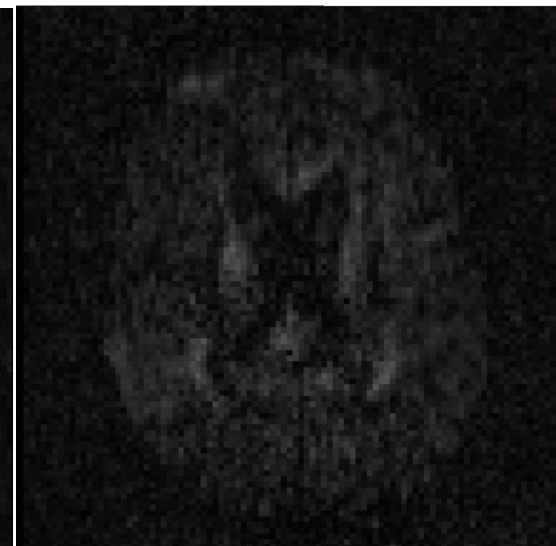
b=1000



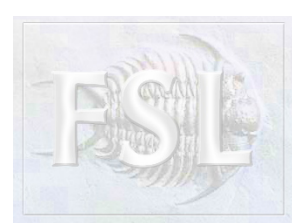
b=2000



b=3000



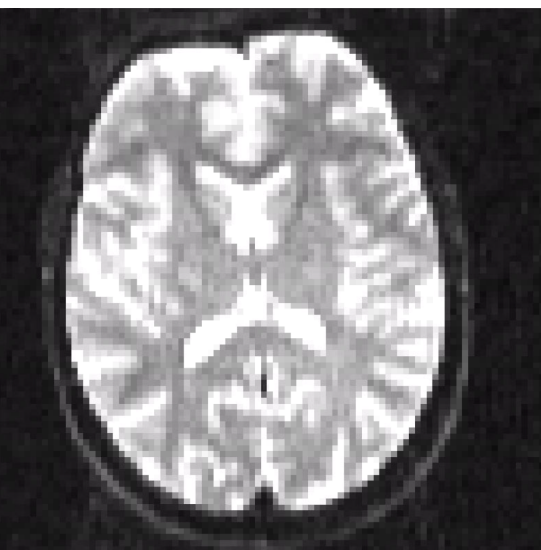
More diffusion contrast with higher b :)
...But less signal left - exponential decay :(



Measuring Diffusion with MRI: Diffusion MRI (dMRI)

Diffusion contrast can be modulated by:
B) Gradient Direction $\mathbf{x}$

$b=0$

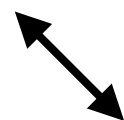


$b=1000$



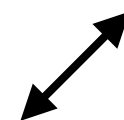
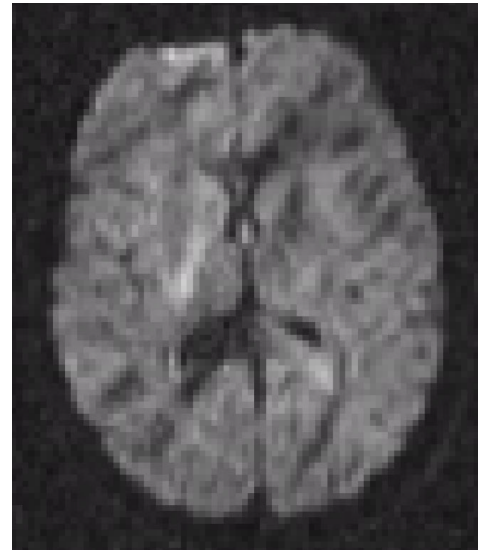
$\mathbf{x}$

$b=1000$



$\mathbf{x}$

$b=1000$



$\mathbf{x}$

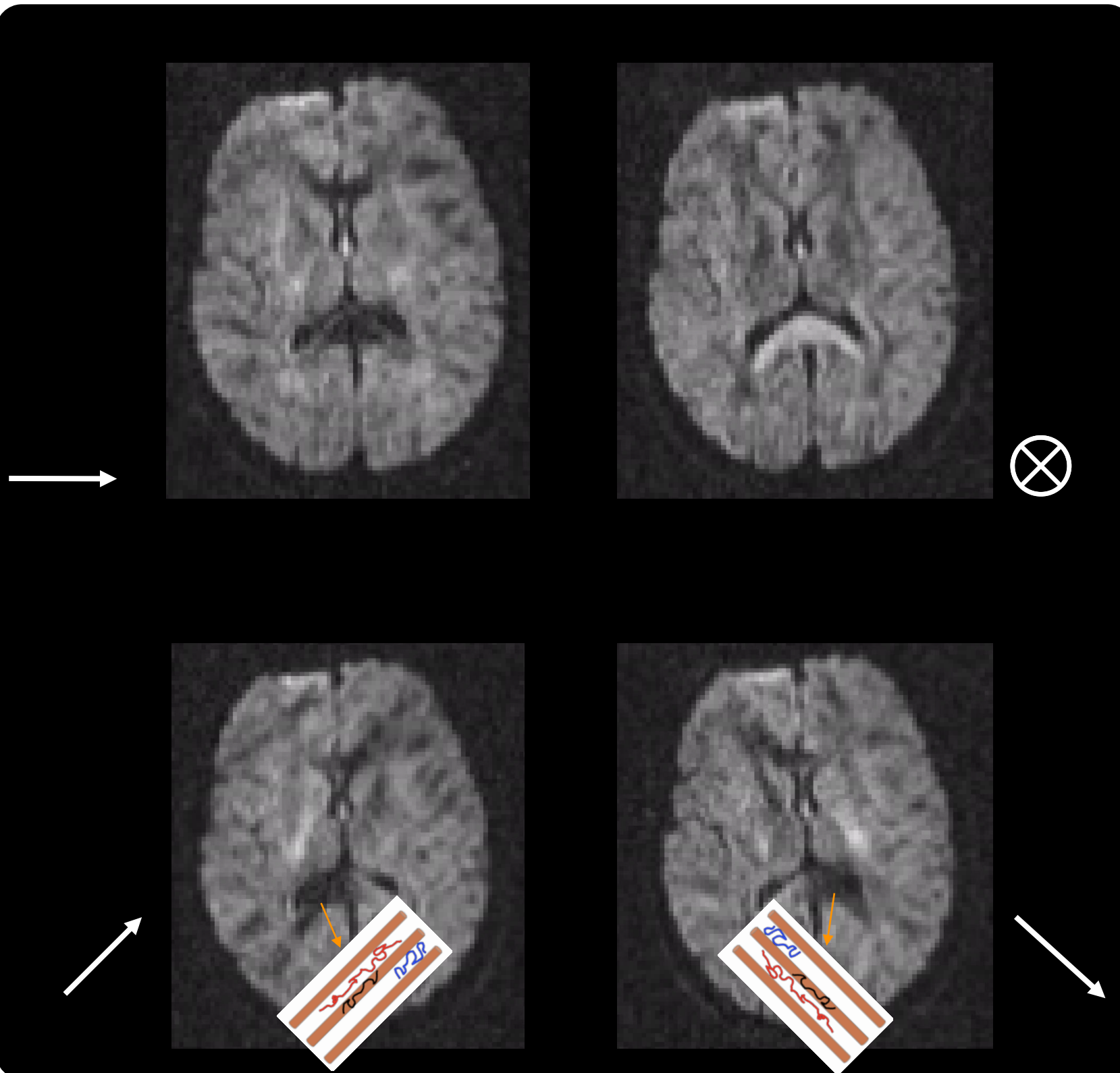
$b=1000$



$\mathbf{x}$



Orientation Contrast in dMRI



Because diffusion is anisotropic in WM, applying a gradient G along different directions $\mathbf{x}$, gives different contrast in WM.

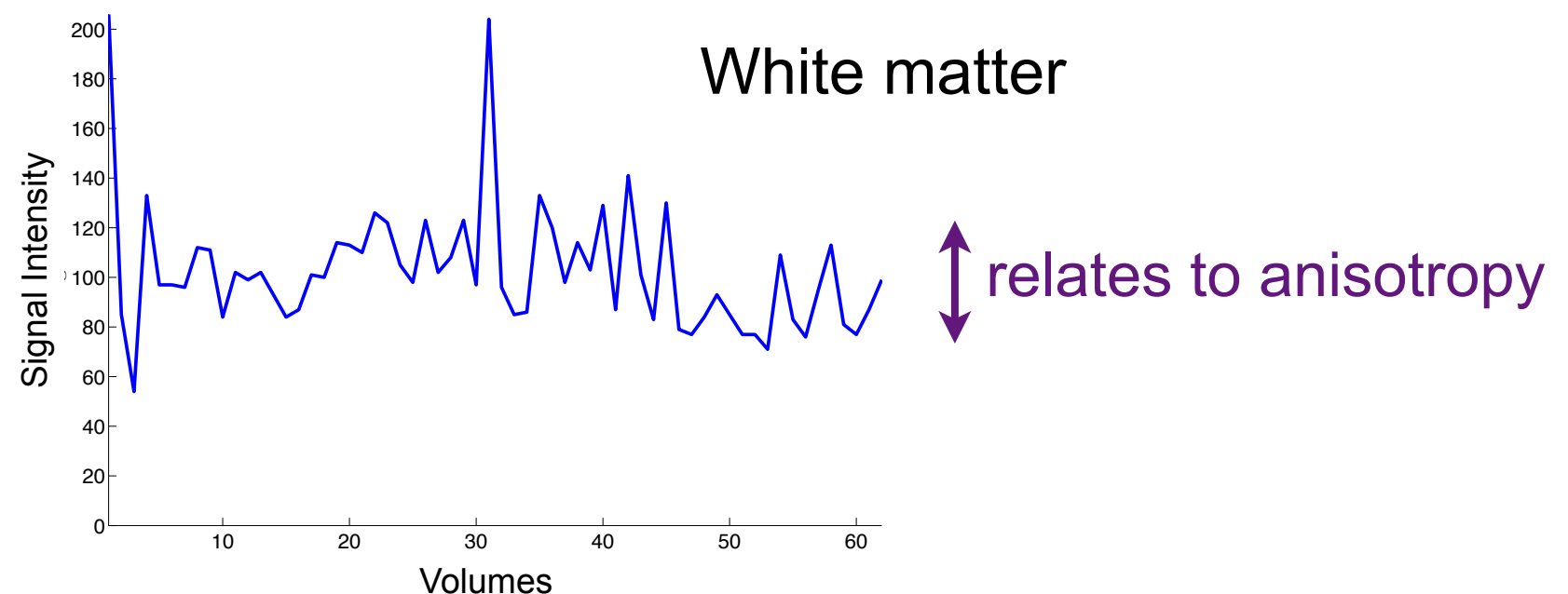
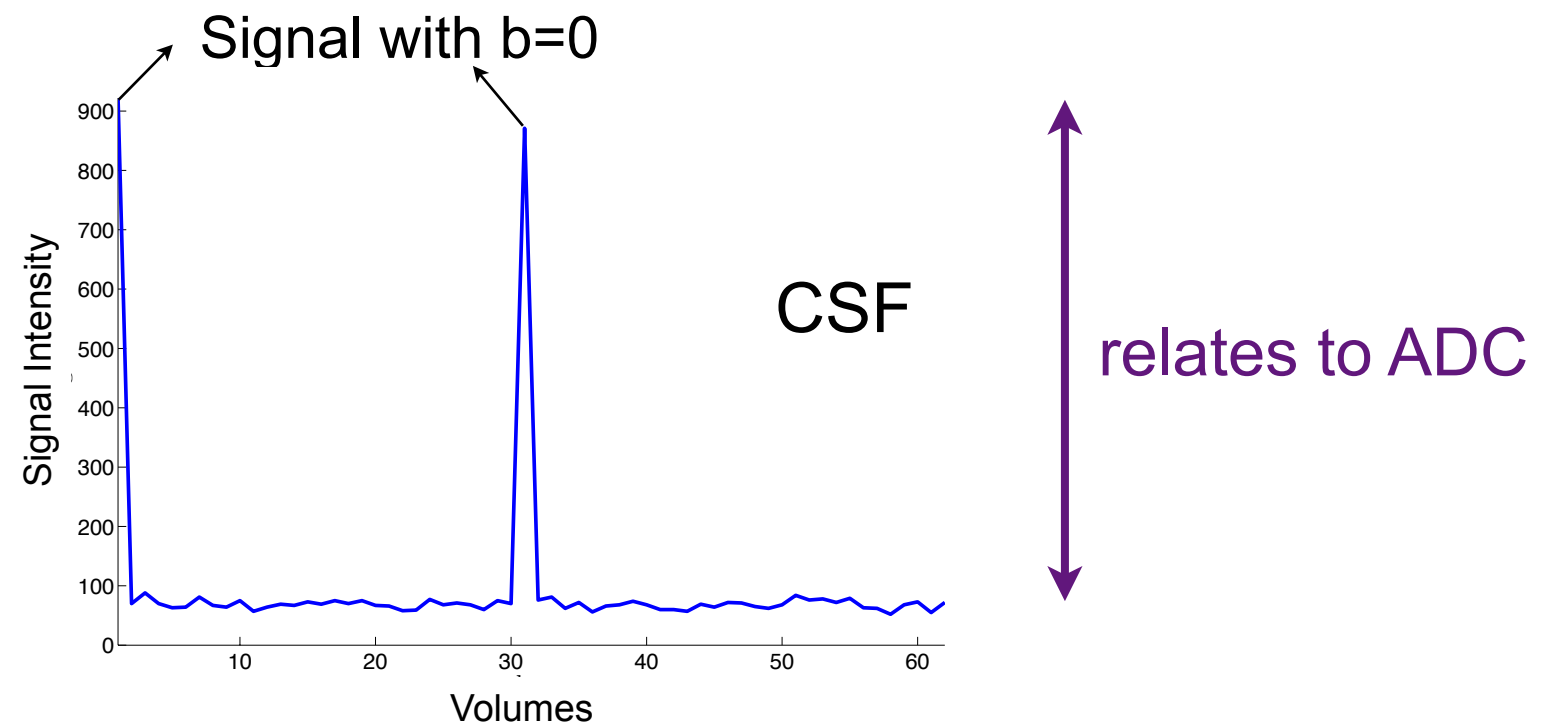
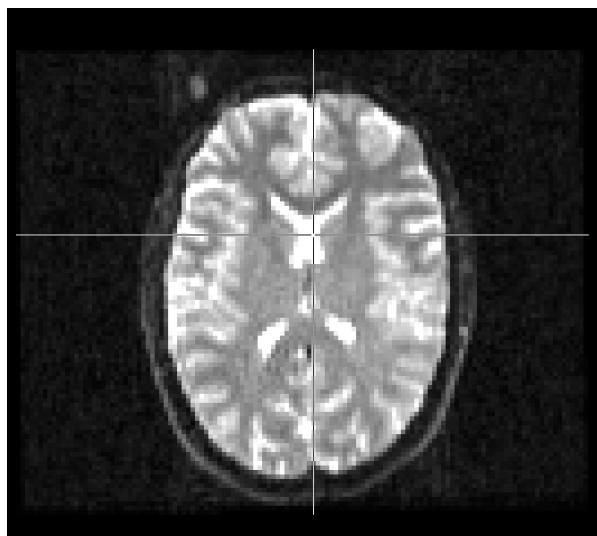
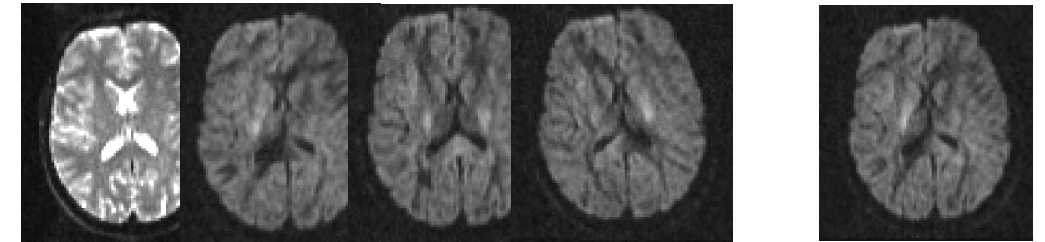
Anisotropic measurements in WM!

Roughly **Isotropic** in GM and CSF.



A Typical dMRI Protocol

- Normally a few (at least one) $b=0$ volumes acquired, along with shells at higher b (~ 1000 s/mm²).
- A shell is a set of volumes acquired with the same b -value, but different gradient orientation



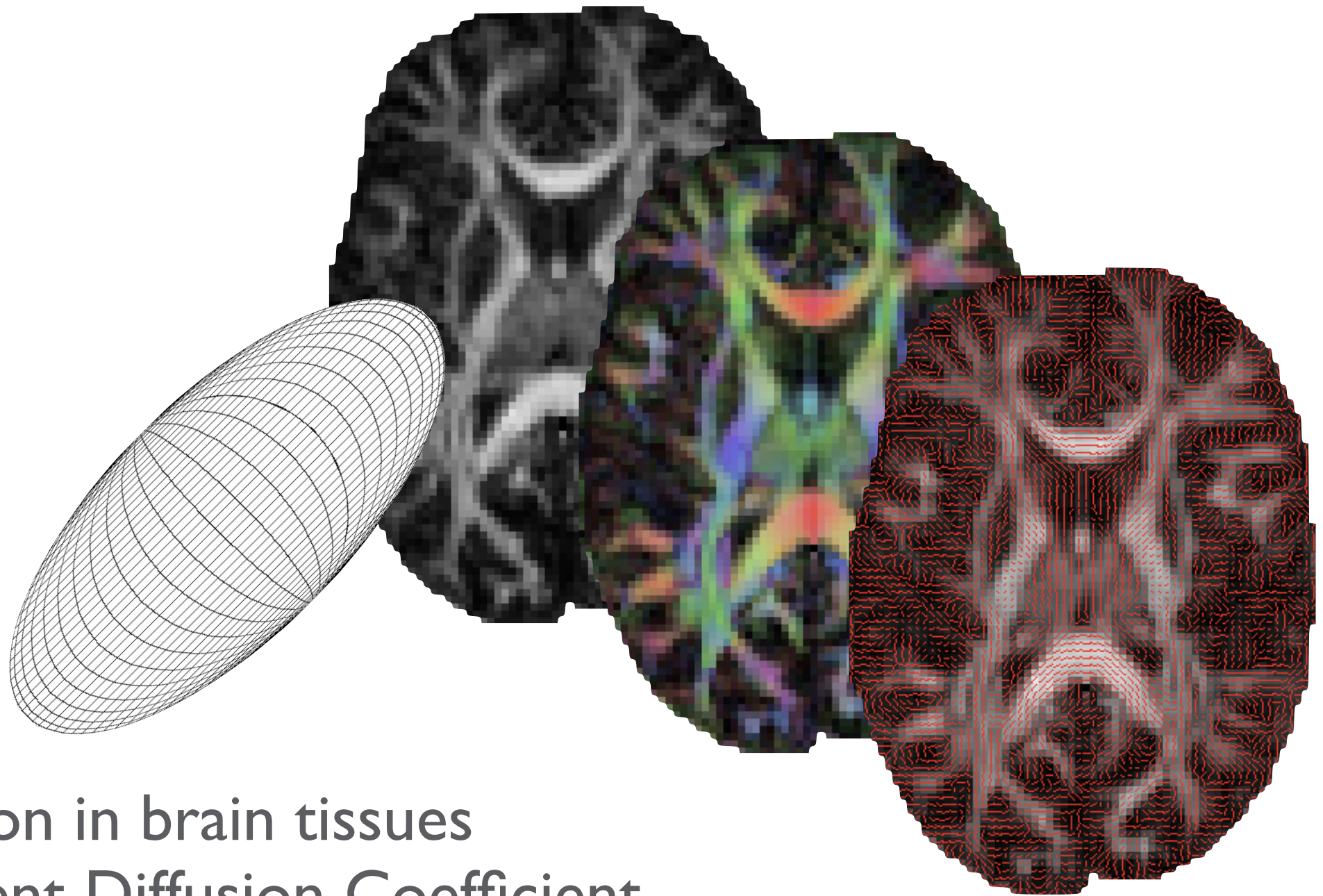


dMRI Summary

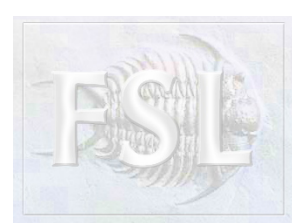
- Images acquired with a Gradient along $\mathbf{x}$, have contrast that is sensitive to diffusion of water molecules along $\mathbf{x}$.
- Images acquired with higher b-values (stronger gradient/ longer diffusion time) are more sensitive to diffusion along $\mathbf{x}$.
- When diffusion occurs, signal is attenuated compared to the one with no diffusion-weighting.
- In WM, measurements are anisotropic.
- In GM and CSF, measurements are roughly isotropic.



Diffusion Tensor Imaging - basic principles

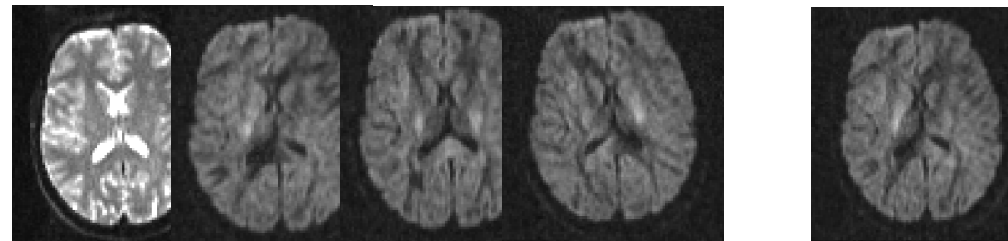


- Diffusion in brain tissues
- Apparent Diffusion Coefficient
- Diffusion Tensor model
- Tensor-derived measures



Diffusion Tensor Imaging (DTI)

- Apply **the diffusion tensor model** to a set of dMRI images.



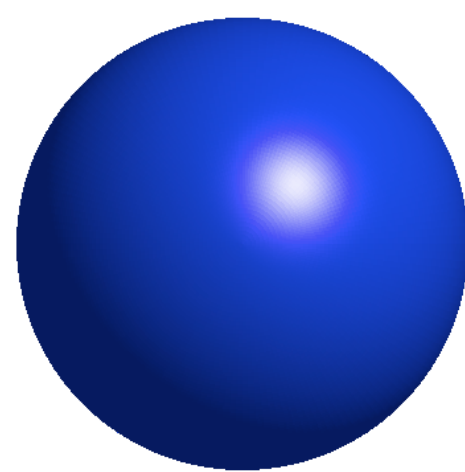
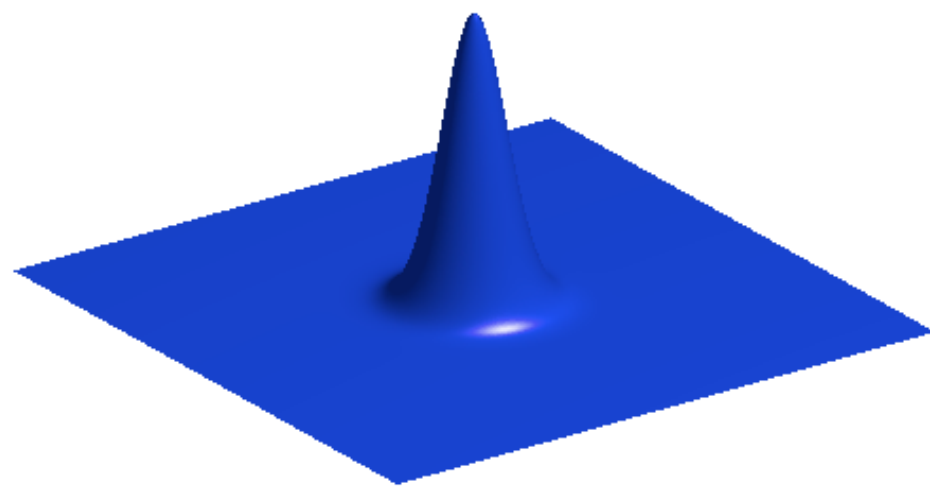


Diffusion Tensor Imaging (DTI)

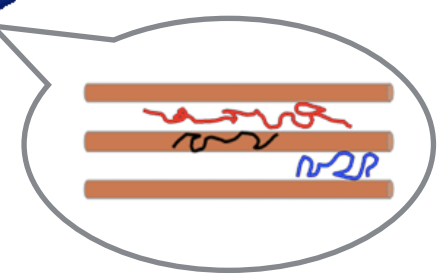
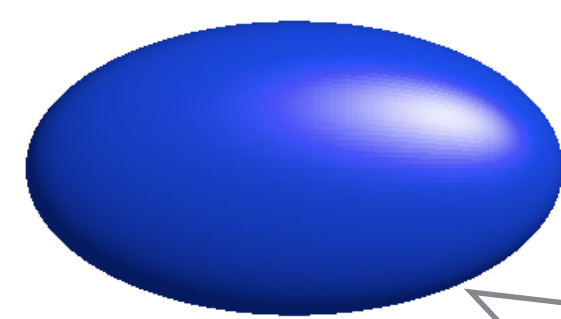
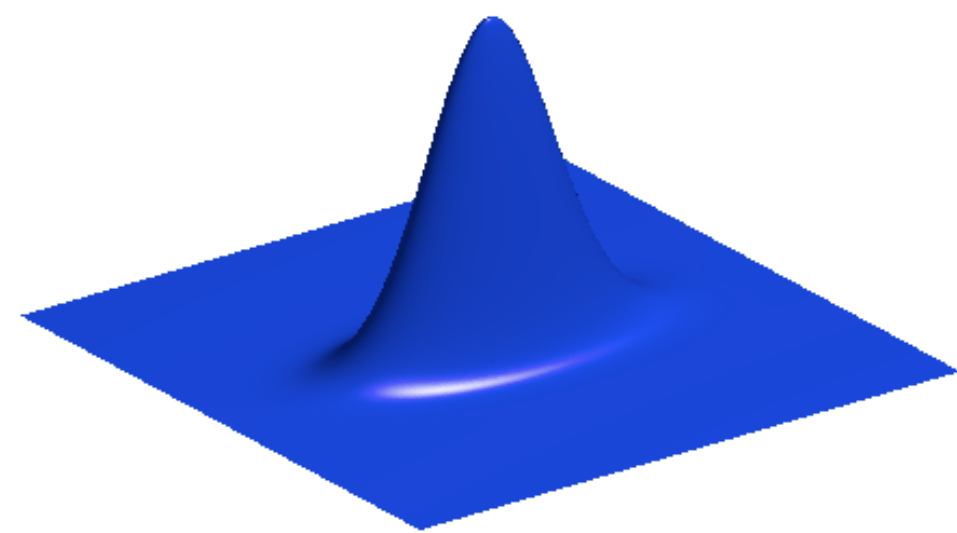
Two dimensions

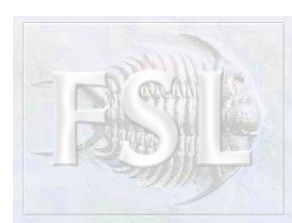
Three dimensions

Scalar D (same D for all directions)



Tensor D - DTI (D can be different for different directions)





Diffusion Tensor Imaging (DTI)

Diffusion Tensor Model. In each voxel:

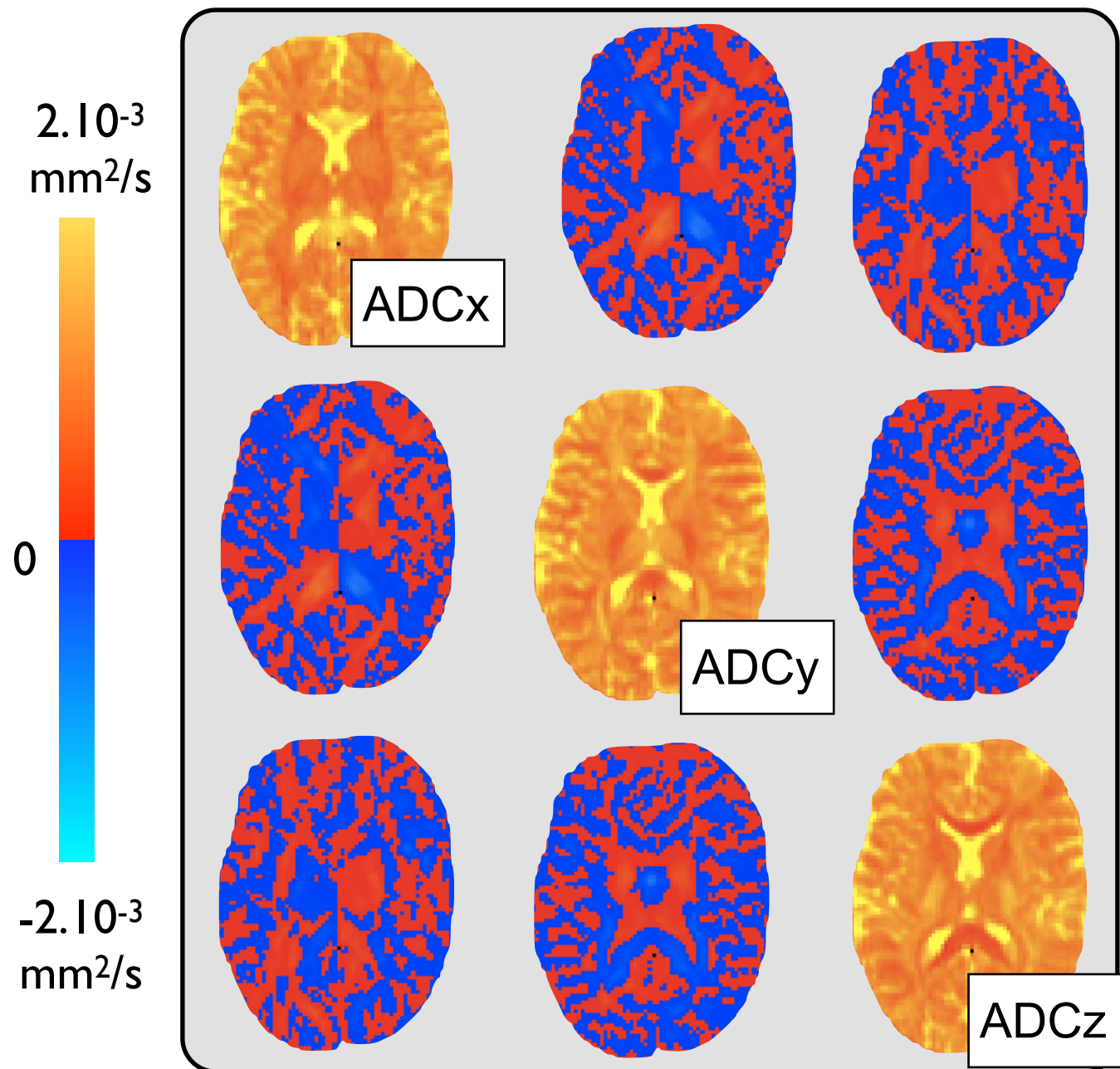
$$S_j = S_0 \exp(-b_j \mathbf{x}_j^T \mathbf{D} \mathbf{x}_j)$$

Diagram illustrating the Diffusion Tensor Model equation and its components:

- S_j : Signal measured after applying a Gradient j with direction $\mathbf{x}_j$ and b-value b_j (measured)
- S_0 : Signal measured with no diffusion gradient applied (measured)
- b_j : b-value for gradient j (known)
- $\mathbf{x}_j$: Unit vector representing the direction of gradient j (known)
- $\mathbf{D}$: 3x3 Diffusion Tensor (unknown)



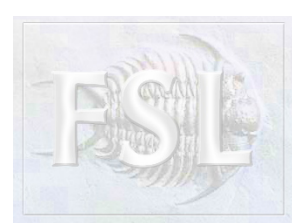
The Elements of the Diffusion Tensor



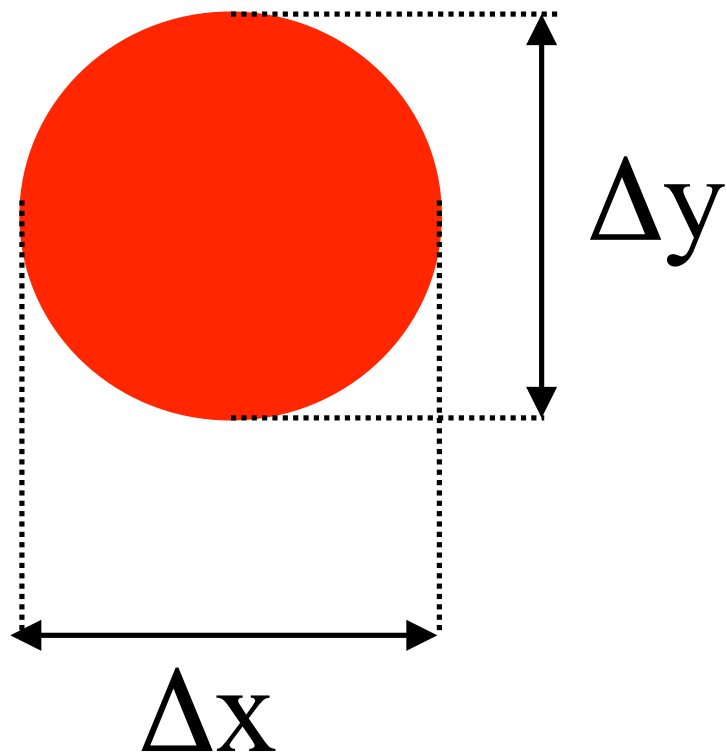
$$\mathbf{D} = \begin{bmatrix} D_{xx} & D_{xy} & D_{xz} \\ D_{xy} & D_{yy} & D_{yz} \\ D_{xz} & D_{yz} & D_{zz} \end{bmatrix}$$

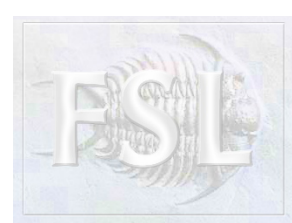
- Tensor is **symmetric** (6 unknowns)
- **Diagonal Elements** are proportional to the diffusion displacement variances (**ADCs**) along the three directions of the experiment coordinate system
- **Off-diagonal Elements** are proportional to the **correlations** (covariances) of displacements along these directions

$$N_3(0, 2t\mathbf{D})$$

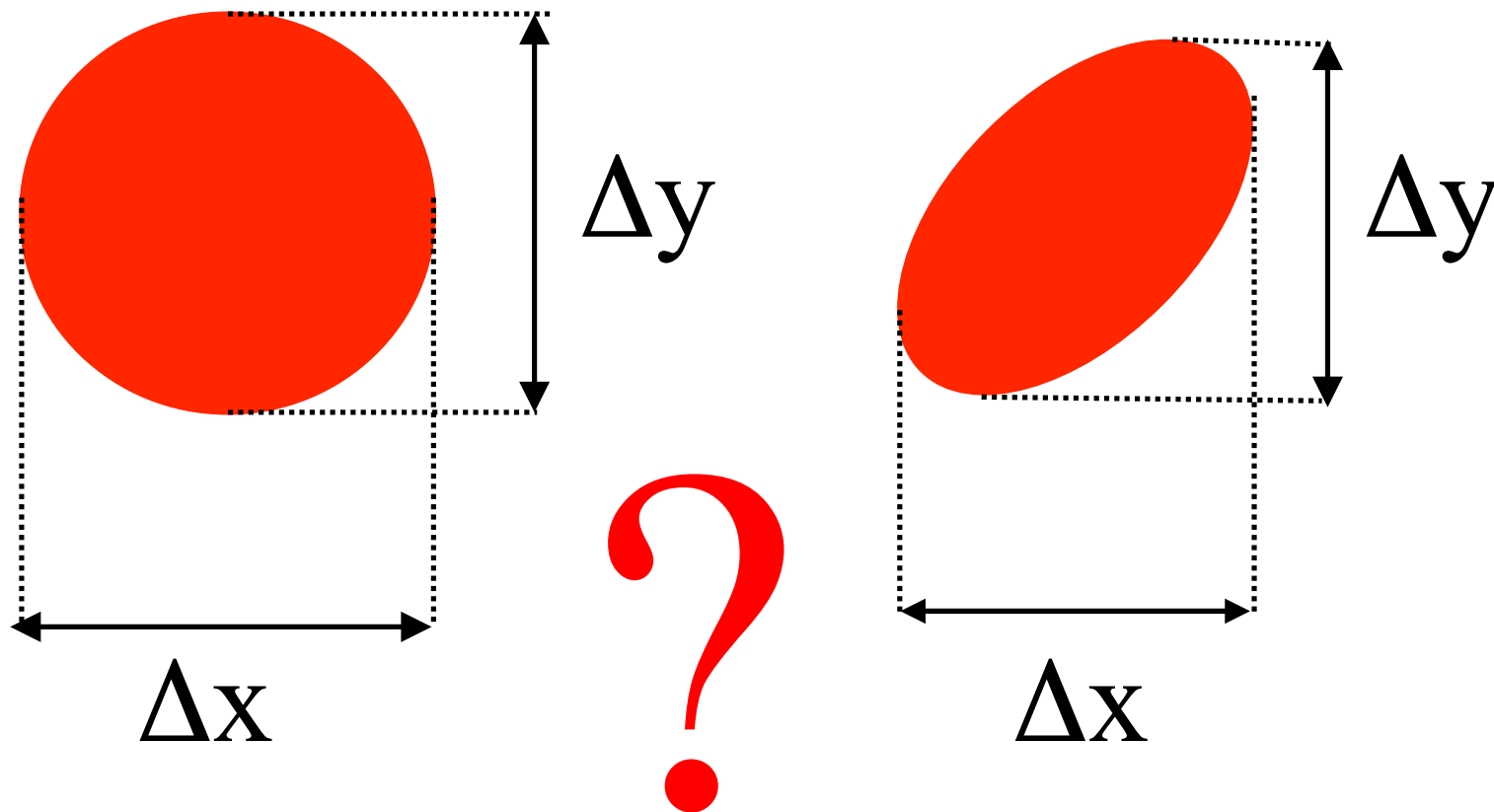


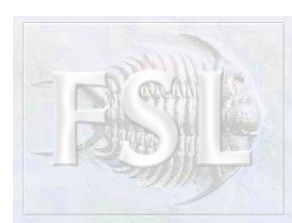
Why do we need a tensor?



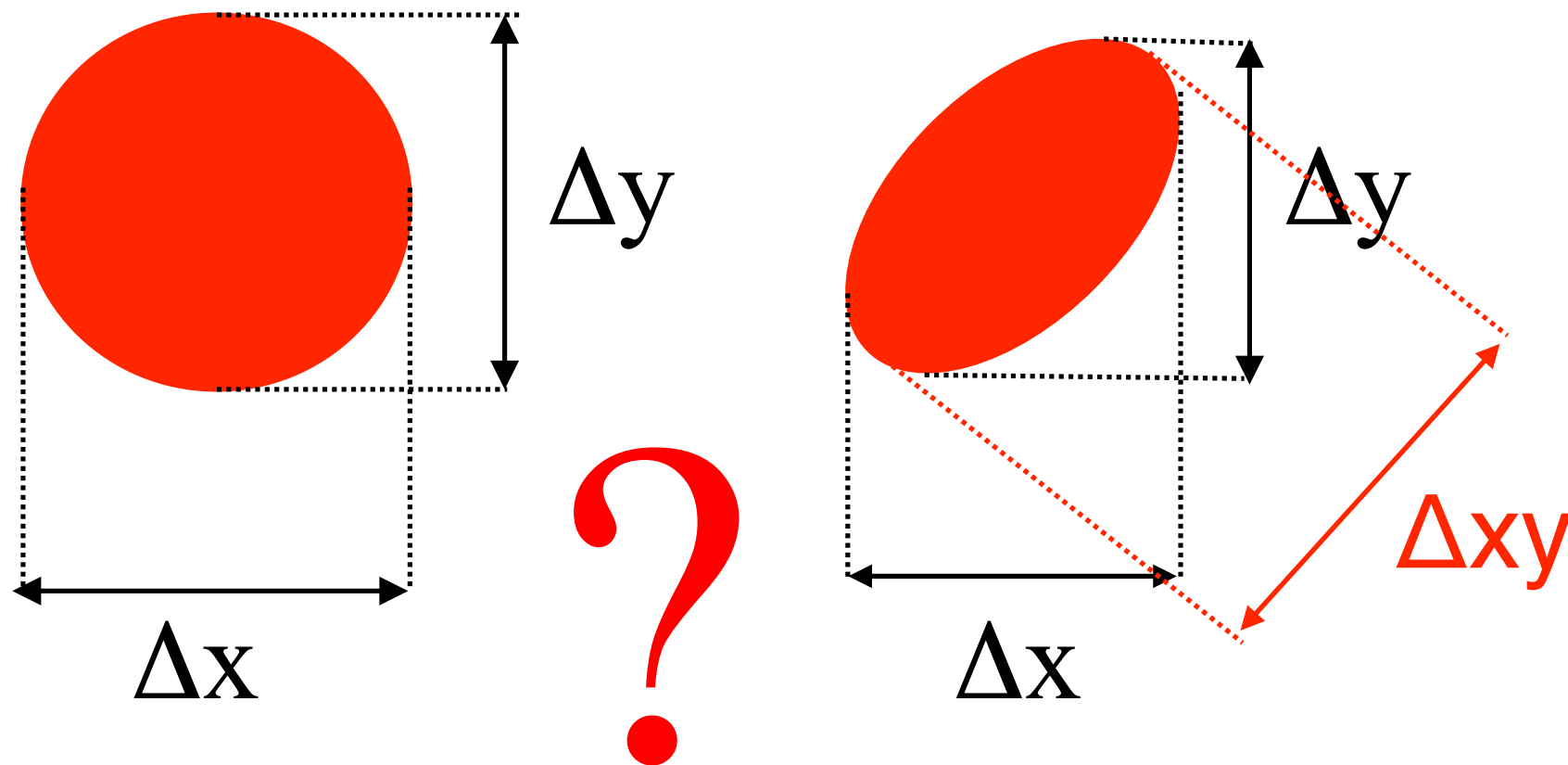


Why do we need a tensor?





Why do we need a tensor?



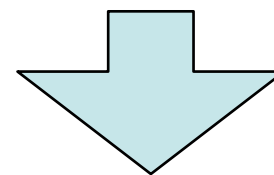
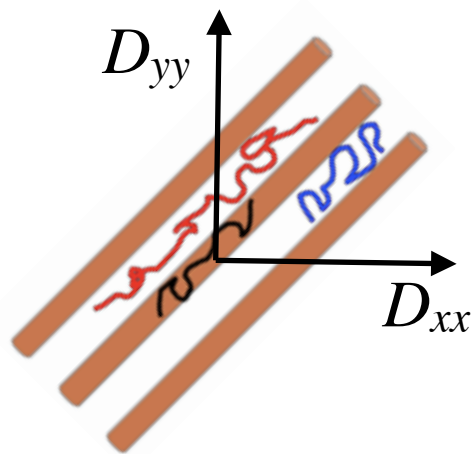
$$\begin{bmatrix} D_x & D_{xy} \\ D_{xy} & D_y \end{bmatrix}$$



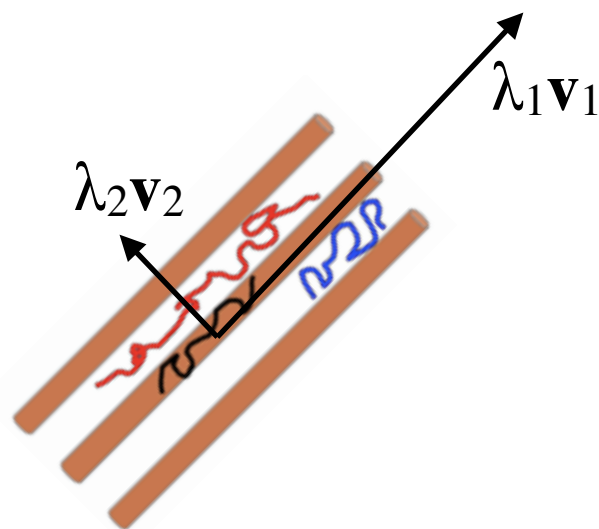
The Diffusion Tensor Eigenspectrum

$$\mathbf{D} = \begin{bmatrix} D_{xx} & D_{xy} & D_{xz} \\ D_{xy} & D_{yy} & D_{yz} \\ D_{xz} & D_{yz} & D_{zz} \end{bmatrix}$$

Once $\mathbf{D}$ is estimated, we get ADCs along the scanner's coordinate system. But we want ADCs along a local coordinate system in each voxel, determined by the anatomy.



Diagonalize the estimated tensor in each voxel



$$\mathbf{D} = [\mathbf{v}_1 | \mathbf{v}_2 | \mathbf{v}_3]^T \begin{bmatrix} \lambda_1 & 0 & 0 \\ 0 & \lambda_2 & 0 \\ 0 & 0 & \lambda_3 \end{bmatrix} [\mathbf{v}_1 | \mathbf{v}_2 | \mathbf{v}_3]$$

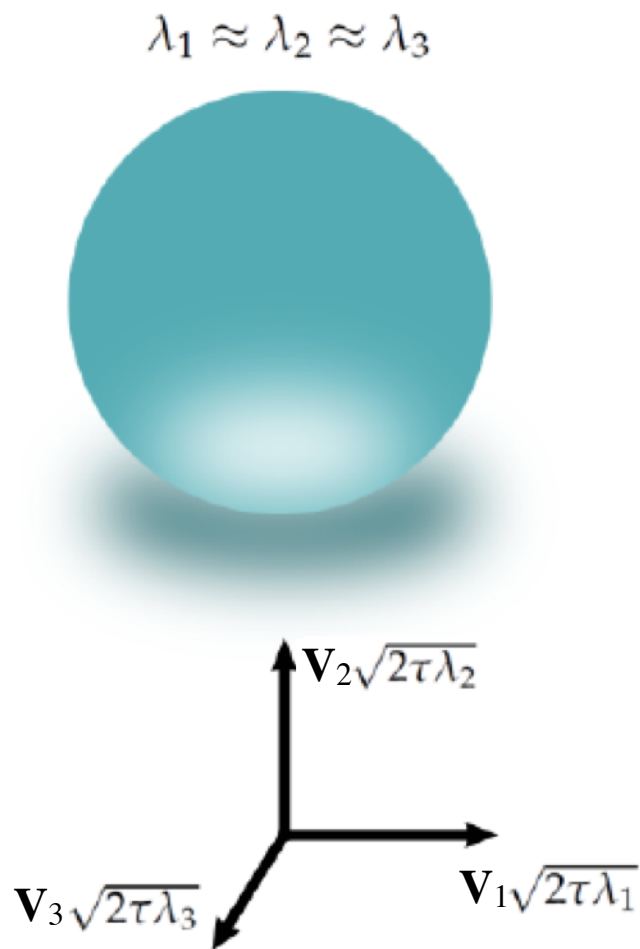
eigenvalues: ADCs along $\mathbf{v}_1, \mathbf{v}_2, \mathbf{v}_3$

eigenvectors - $\mathbf{v}_1$ =direction of max diffusivity

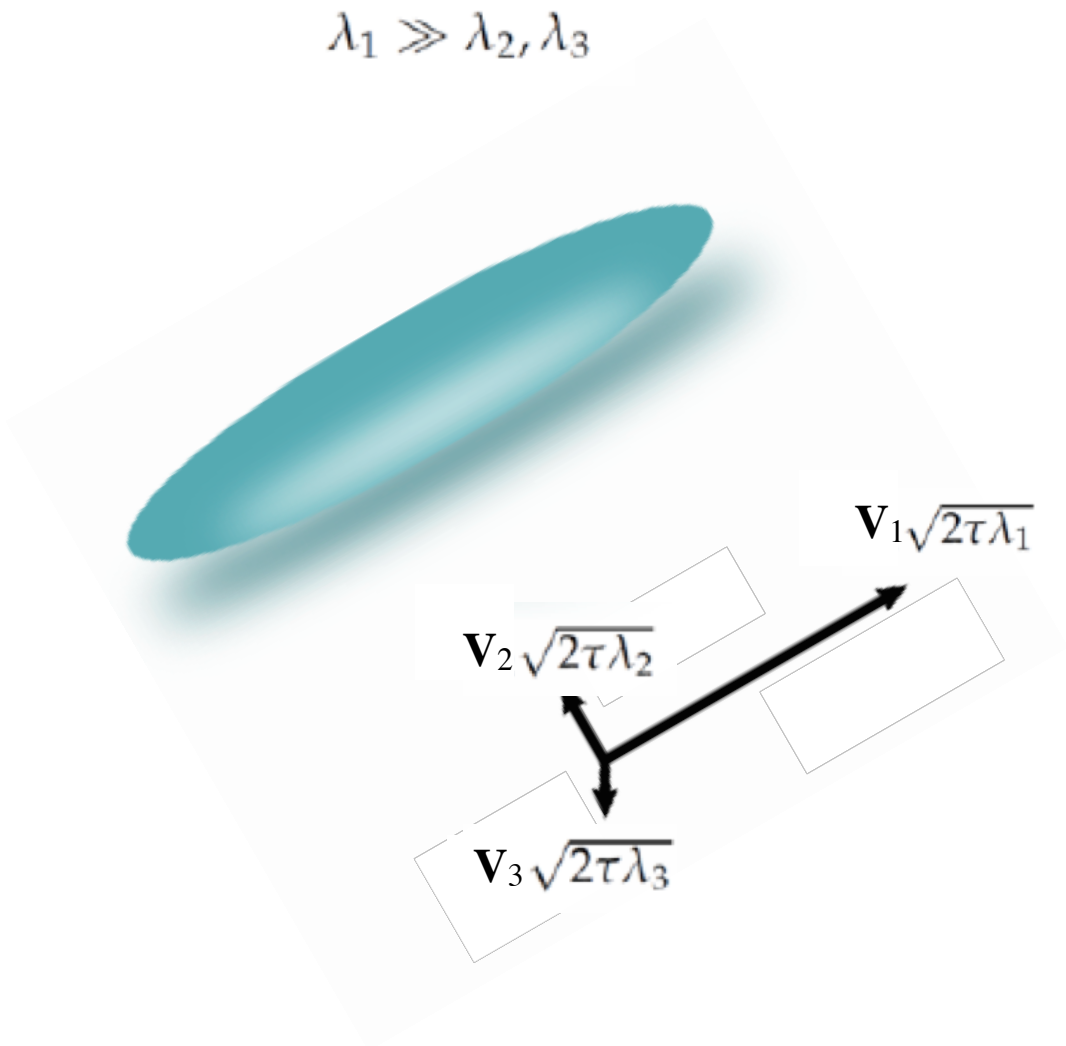


The Diffusion Tensor Ellipsoid

Isotropic voxel

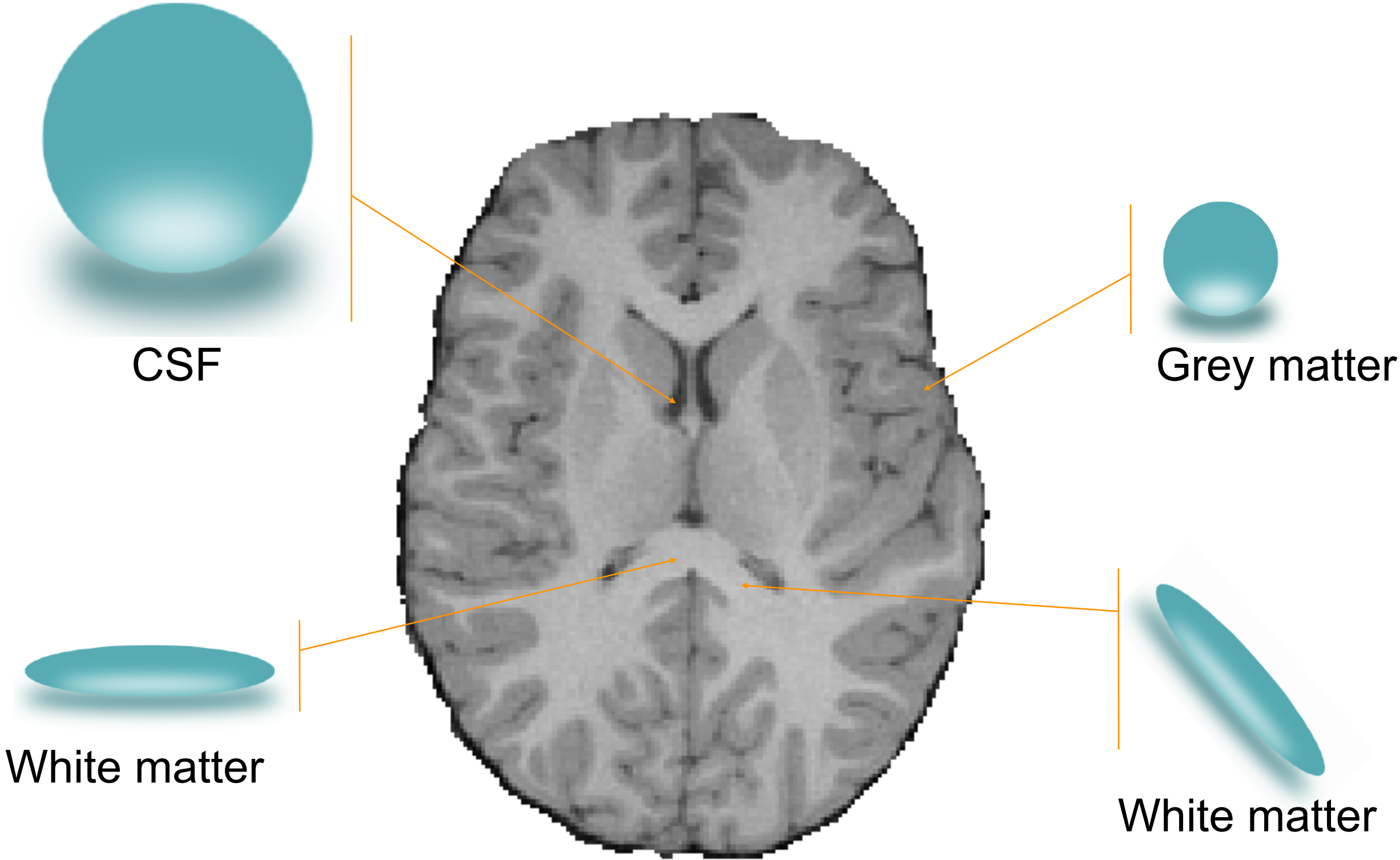


Anisotropic voxel





The Diffusion Tensor Ellipsoid



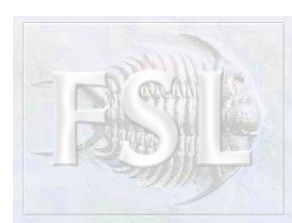


Quantitative Diffusion Maps

Fractional Anisotropy (FA) ~ Eigenvalues Variance (normalised)
Mean Diffusivity (MD) = Eigenvalues Mean

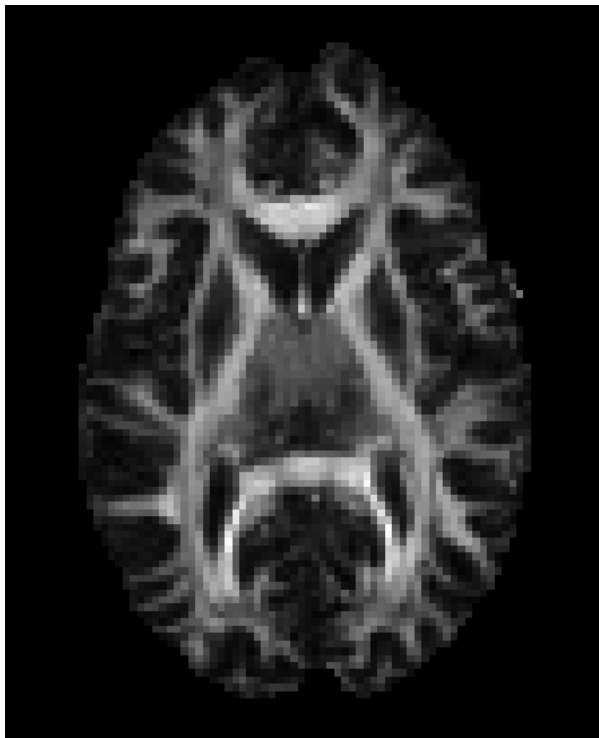
$$FA = \sqrt{\frac{3 \sum_{i=1}^3 (\lambda_i - \bar{\lambda})^2}{2 \sum_{i=1}^3 \lambda_i^2}}, \quad FA \text{ in } [0,1]$$

$$MD = \frac{D_{xx} + D_{yy} + D_{zz}}{3} = \frac{\lambda_1 + \lambda_2 + \lambda_3}{3}$$



Quantitative Diffusion Maps

FA



MD



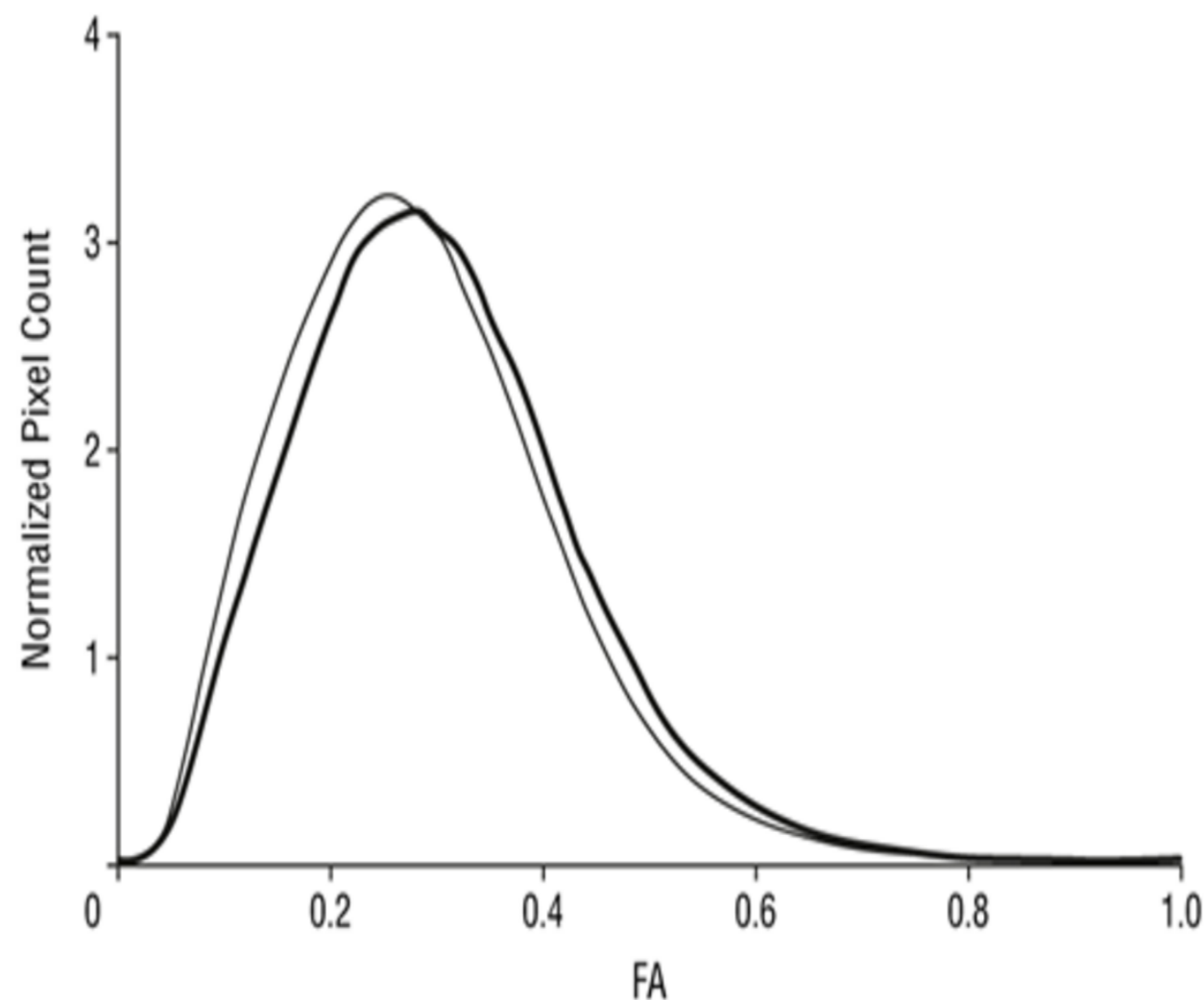


Quantitative Diffusion Maps

FA decrease/ MD increase has been associated in many studies with tissue breakdown (loss of structure).



Rovaris et al, Arch Neurol 2002
Gallo et al, Arch Neurol 2005



Fractional Anisotropy changes in MS normal appearing white matter

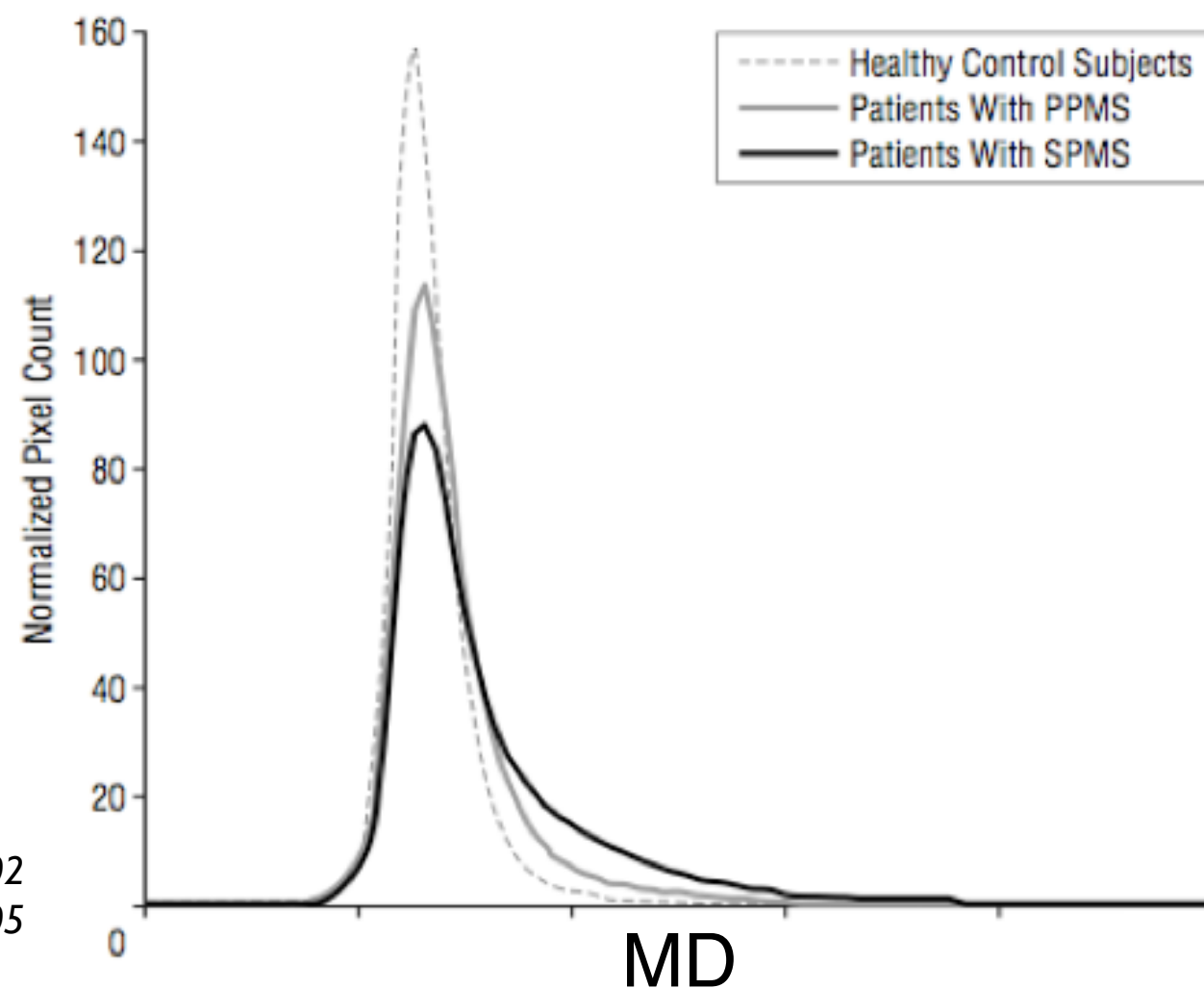


Quantitative Diffusion Maps

FA decrease/ MD increase has been associated in many studies with tissue breakdown (loss of structure).



Rovaris et al, Arch Neurol 2002
Gallo et al, Arch Neurol 2005

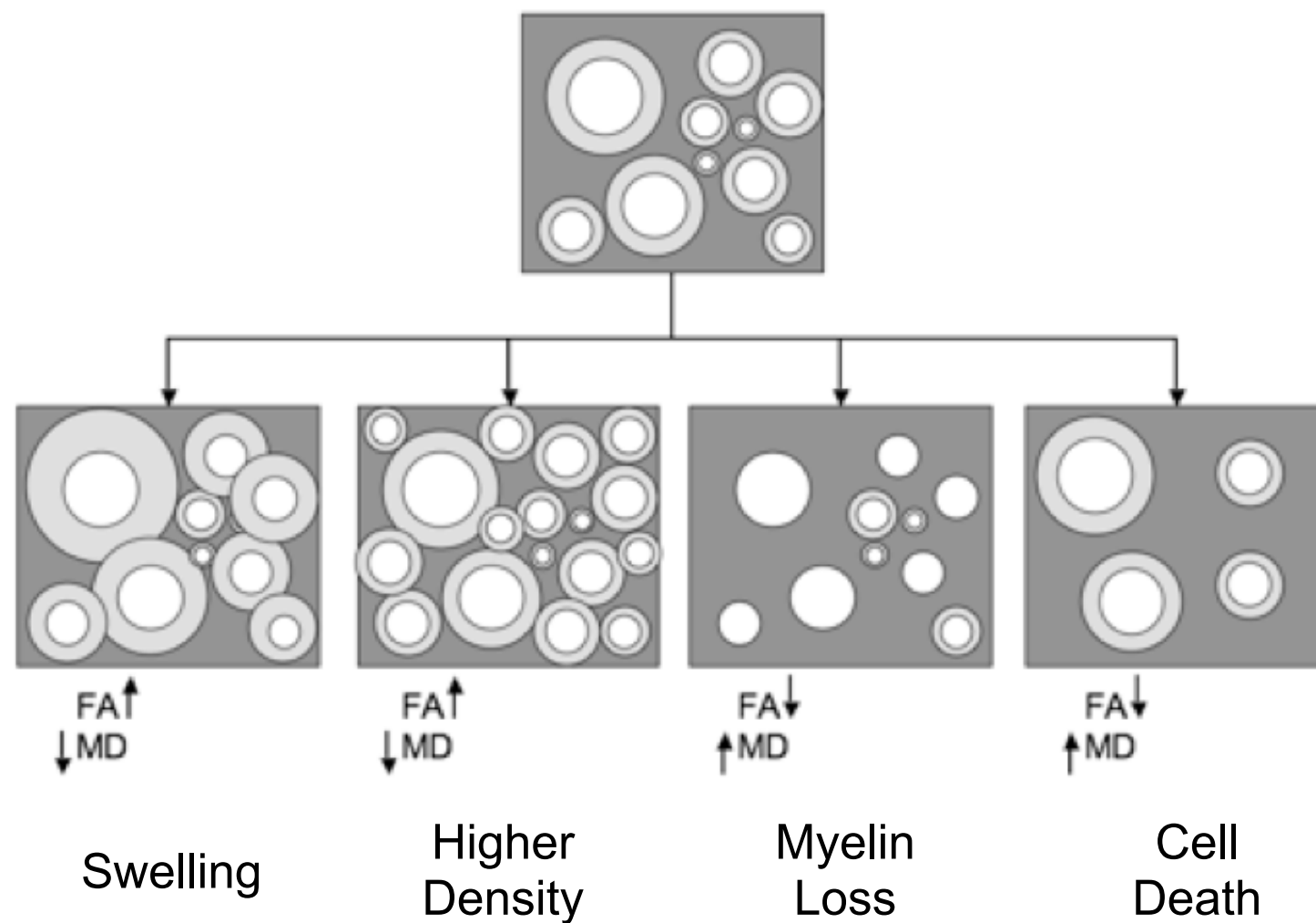


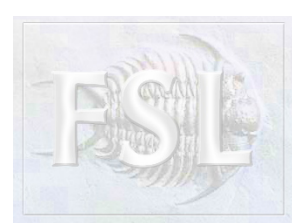
Fractional Anisotropy changes in MS normal appearing white matter



Quantitative Diffusion Maps

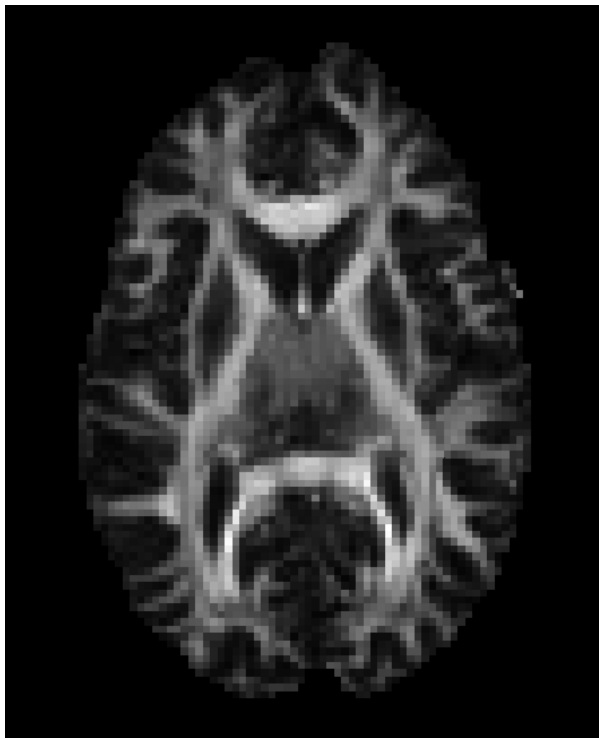
Different scenarios can have same effect on FA, MD





Quantitative Diffusion Maps

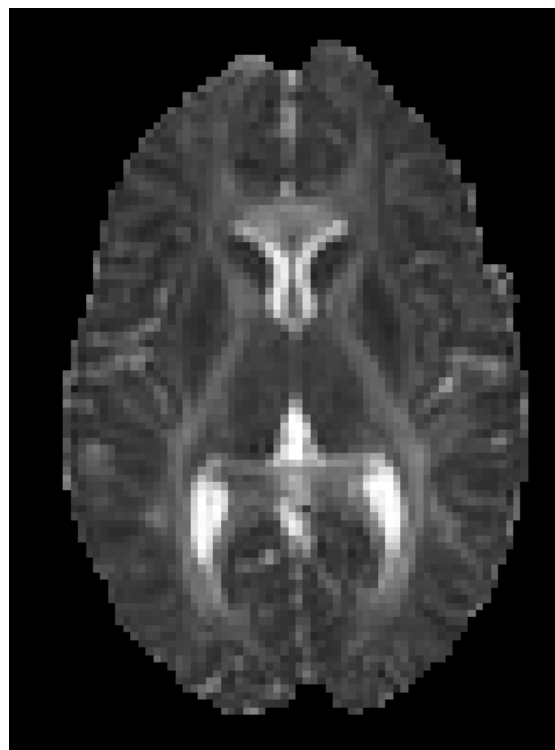
FA



MD



Longitudinal/axial/parallel ADC
(λ_1)



Transverse/radial/perpendicular ADC
($\lambda_2 + \lambda_3$)/2





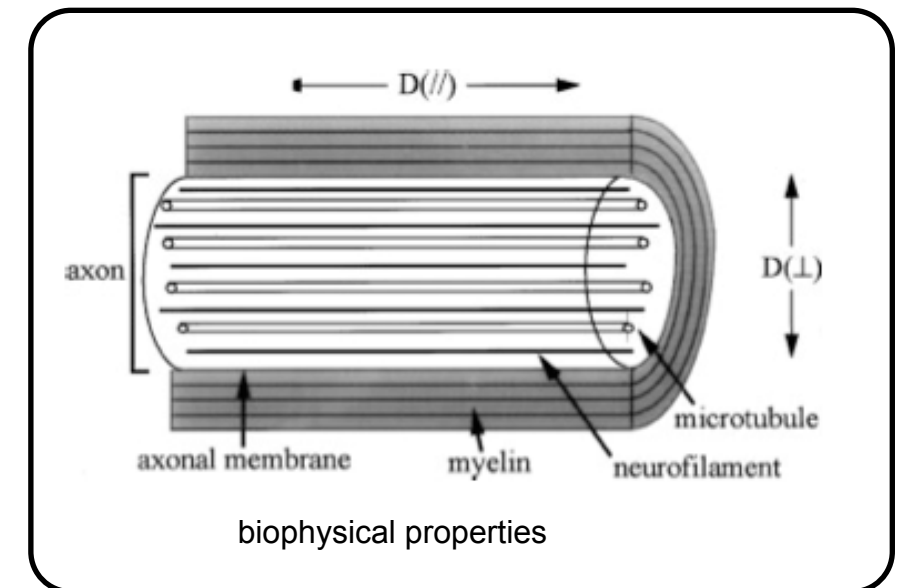
Quantitative Diffusion Maps

FA decrease in WM can be caused:

a) Decrease of longitudinal ADC.
Axonal breakdown?

b) Increase of transverse ADC.
Myelin breakdown?

But do not over-interpret your results.
Always keep in mind that the DTI
model is an oversimplification of
reality





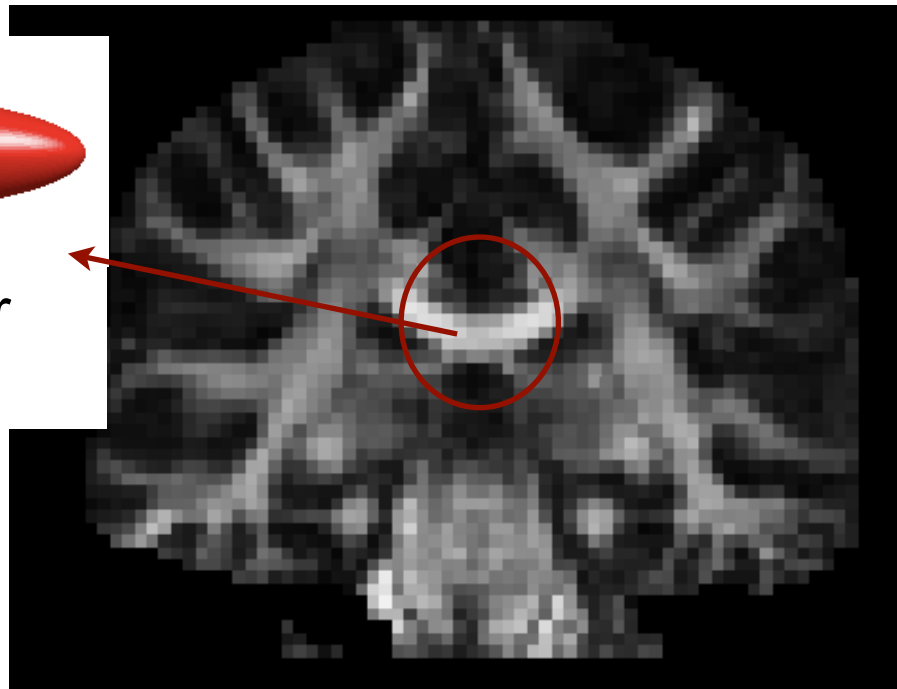
Tensor and FA in Crossing Regions

- In voxels containing two crossing bundles, FA is low and the tensor ellipsoid is pancake-shaped (oblate, planar tensor).



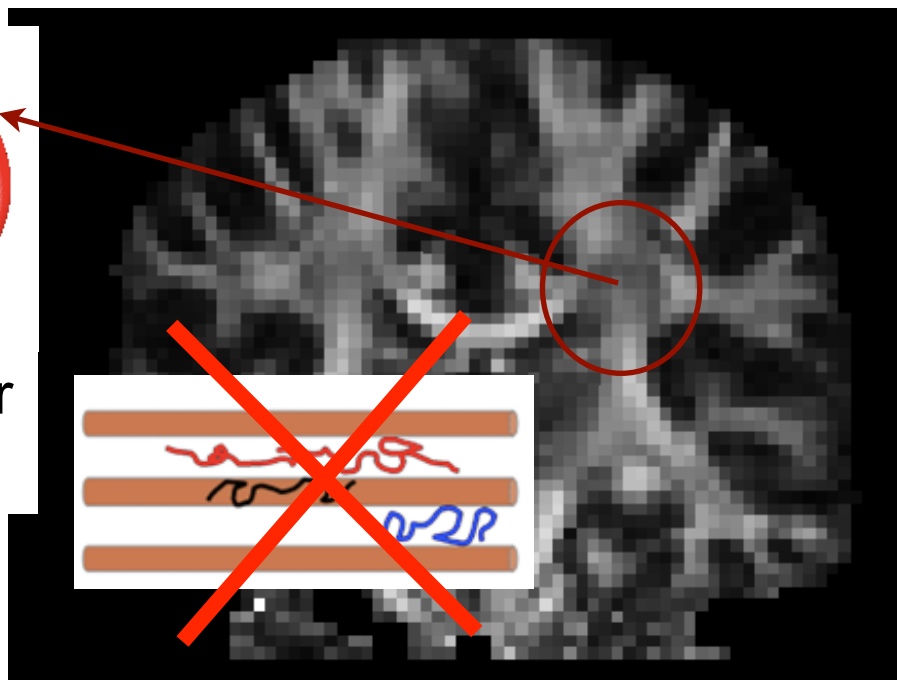
Prolate Tensor

$$\lambda_1 \gg \lambda_2, \lambda_3$$



Oblate Tensor

$$\lambda_1 = \lambda_2 \gg \lambda_3$$



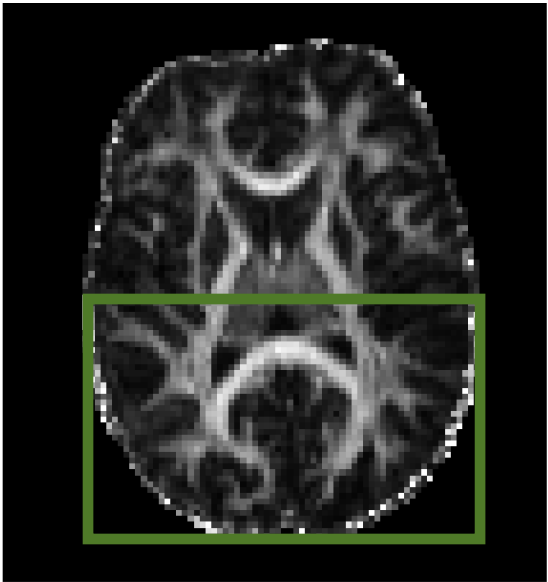
Consequences:

- PDD not necessarily = direction of fibres
- FA changes difficult to interpret

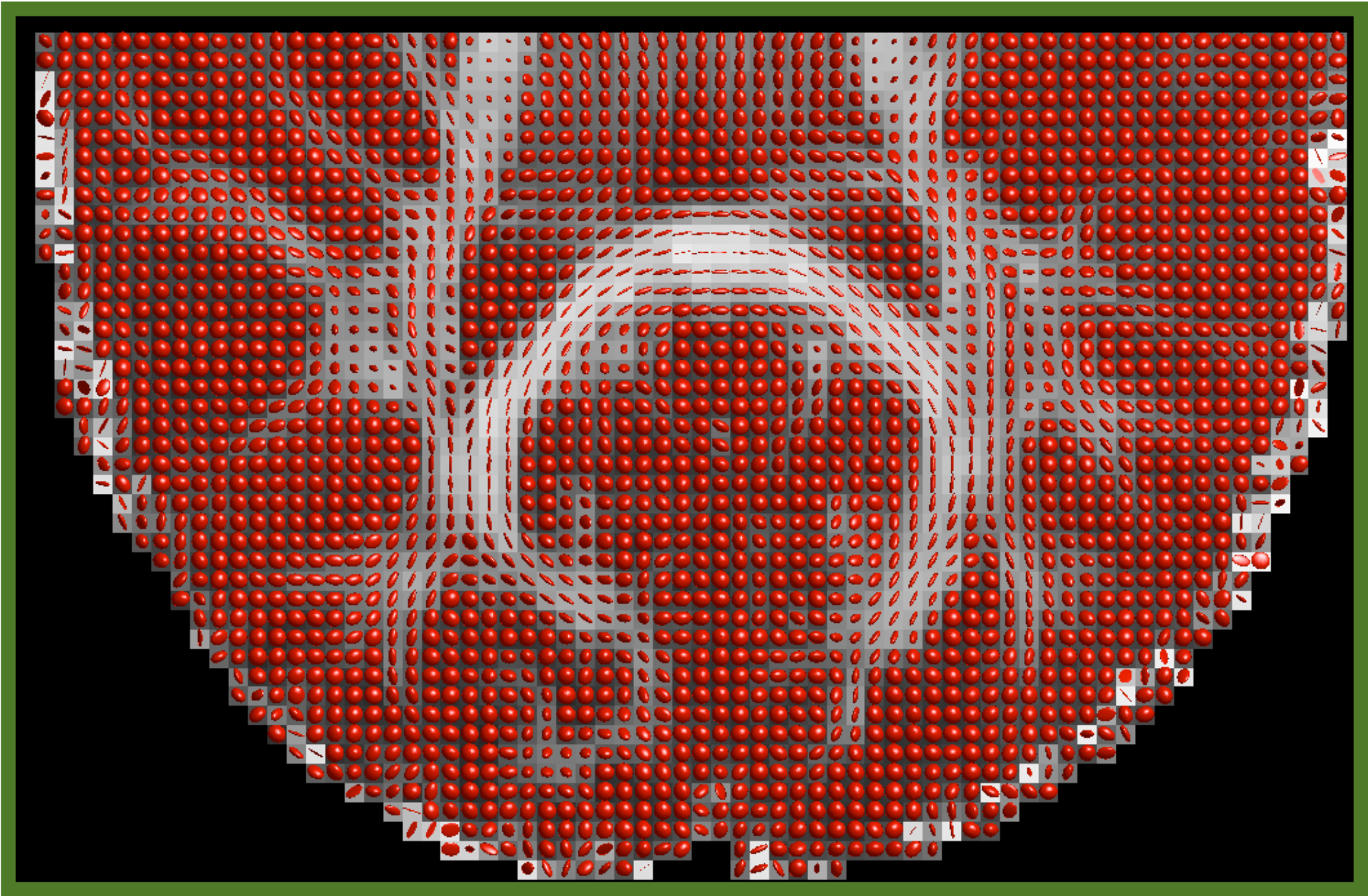
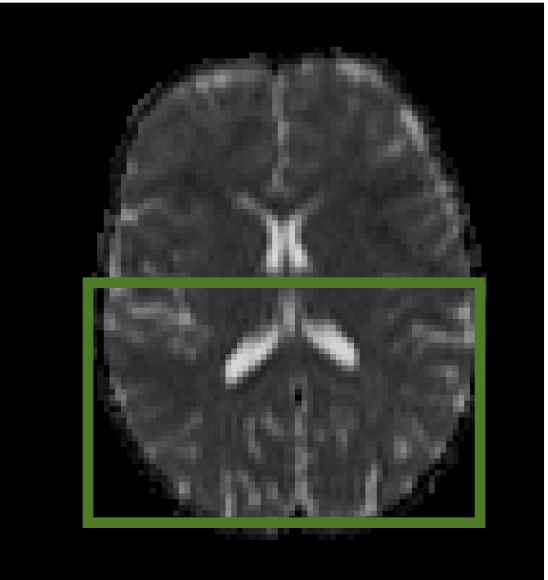


Diffusion Tensor Ellipsoids

Fractional anisotropy

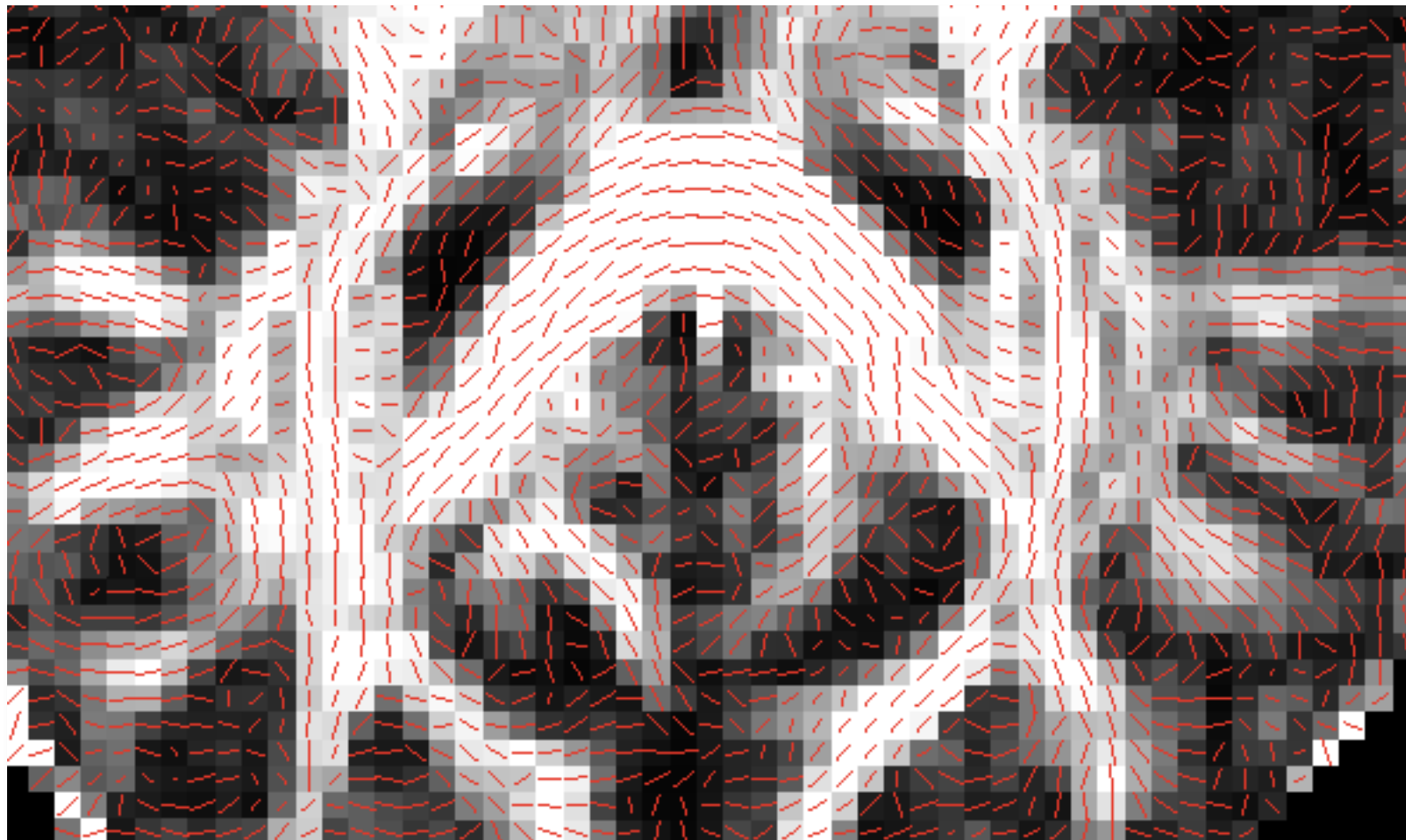


Mean diffusion

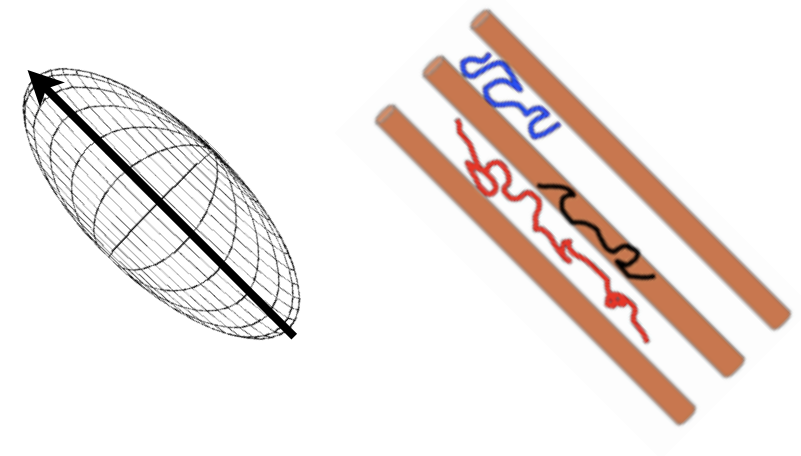


Estimates of Principal Fibre Orientation in WM

v_1 map
Principal Diffusion Direction



Principal Diffusion
Direction

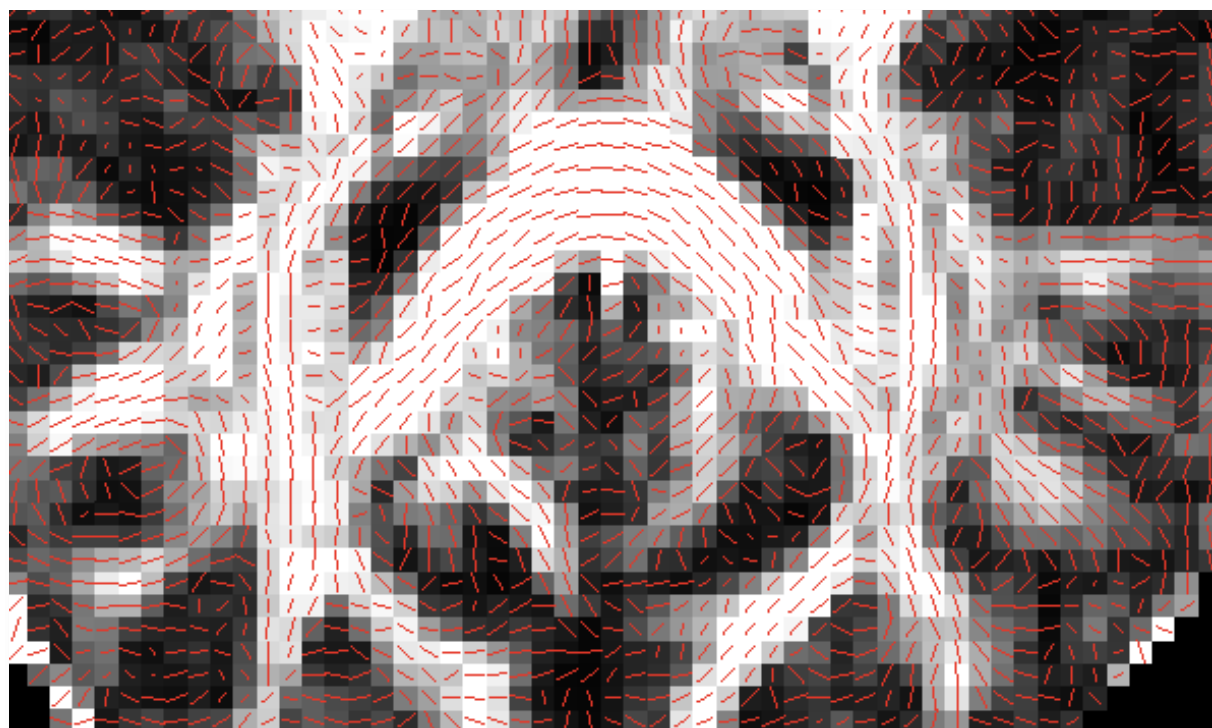


Assumption!!

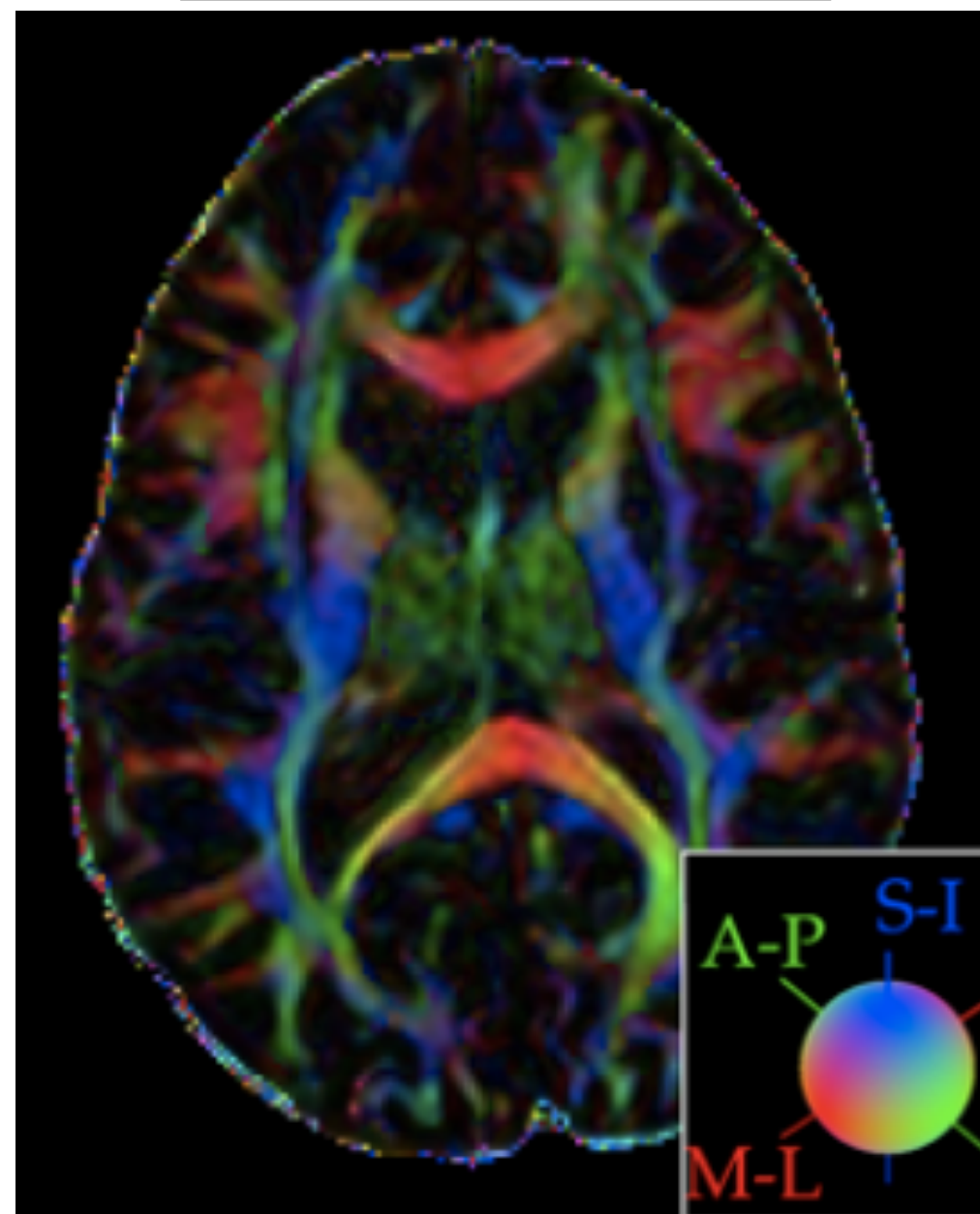
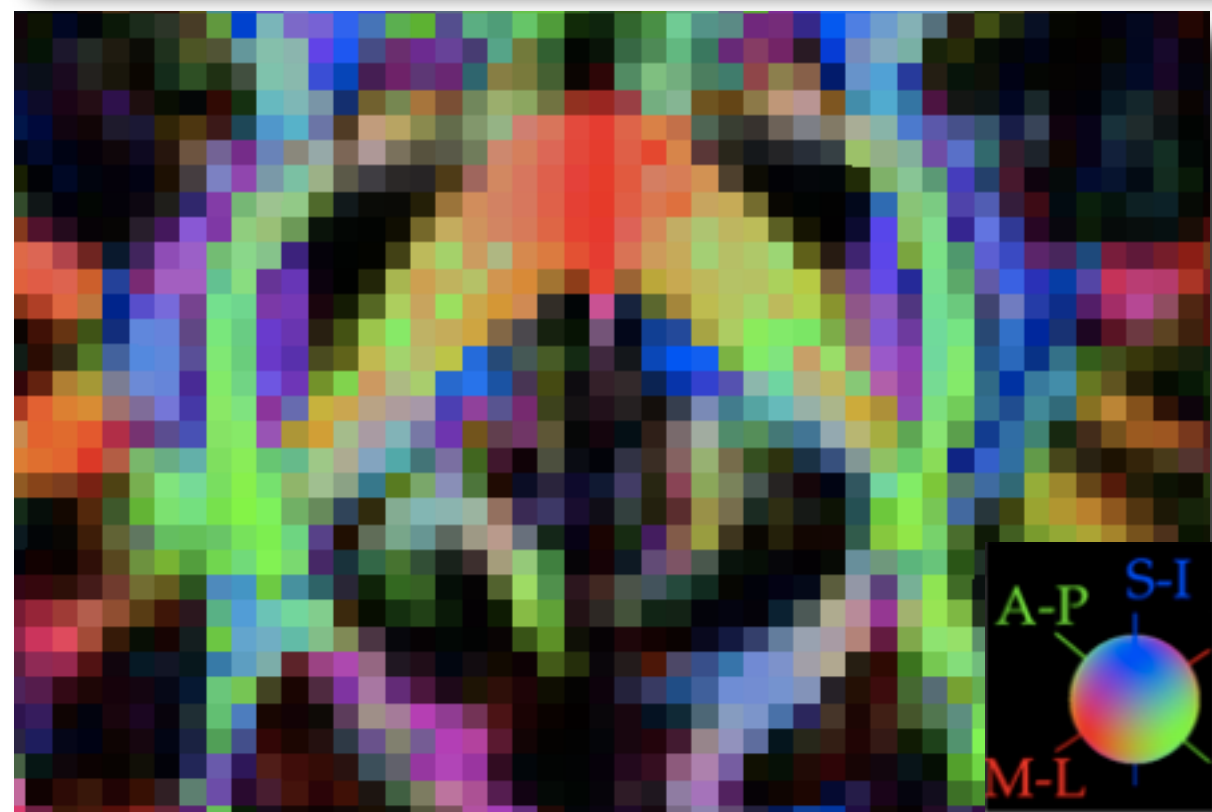
Direction of maximum diffusivity in voxels with anisotropic profile is an estimate of the major fibre orientation.



Estimates of Principal Fibre Orientation in WM

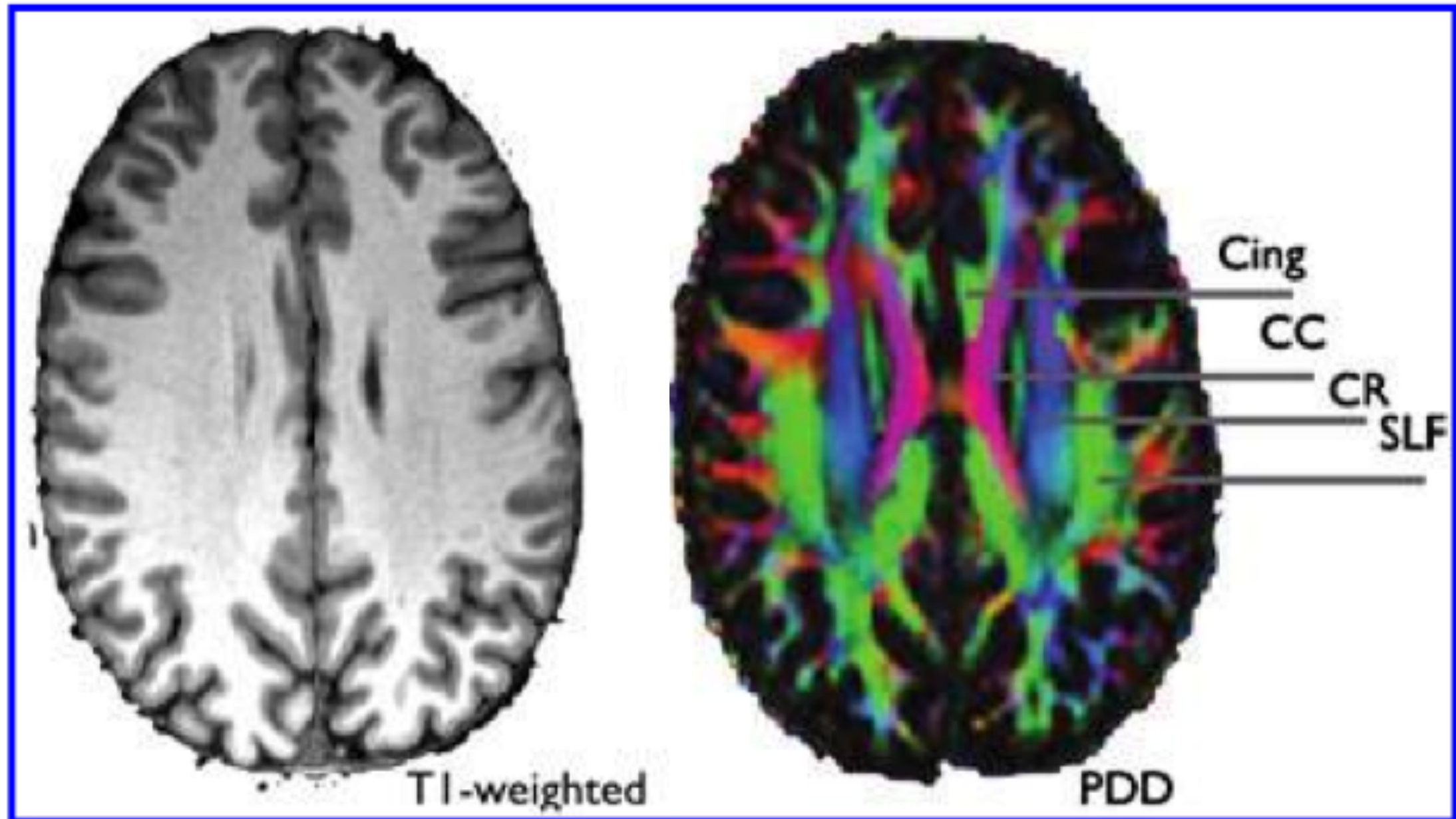


Colour-coded v_1 map





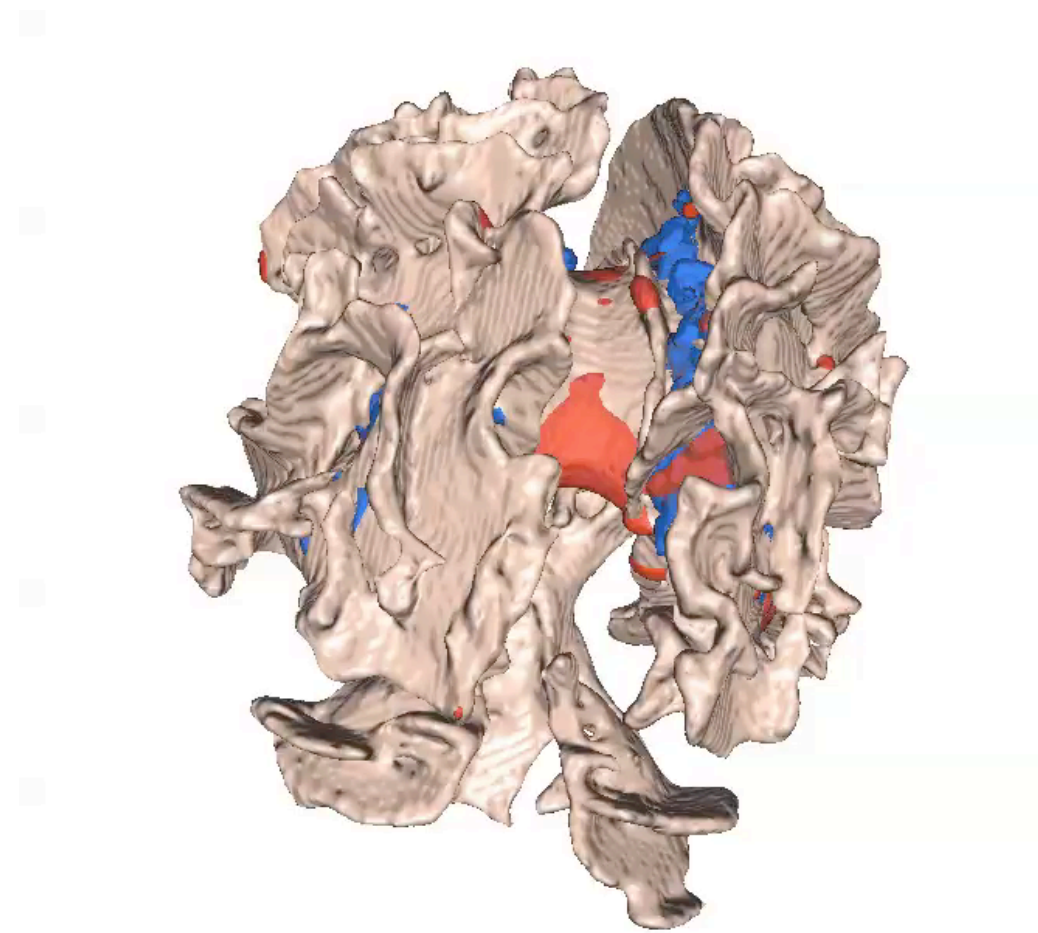
Directional contrast in DTI





TBSS : Tract-Based Spatial Statistics

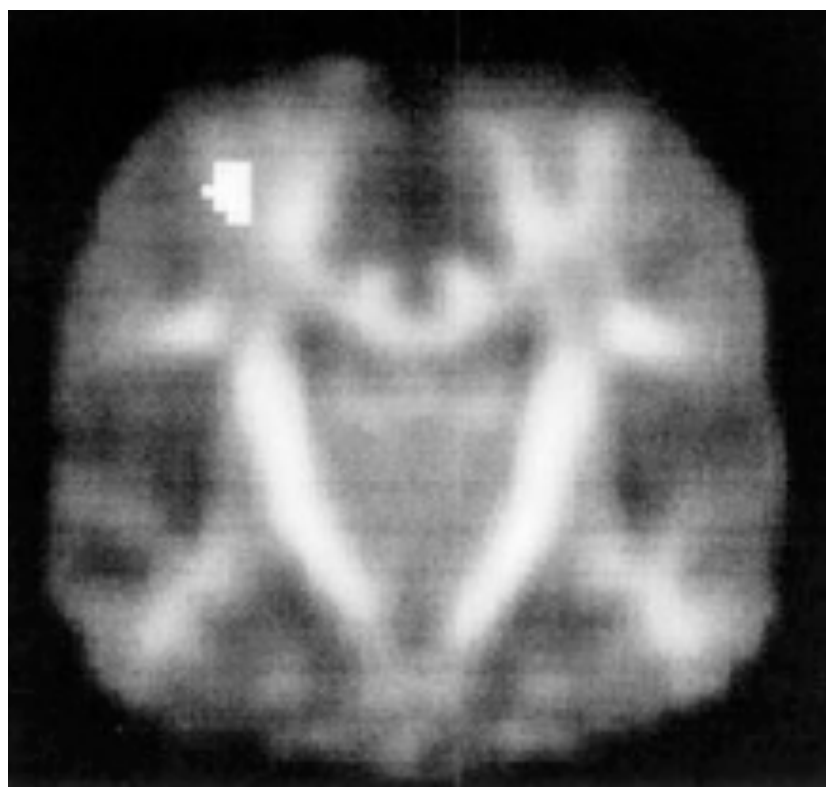
Robust “voxelwise” cross-subject stats
on diffusion-derived measures



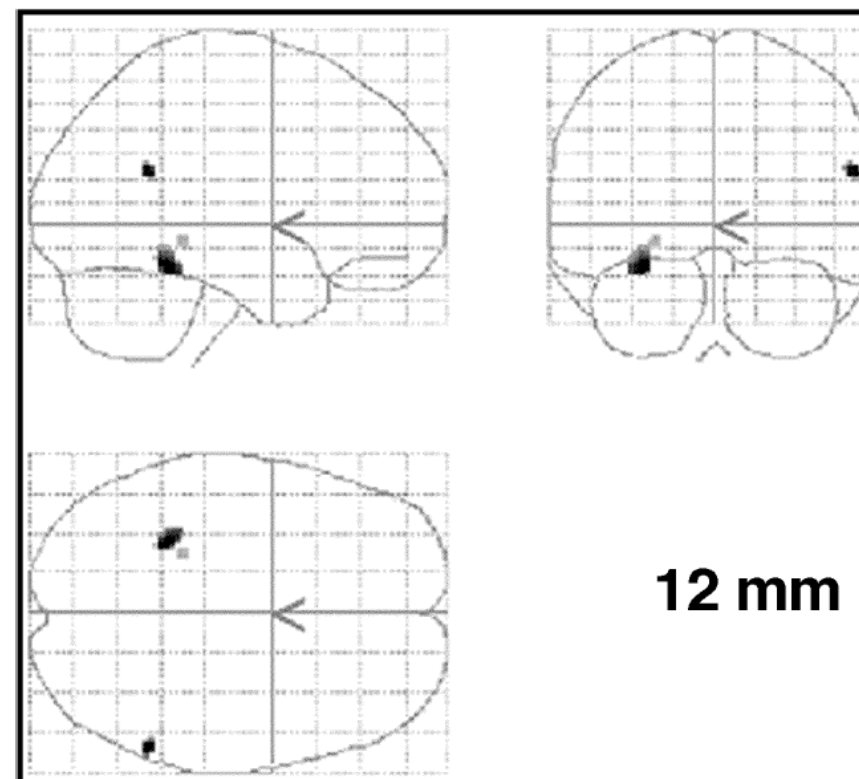


Voxel-wise Analysis of FA

- Compute diffusion tensor
- Align all subjects' data to standard space
 - Diffusion (b0/FA) -> structural -> standard
 - FA -> standard
- Do voxelwise stats (e.g. controls-patients)



Büchel 2004

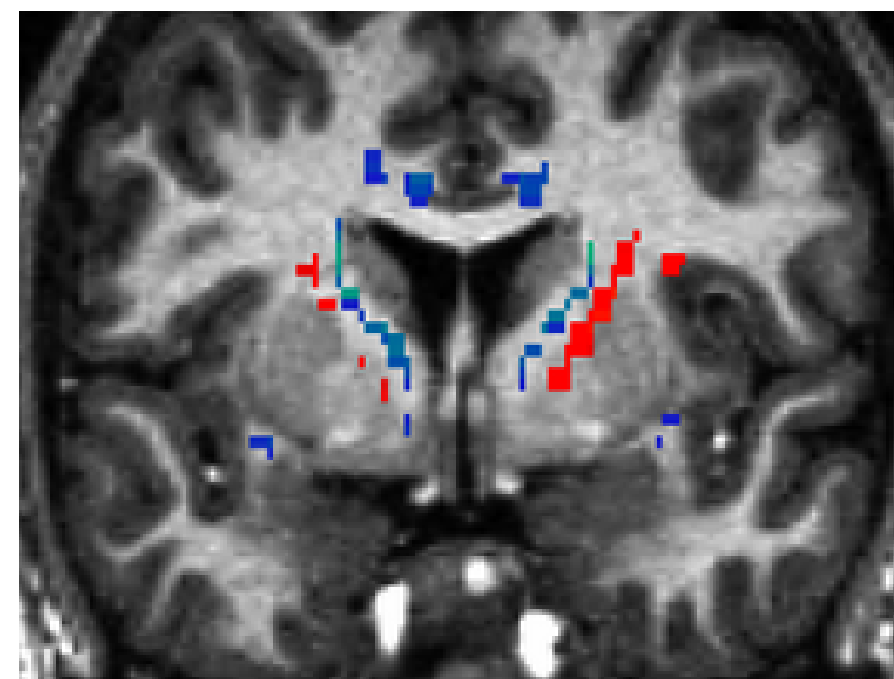
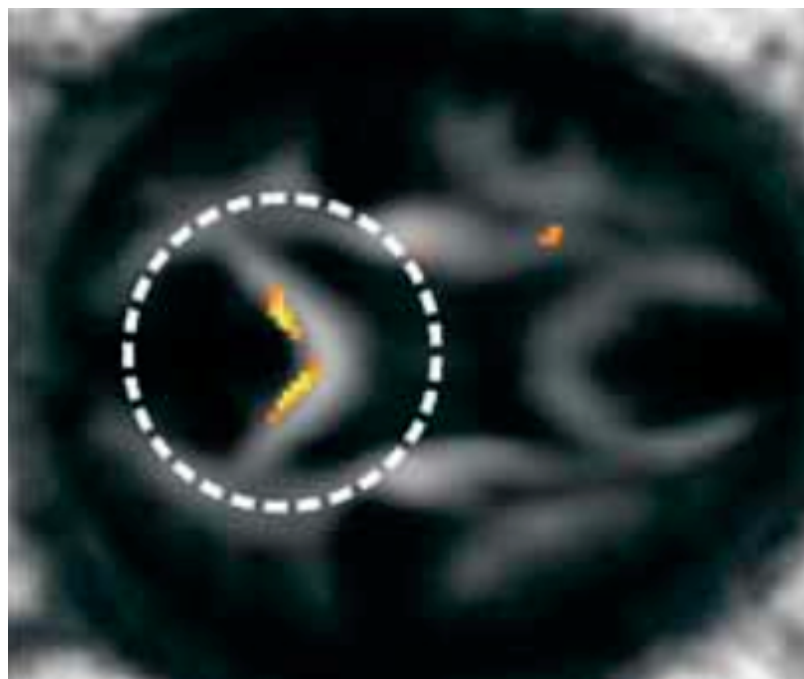
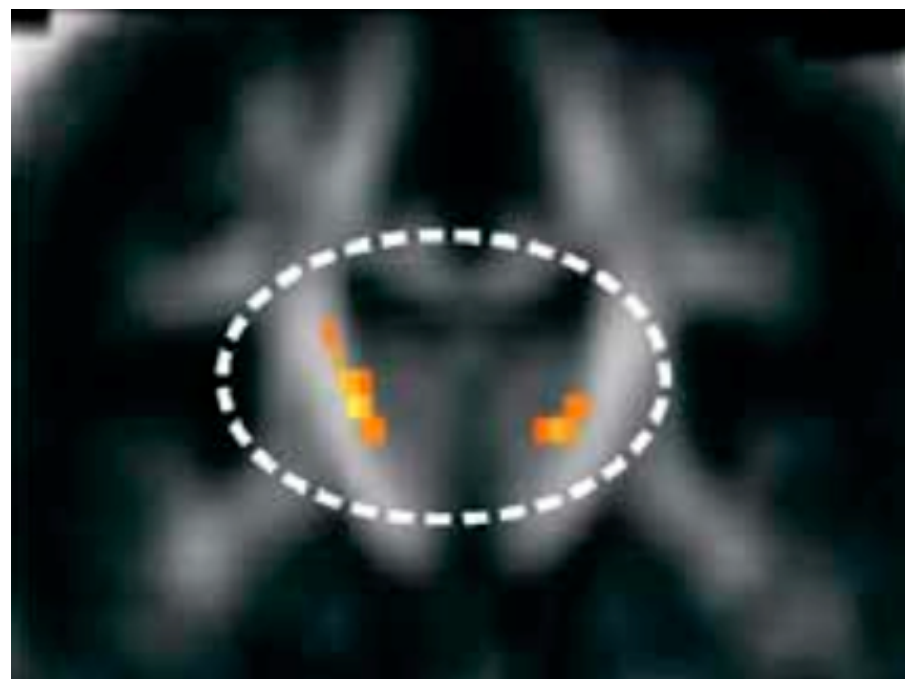


Jones 2005



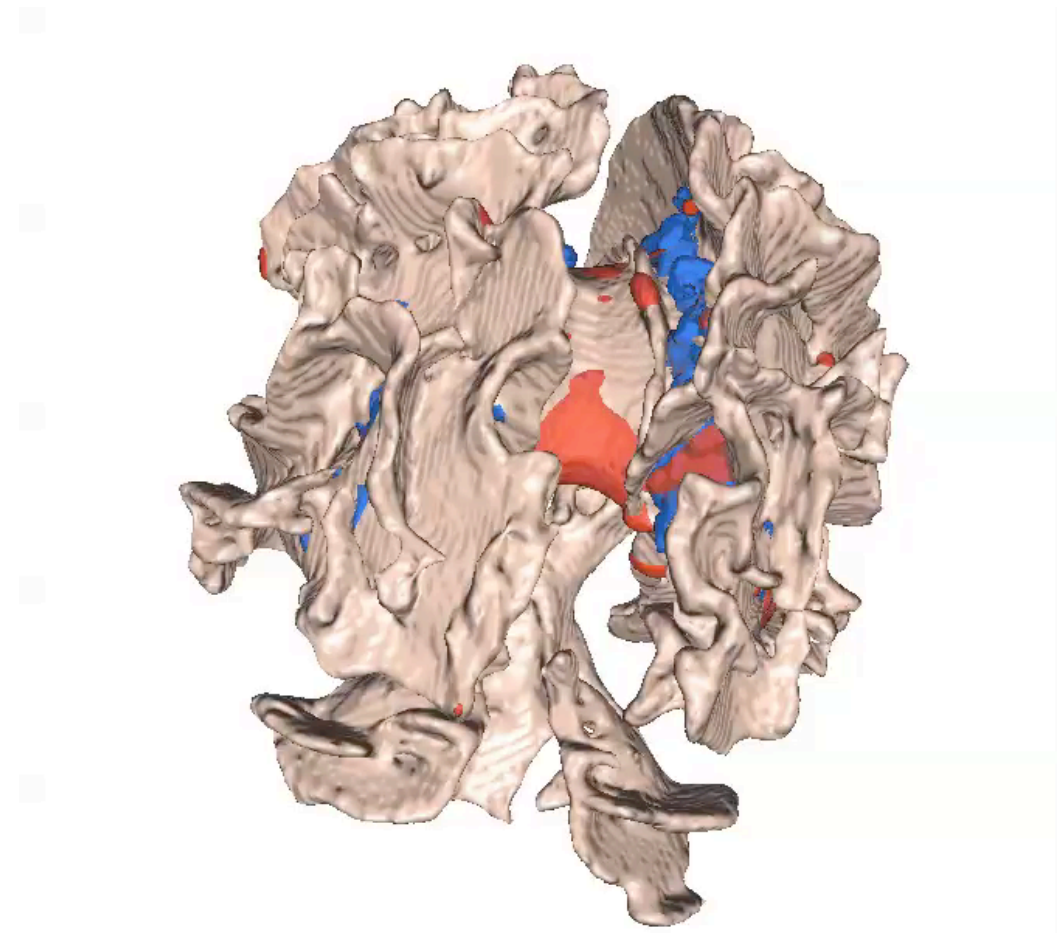
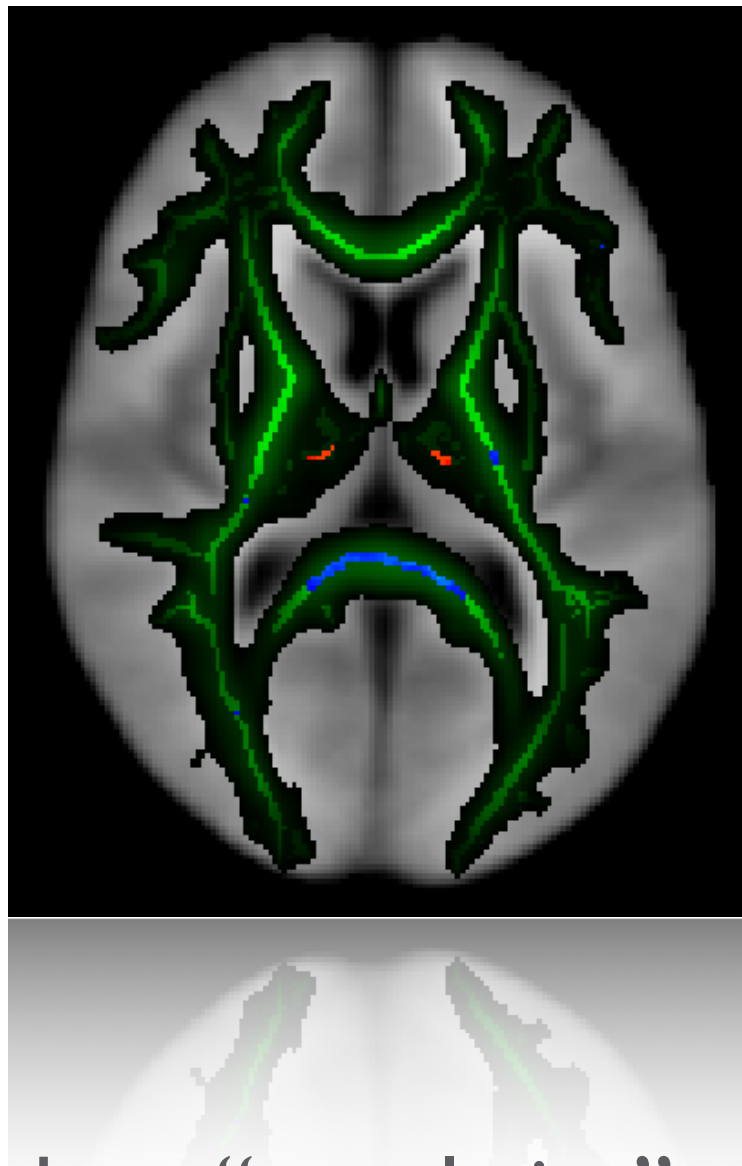
VBM-style Analysis of FA

- Strengths
 - Fully automated & quick
 - Investigates whole brain
- Problems [Bookstein 2001, Davatzikos 2004, Jones 2005]
 - Alignment difficult; smallest systematic shifts between groups can be incorrectly interpreted as FA change
 - Needs smoothing to help with registration problems
 - No objective way to choose smoothing extent





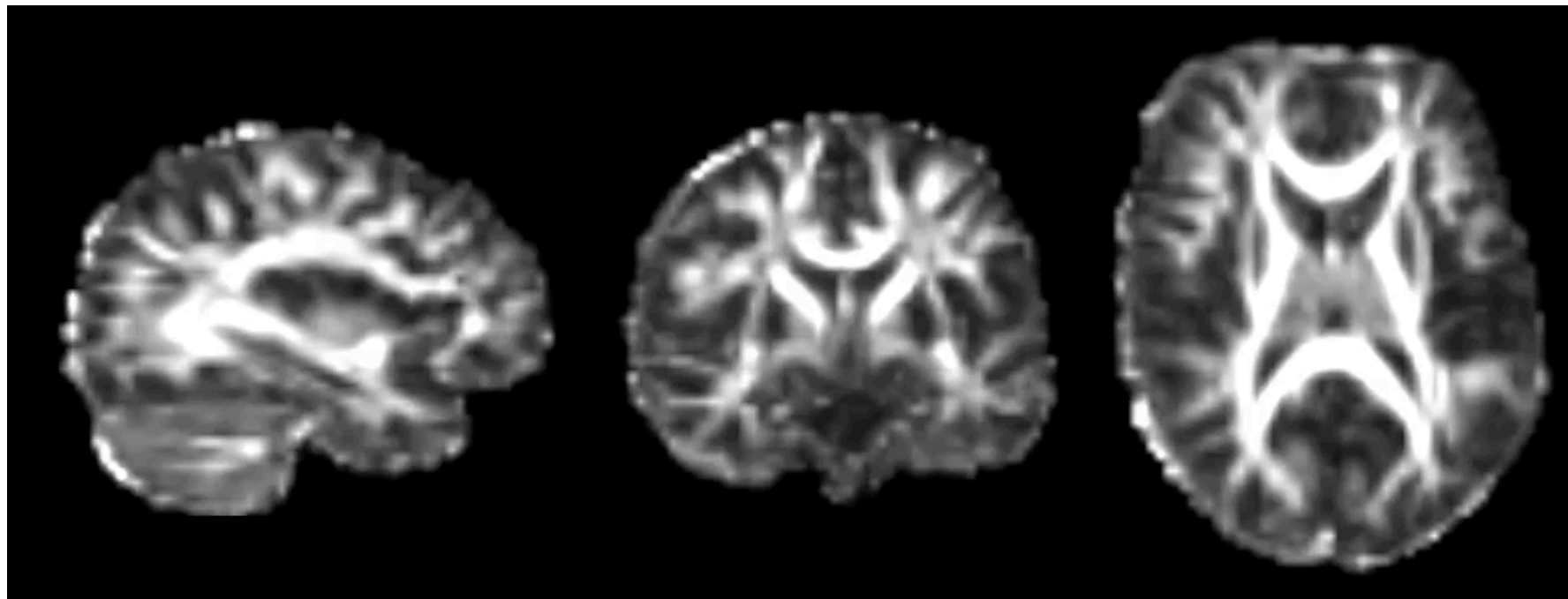
TBSS : Tract-Based Spatial Statistics



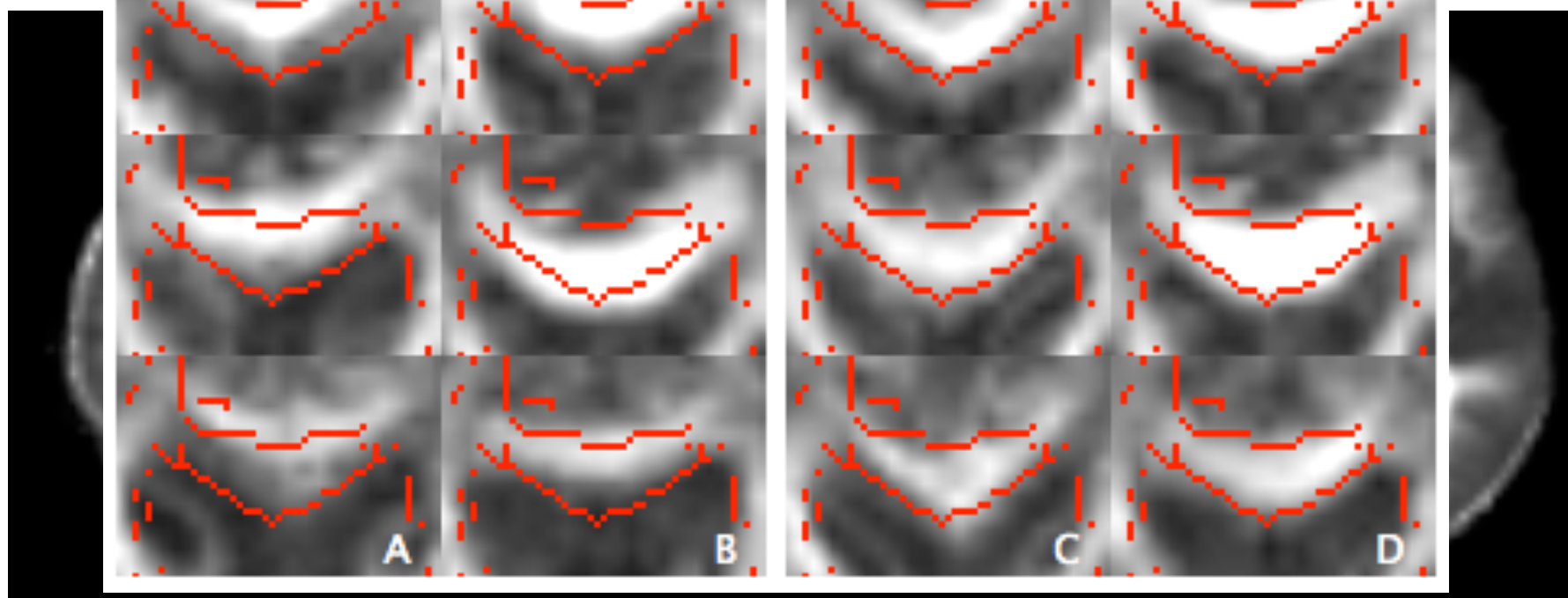
- Need: robust “voxelwise” cross-subject stats on DTI
- Problem: alignment issues confound valid local stats
- TBSS: solve alignment using alignment-invariant features:
- Compare FA taken from tract centres (via skeletonisation)

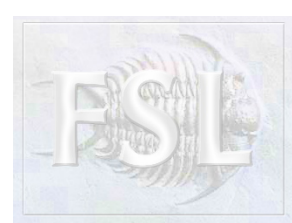


1. Use medium-DoF nonlinear reg to
pre-align all subjects' FA
(nonlinear reg: FNIRT)

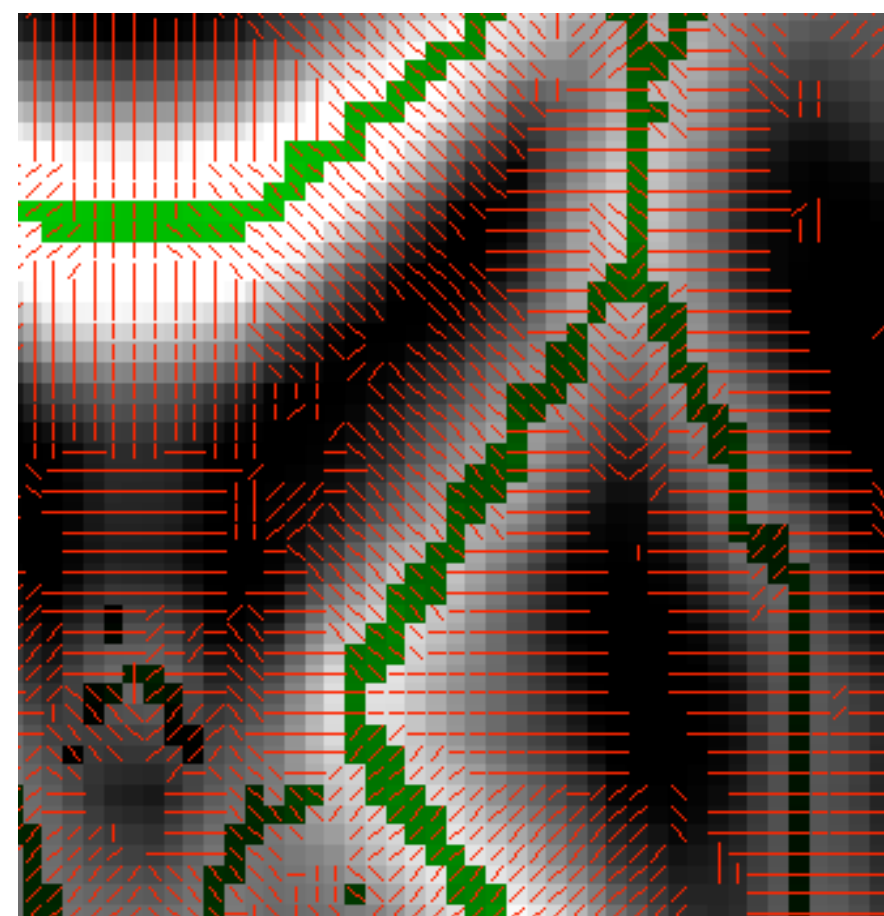
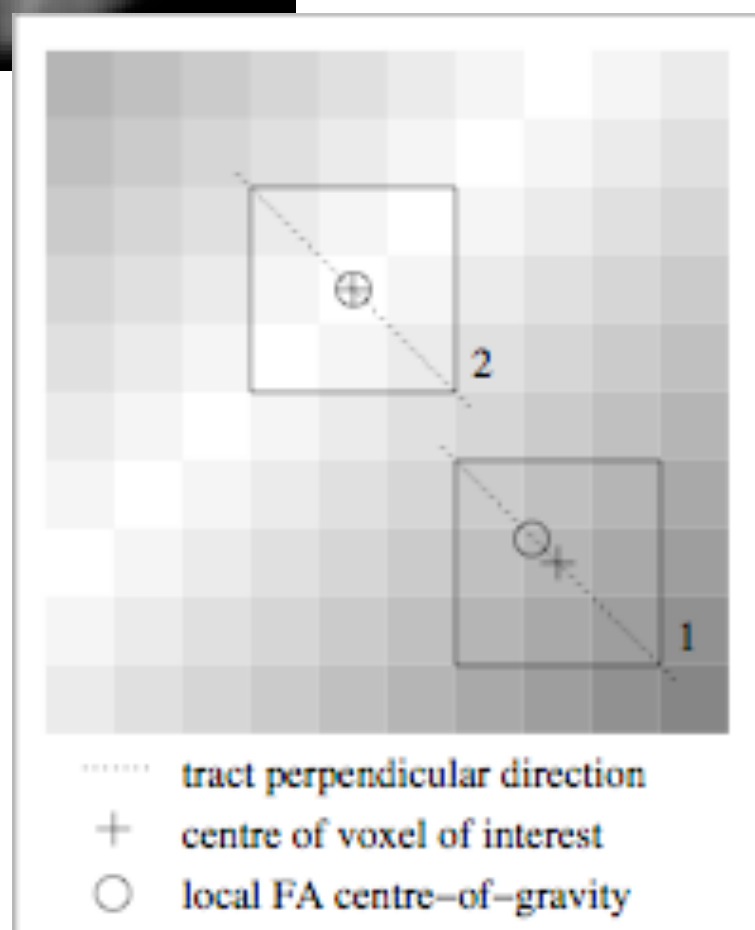
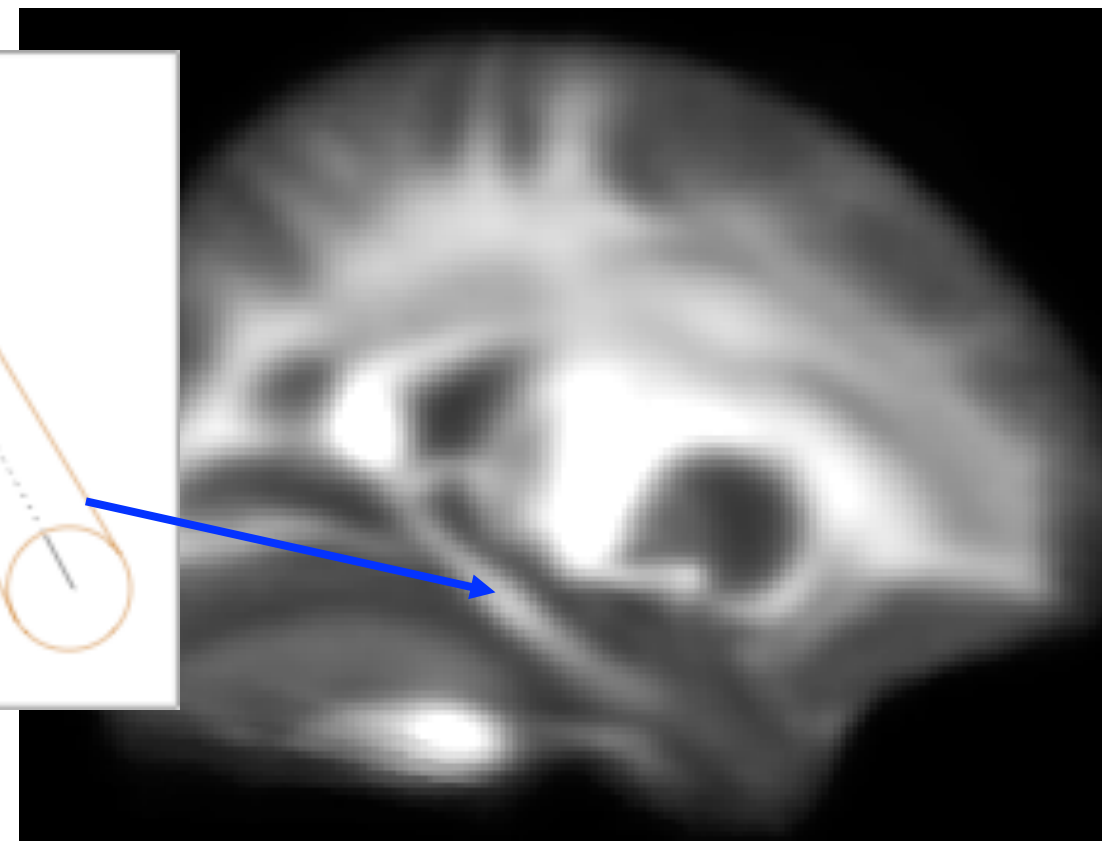
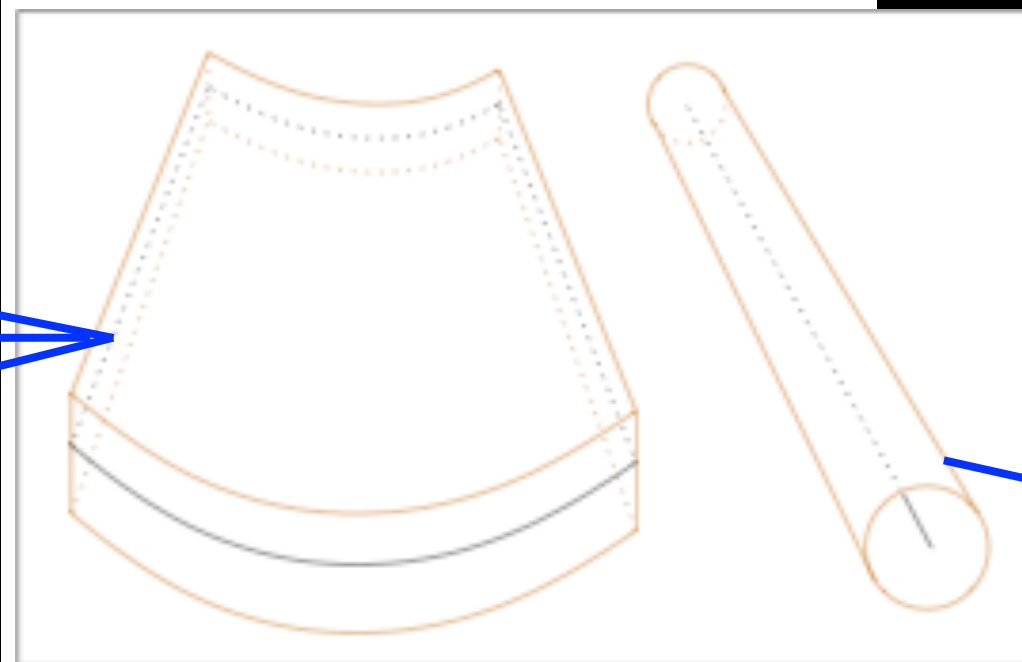
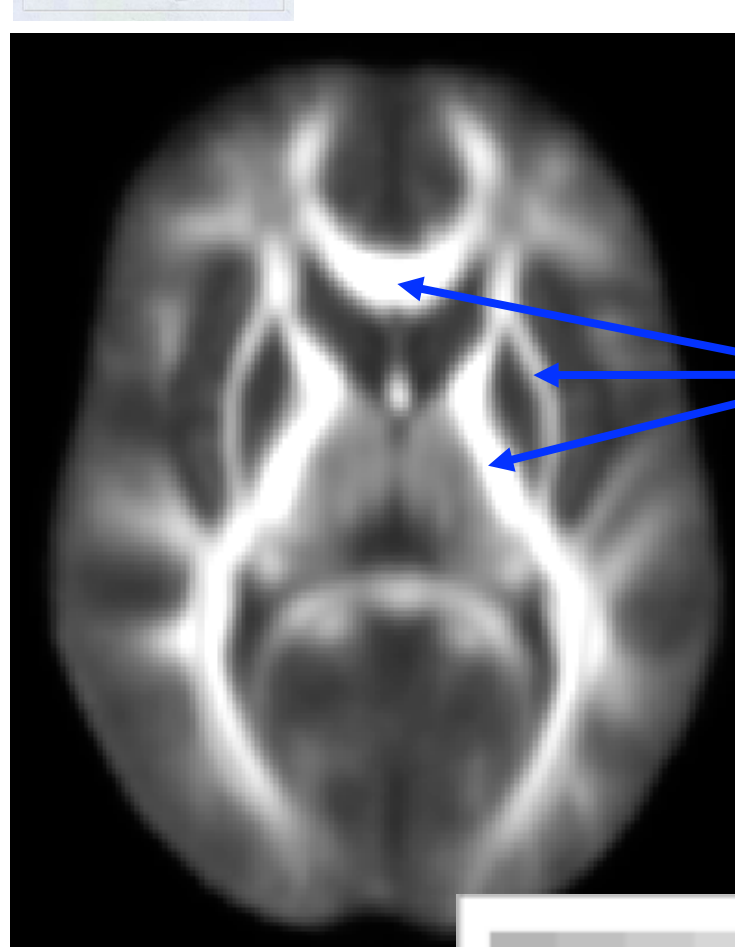


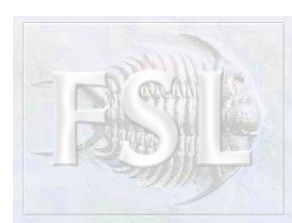
2. Cr (hinging)





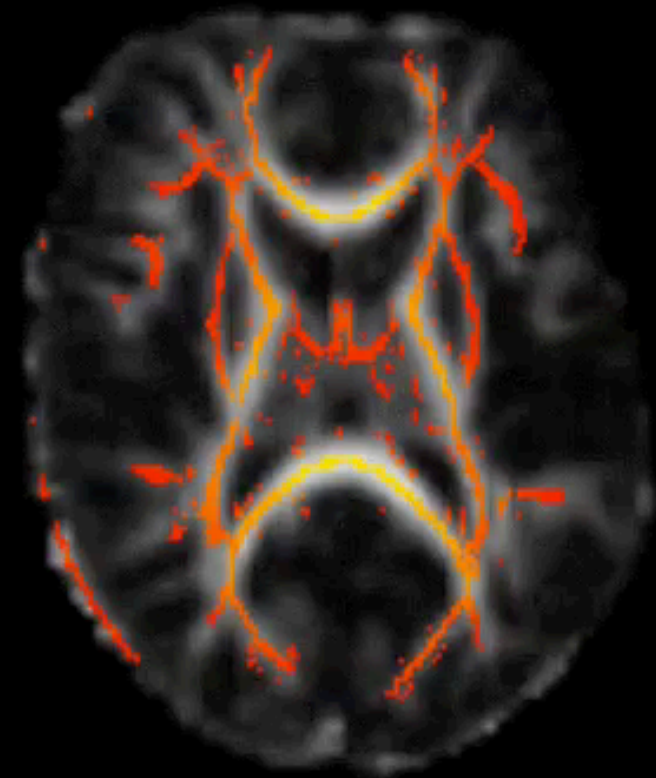
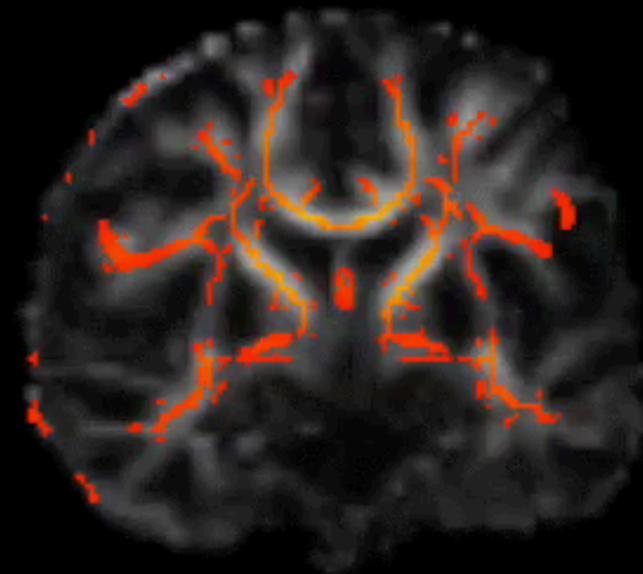
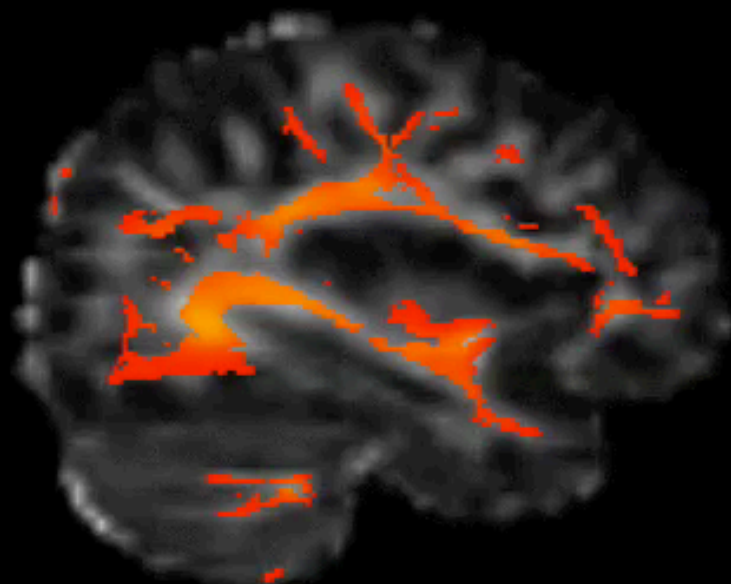
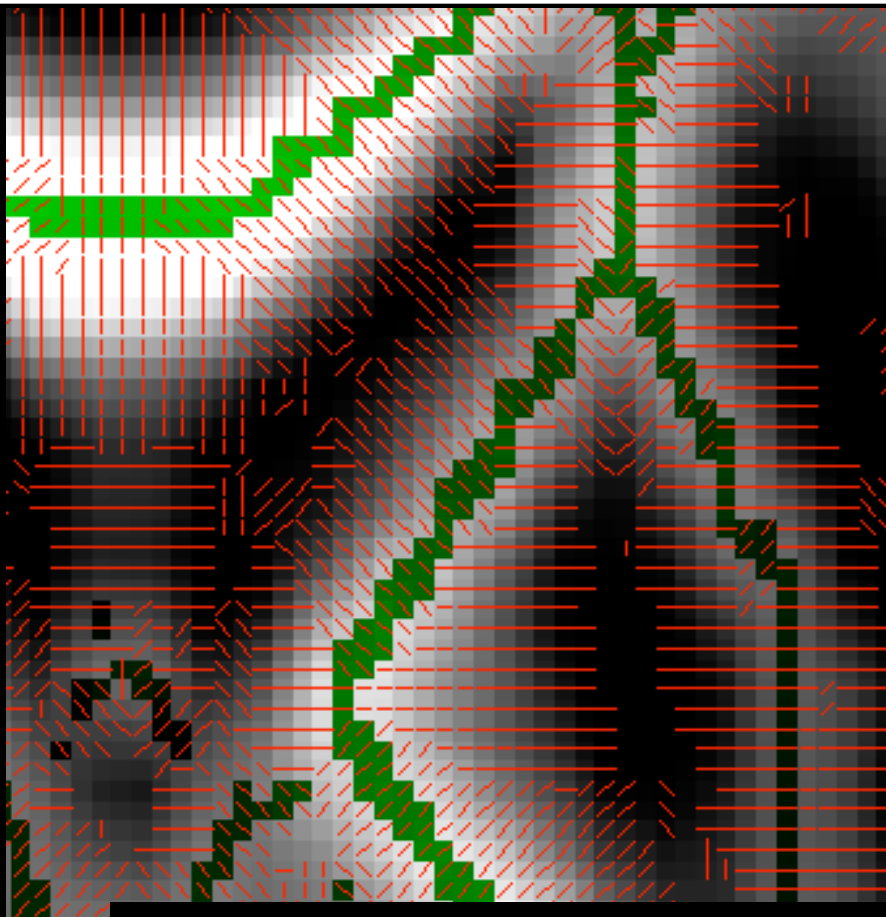
2. “Skeletonise” Mean FA





3. Threshold Mean FA Skeleton

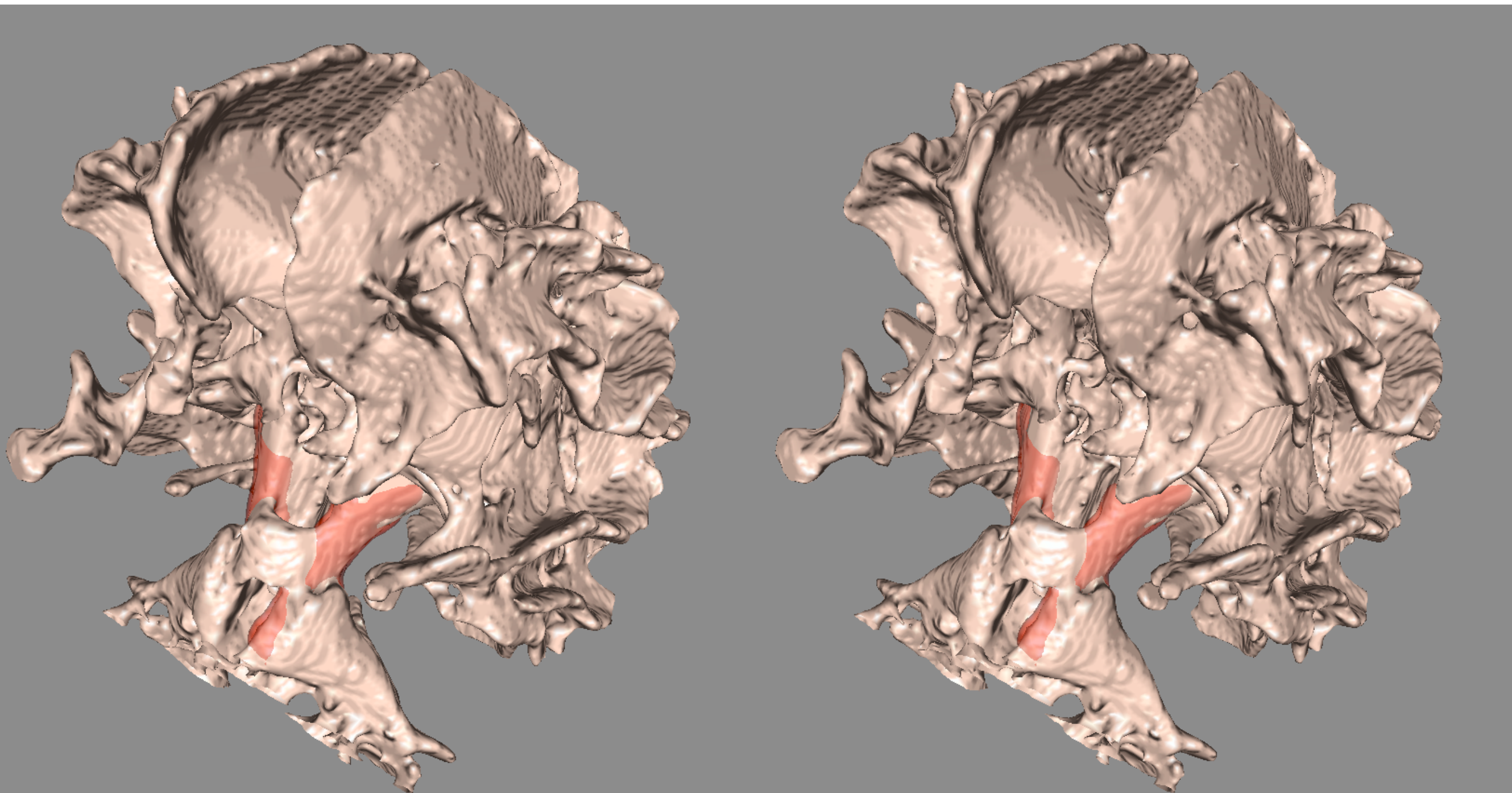
giving “objective” tract map





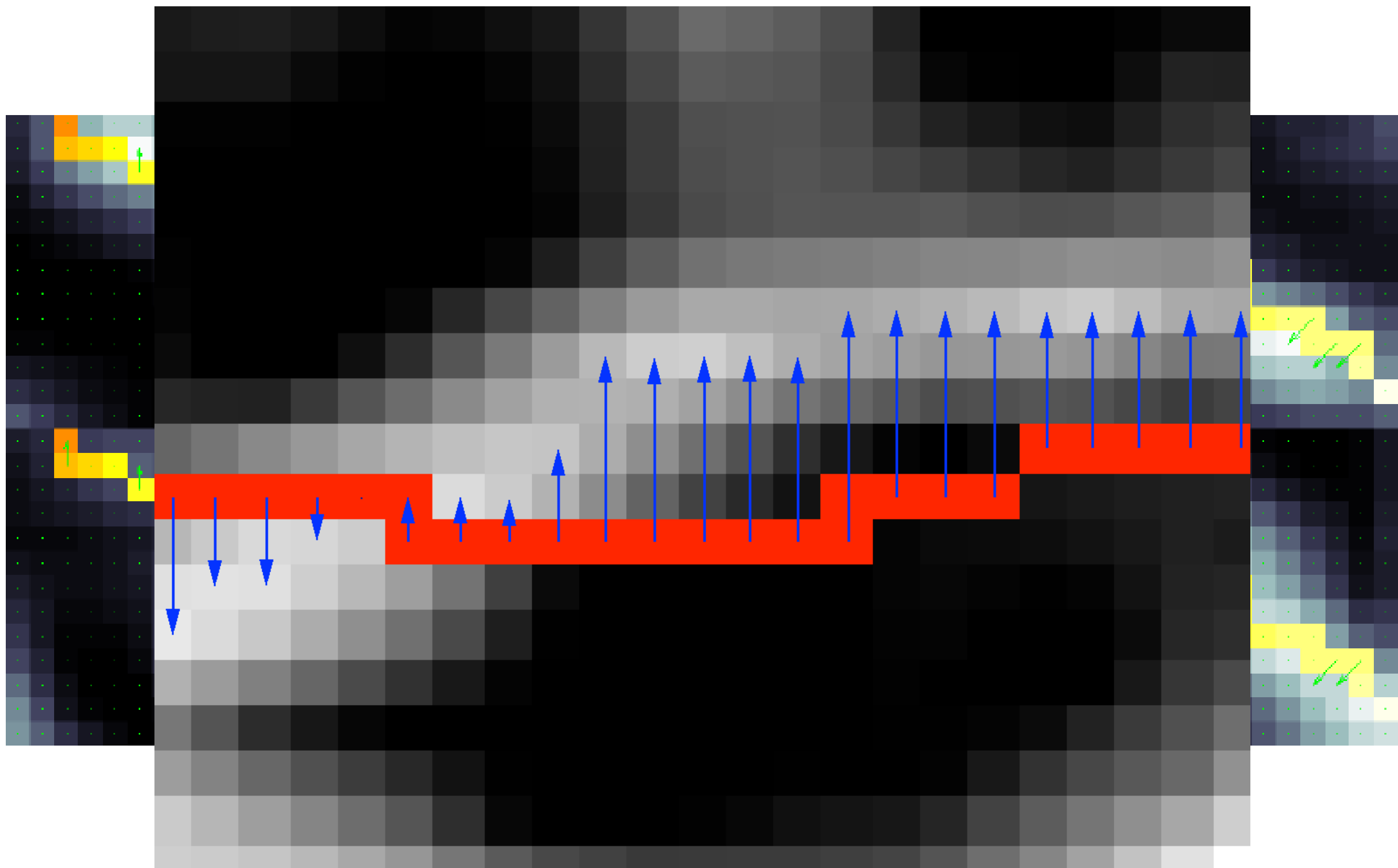
3. Threshold Mean FA Skeleton

giving “objective” tract map

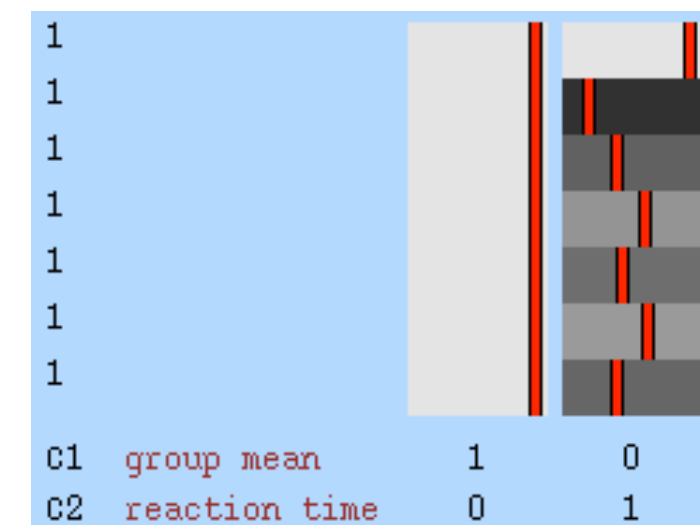
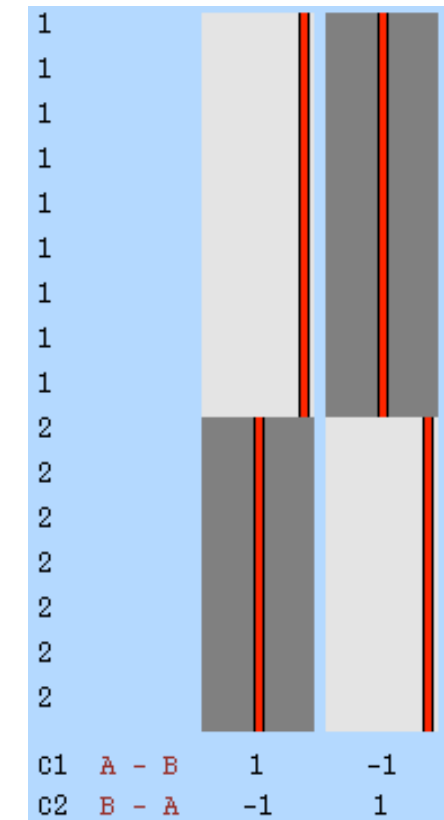
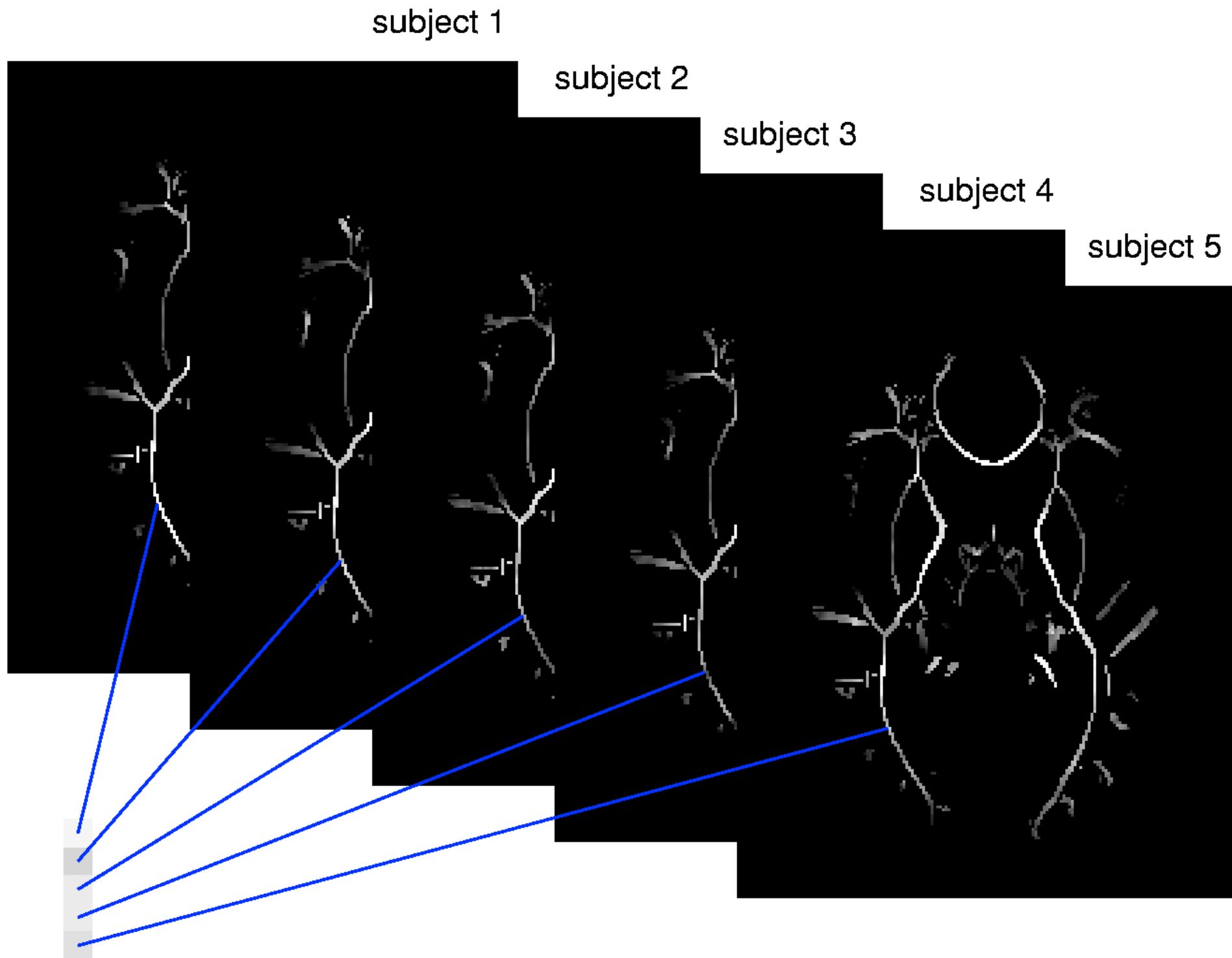


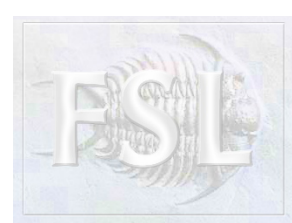


4. For each subject's warped FA, fill each point on the mean-space skeleton with nearest maximum FA value (i.e., from the centre of the subject's nearby tract)



5. Do cross-subject voxelwise stats on skeleton-projected FA and Threshold, (e.g., permutation testing, including multiple comparison correction)

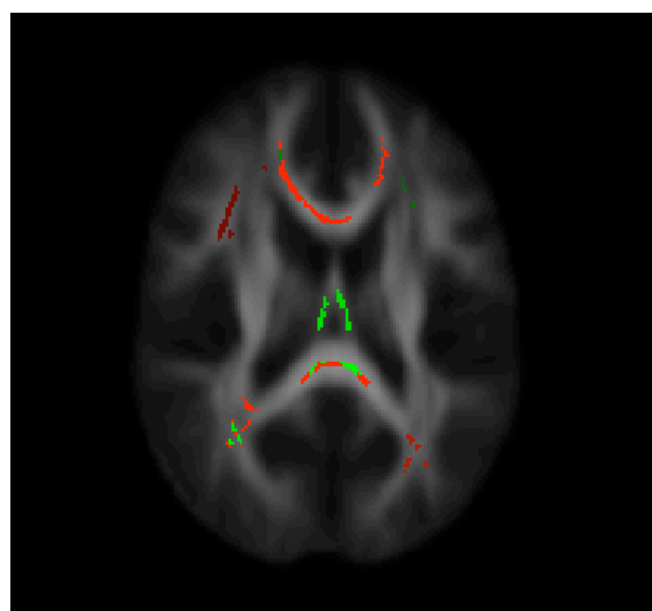
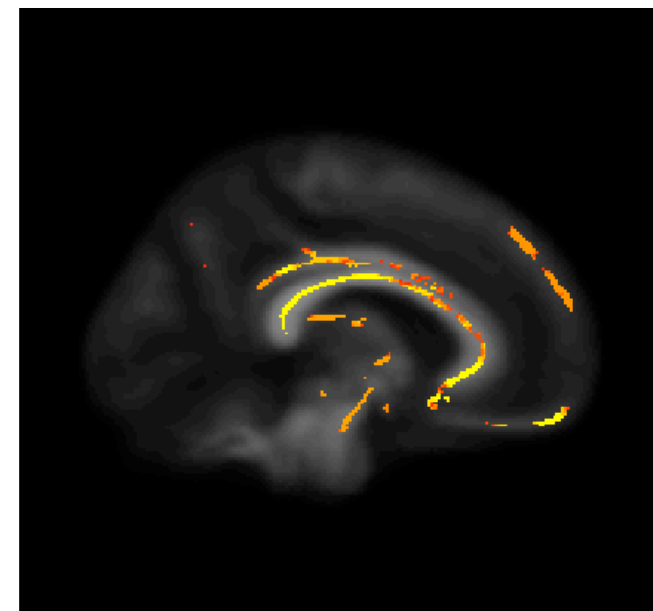
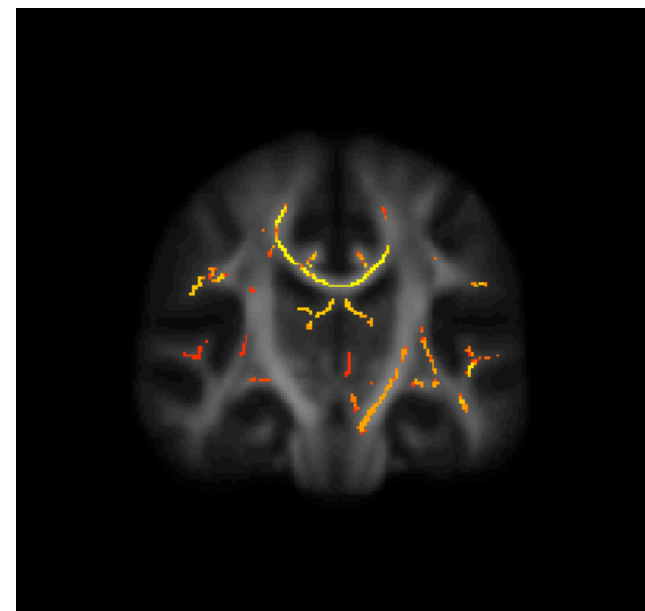
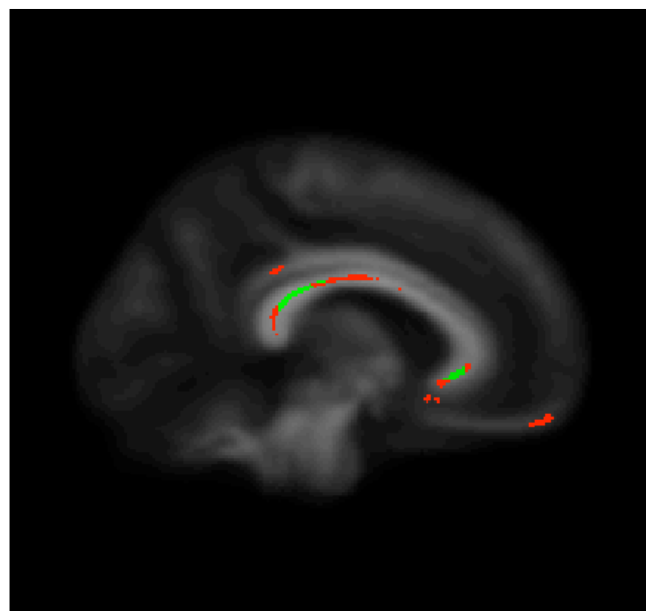
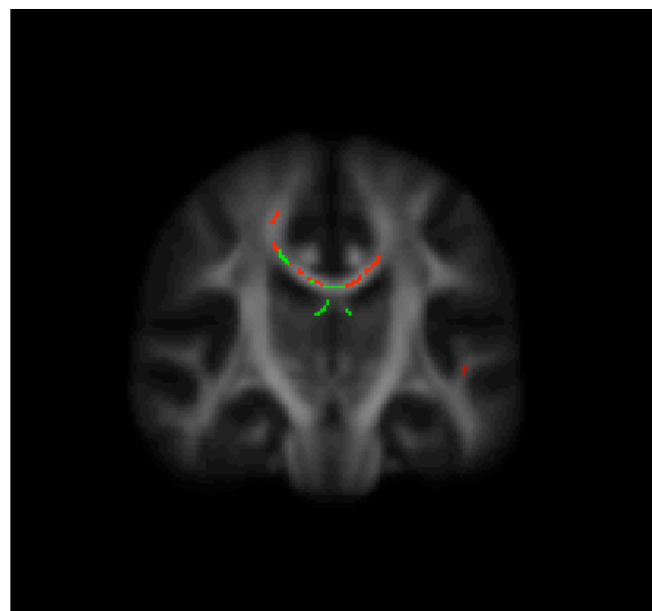




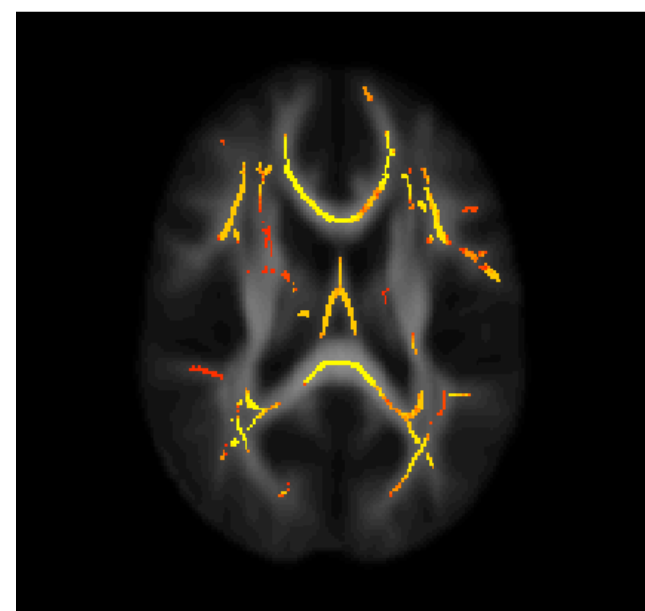
TFCE for TBSS

controls > schizophrenics

$p < 0.05$ corrected for multiple comparisons across space,
using randomise



cluster-based:
cluster-forming
threshold =
2 or **3**



TFCE



Schizophrenia (Mackay)

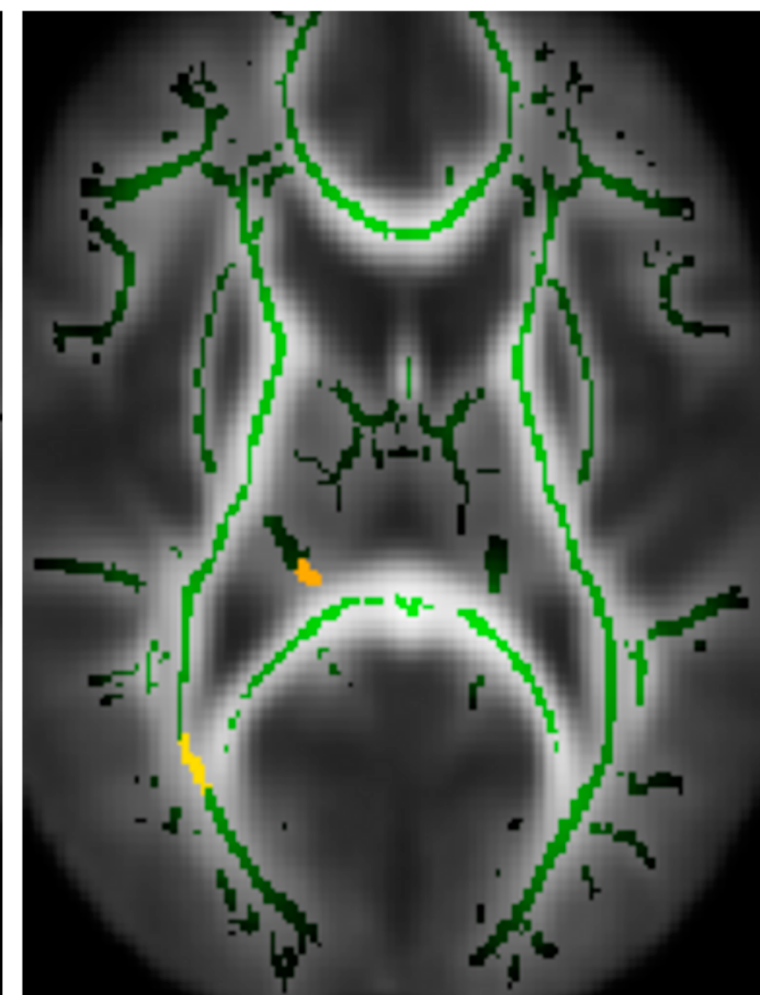
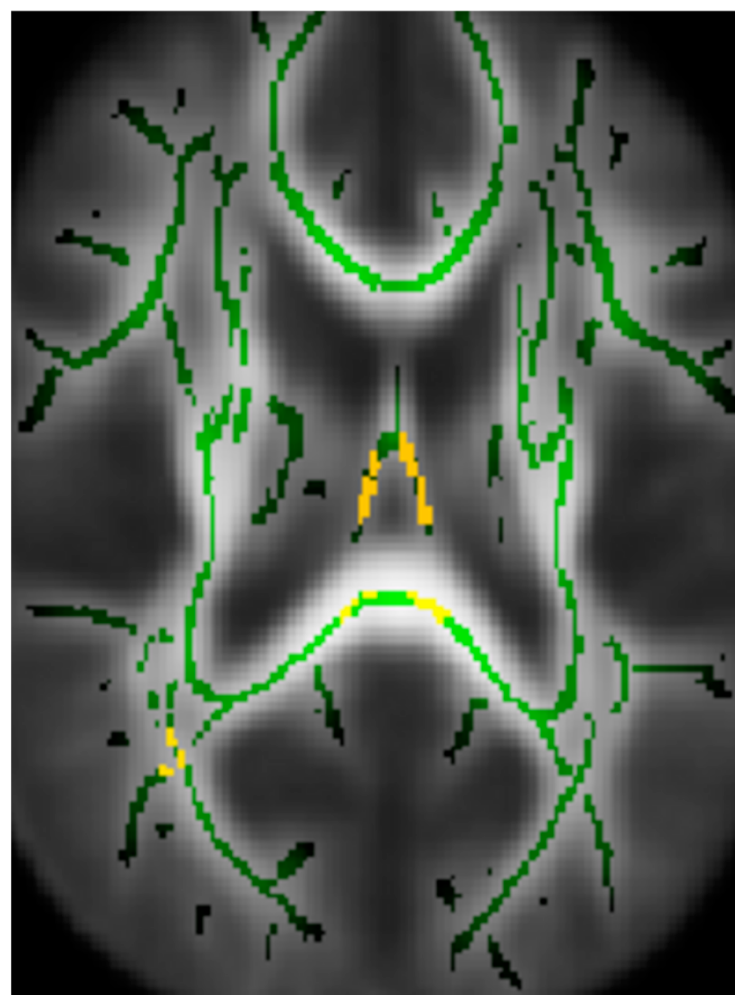
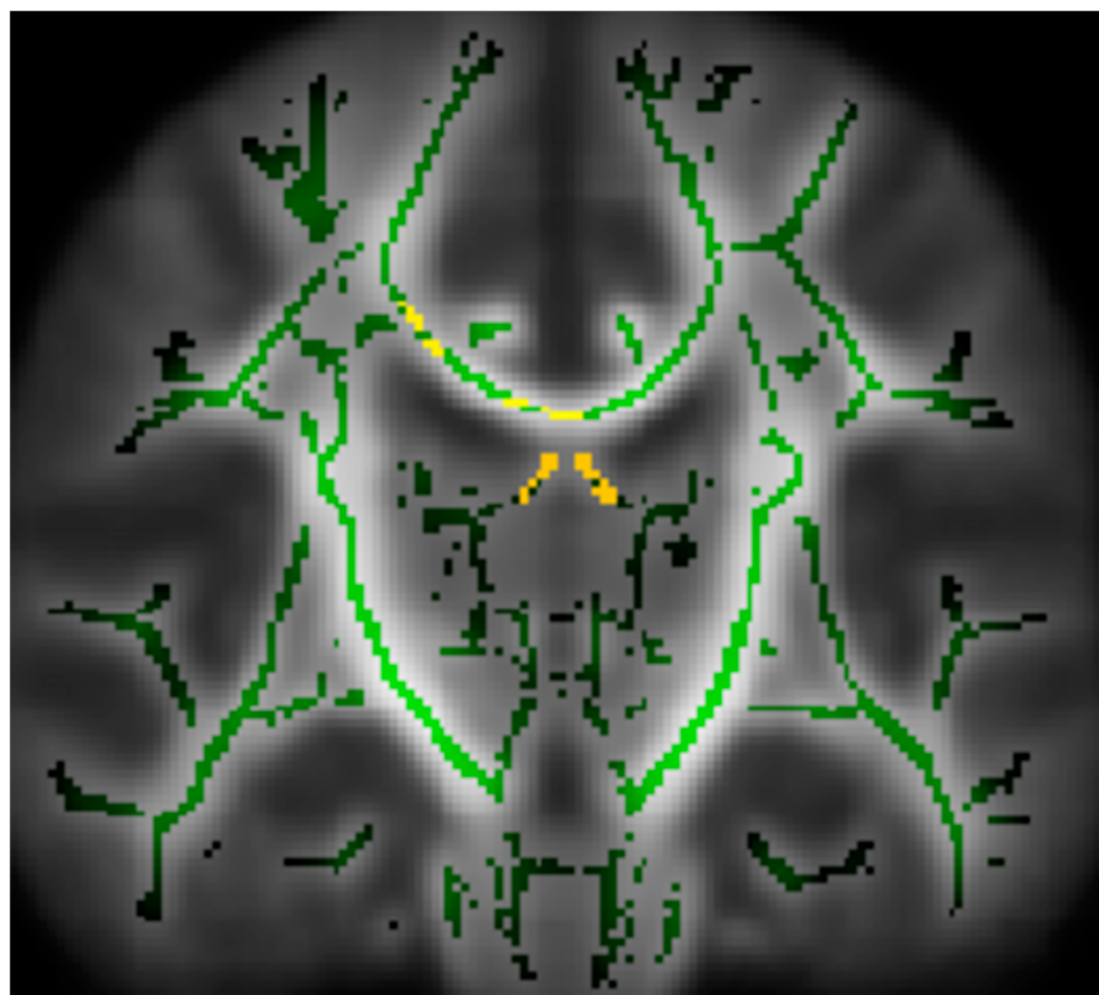
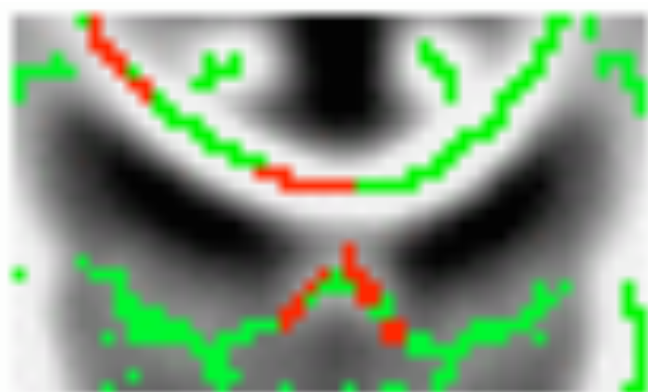
TBSS & voxel-wise show reduced FA in corpus callosum & fornix
VBM shows spurious result in thalamus due to increased ventricles in schiz.

TBSS

voxel-wise

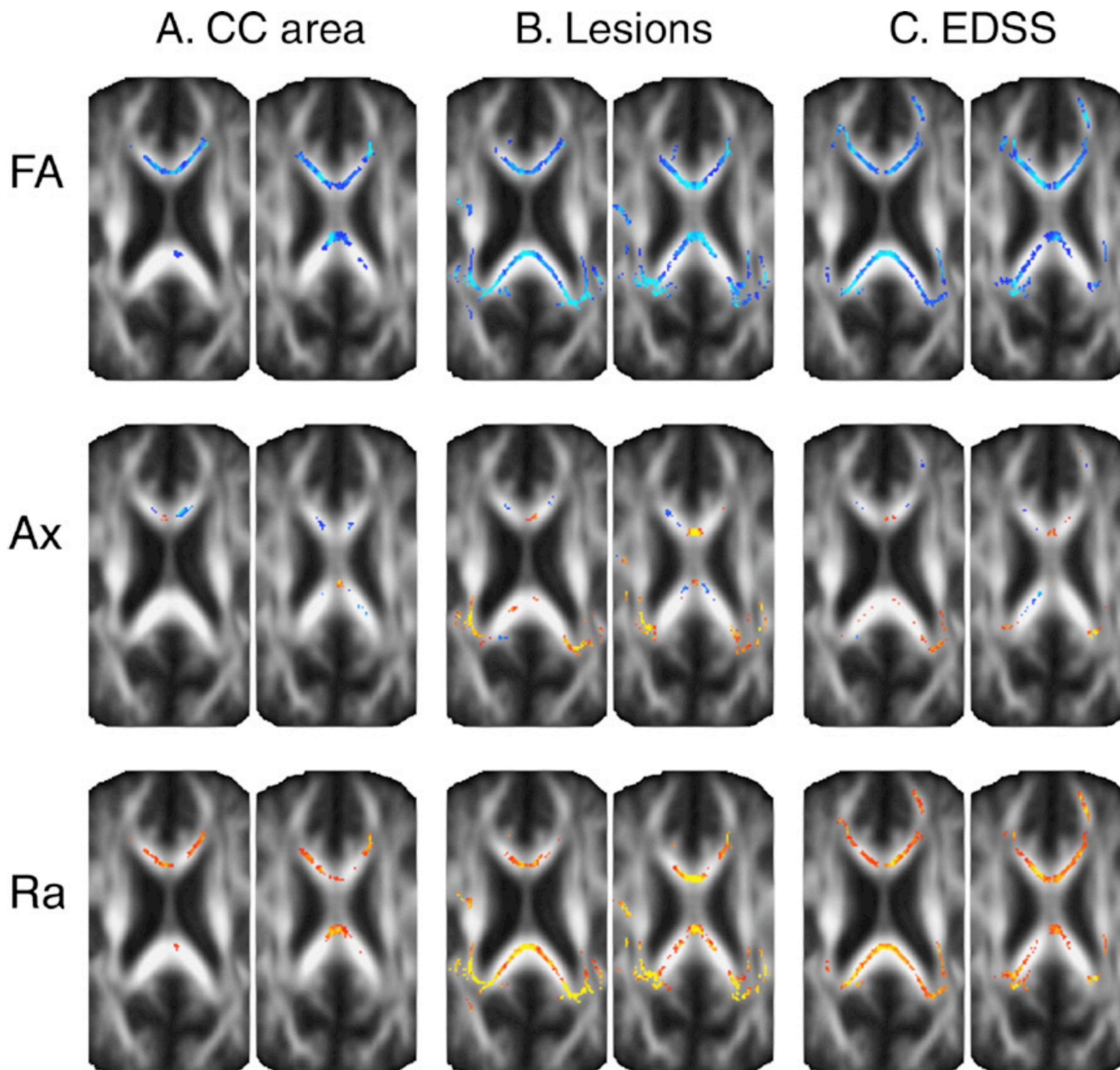
mean FA (controls)

mean FA (schiz.)





Multiple Sclerosis (Cader, Johansen-Berg & Matthews)

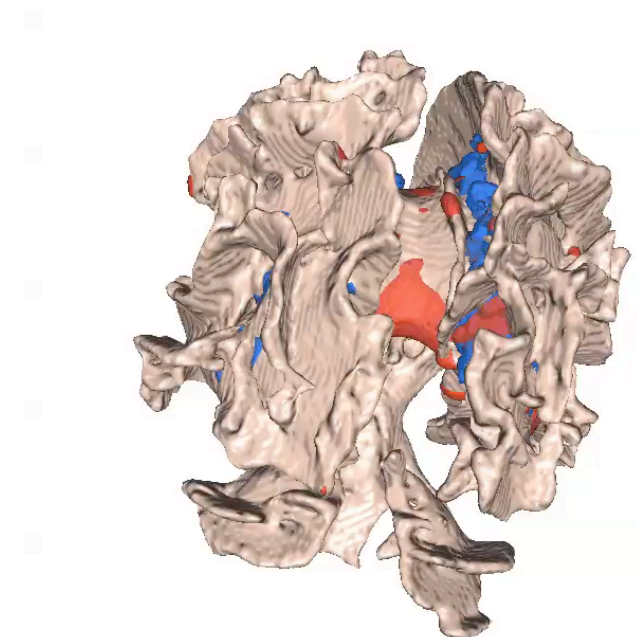
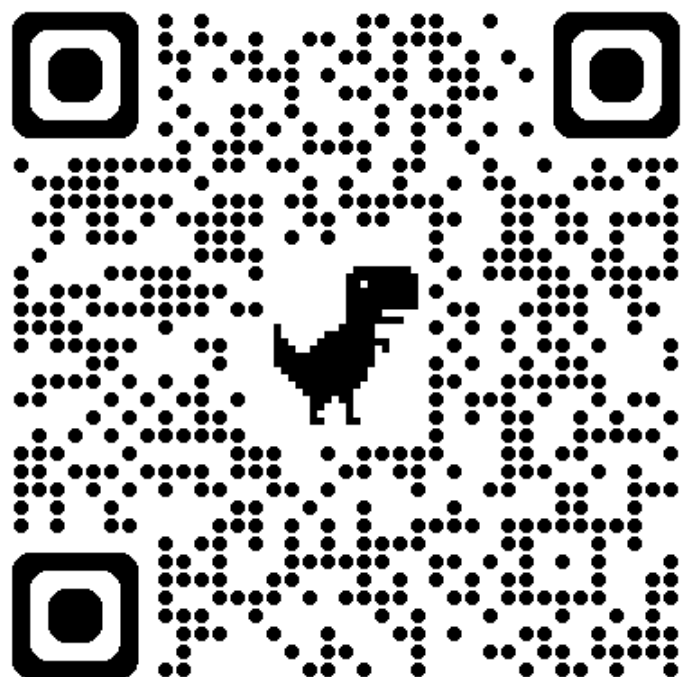




TBSS - Conclusions

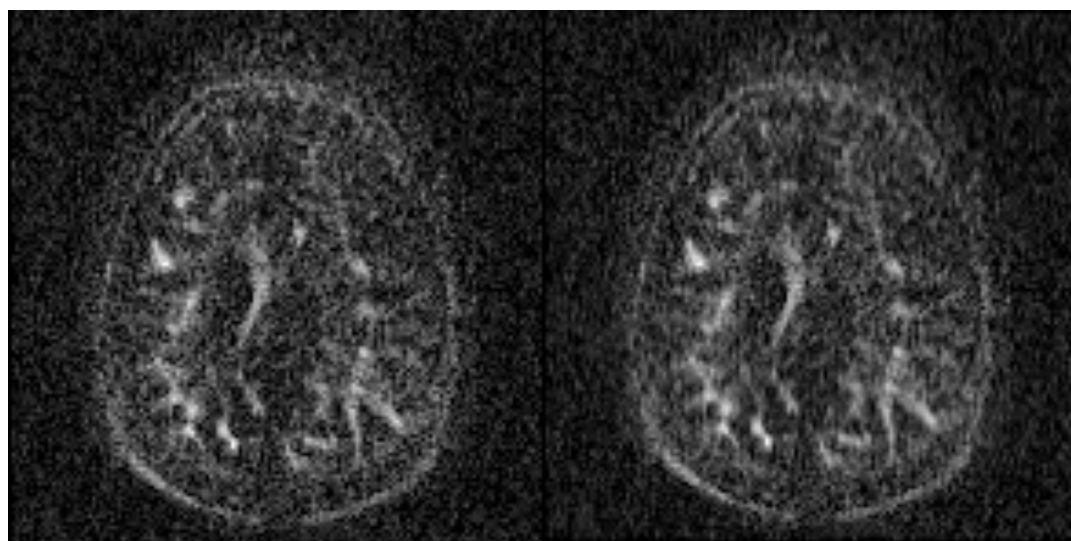
- Diffusion MRI measures direction and size of water diffusion in the brain
- Diffusion tensor (DTI) models this diffusion
- DTI summary measures (FA/MD/axial/radial) can be compared across subjects using TBSS

Submit your questions online

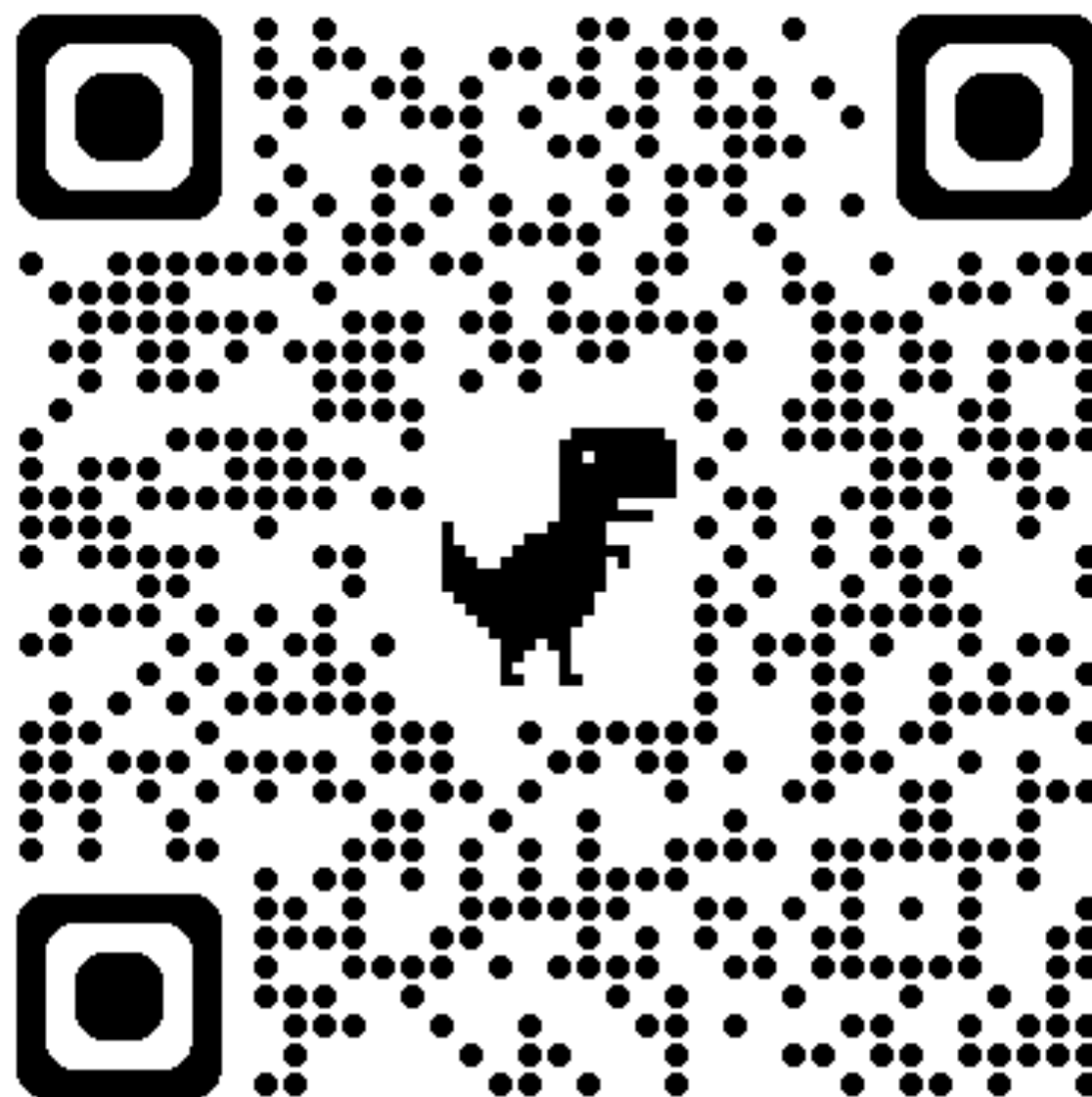




eddy and topup - tools for processing of diffusion data



Submit your questions online



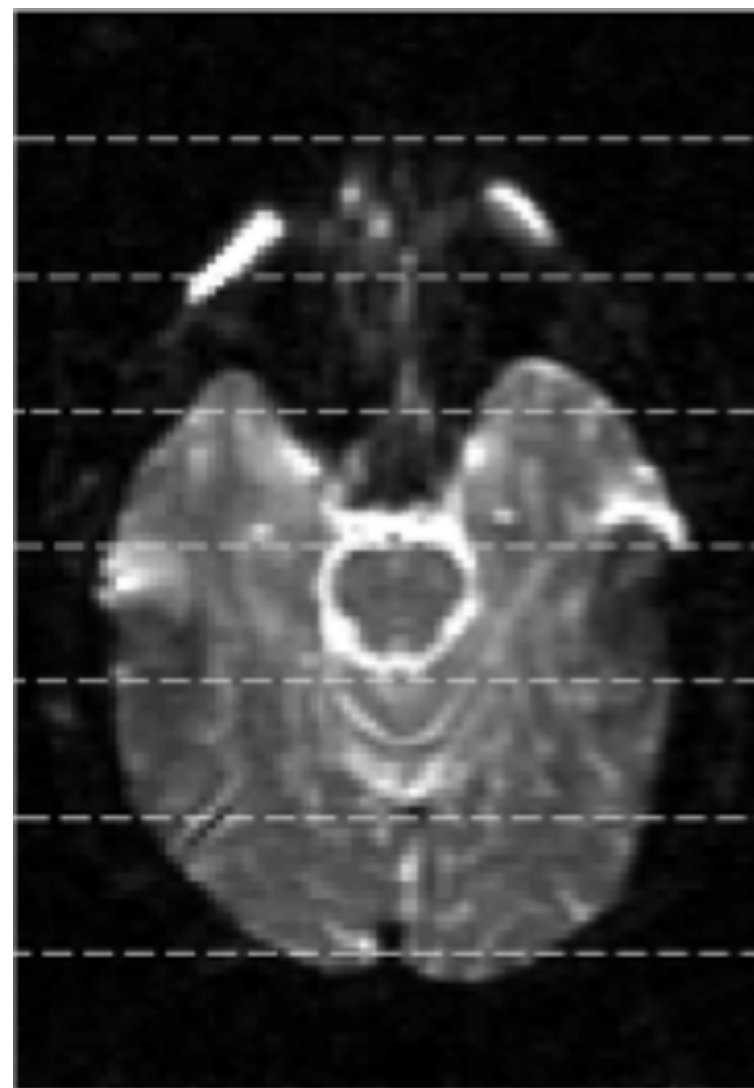
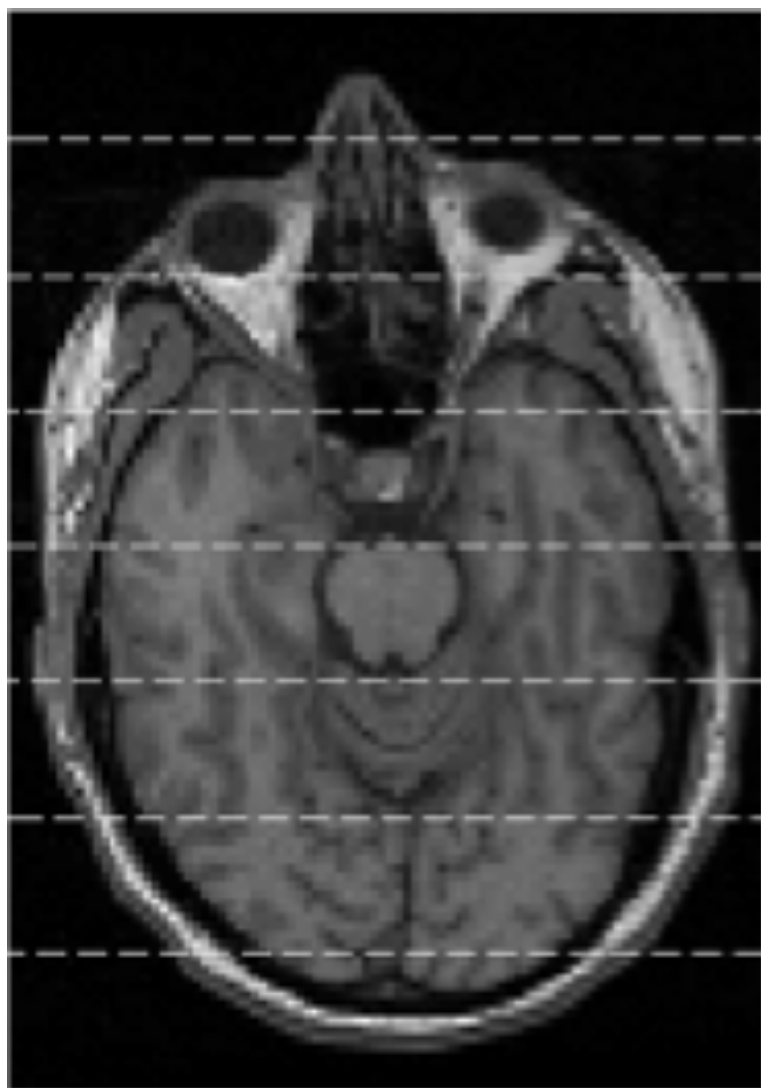


Outline of the talk

- What is the problem with diffusion data?
- Off-resonance field
 - How does it cause distortions?
 - Where does it come from?
- Registering diffusion data
 - How topup works
 - How eddy works
- Practicalities
- Some results
- Quality control
- New eddy features



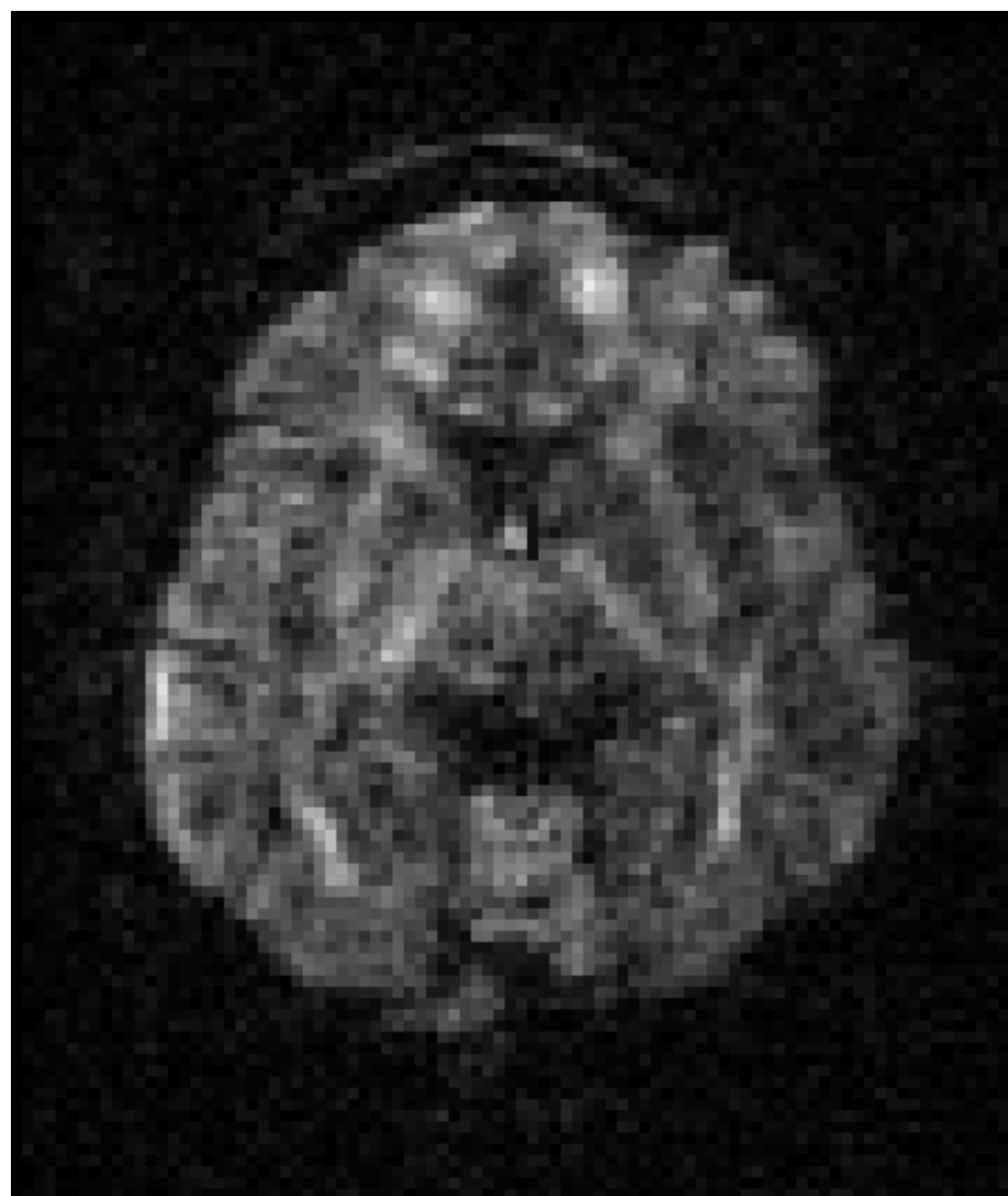
What is the problem with diffusion data?



Well, it isn't very anatomically faithful



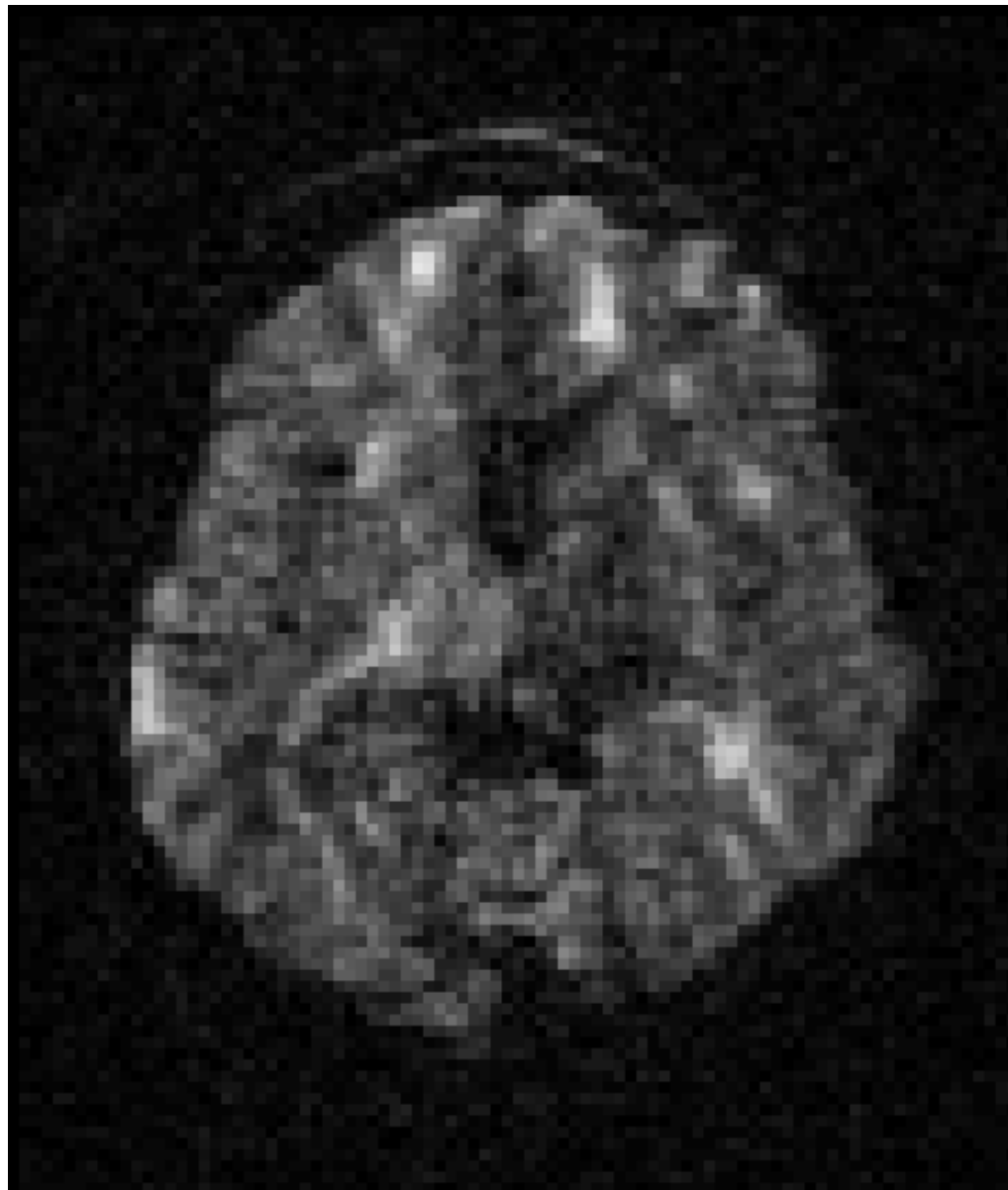
What is the problem with diffusion data?



In fact, it isn't even internally consistent



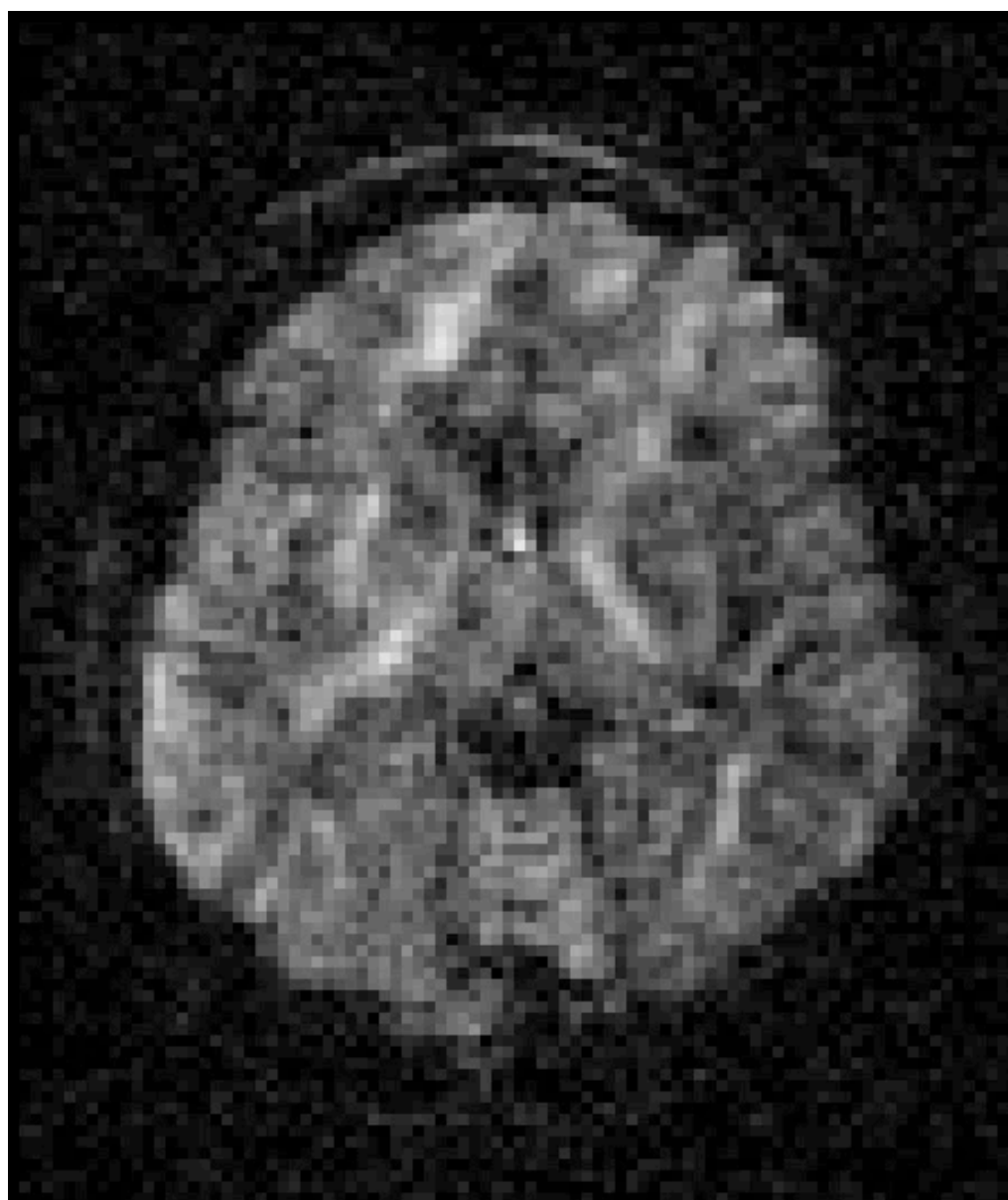
What is the problem with diffusion data?



In fact, it isn't even internally consistent



What is the problem with diffusion data?



In fact, it isn't even internally consistent



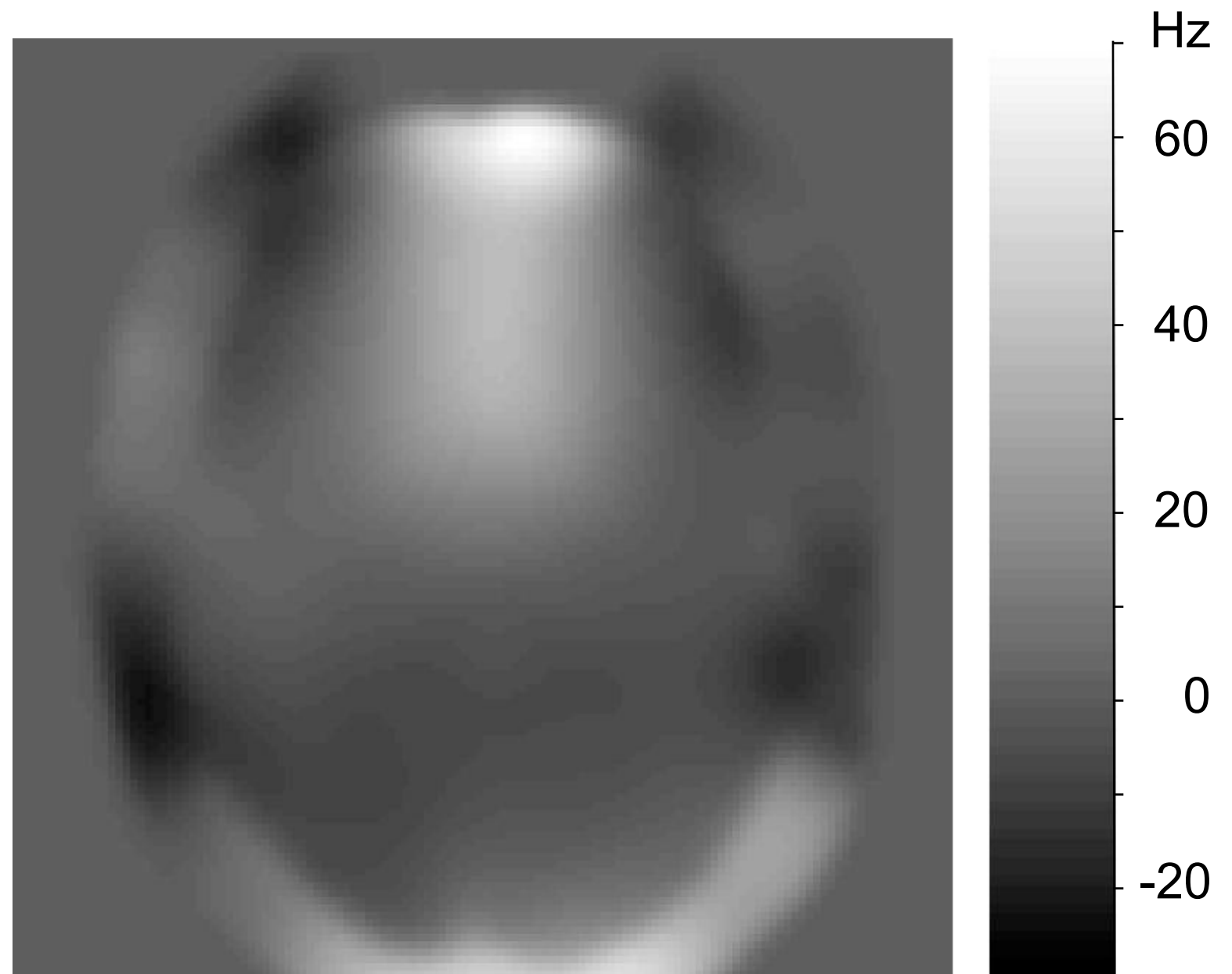
Outline of the talk

- What is the problem with diffusion data?
- Off-resonance field
 - How does it cause distortions?
 - Where does it come from?
- Registering diffusion data
 - How topup works
 - How eddy works
- Practicalities
- Some results
- New eddy features



Off-resonance field $\Rightarrow$ Distortions

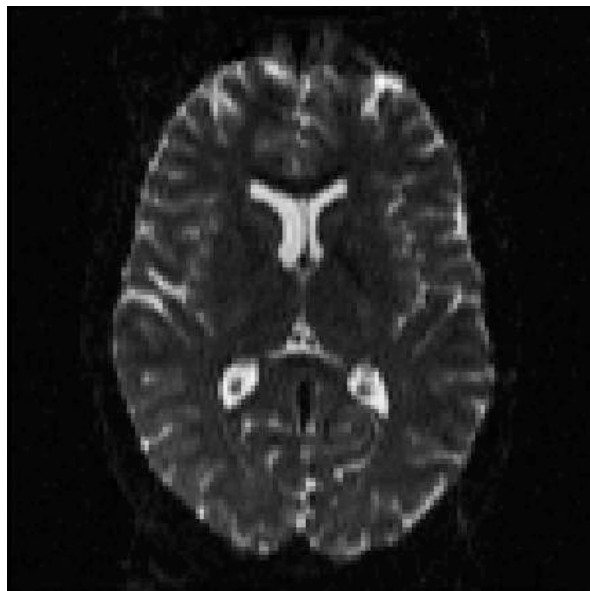
An “off-resonance” field is a map of the difference between what we think the field is and what it really is.



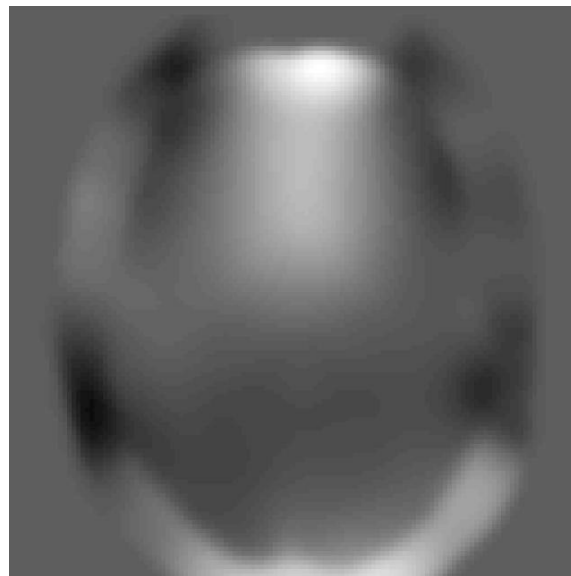
It is all caused by an “off-resonance” field



Off-resonance field $\Rightarrow$ Distortions



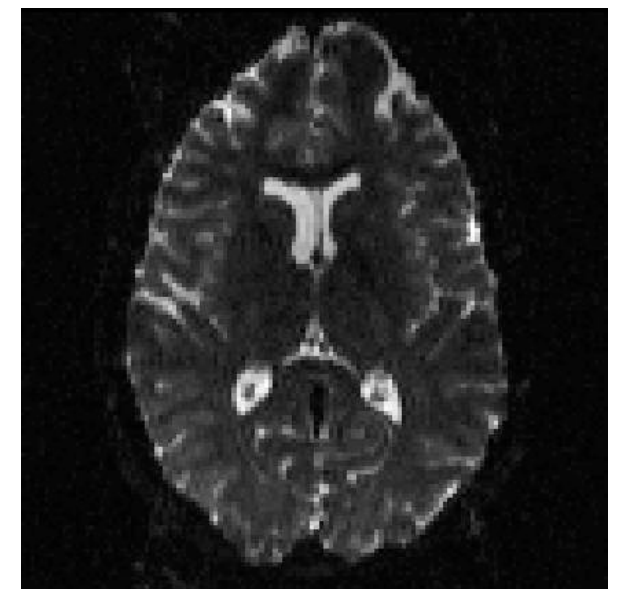
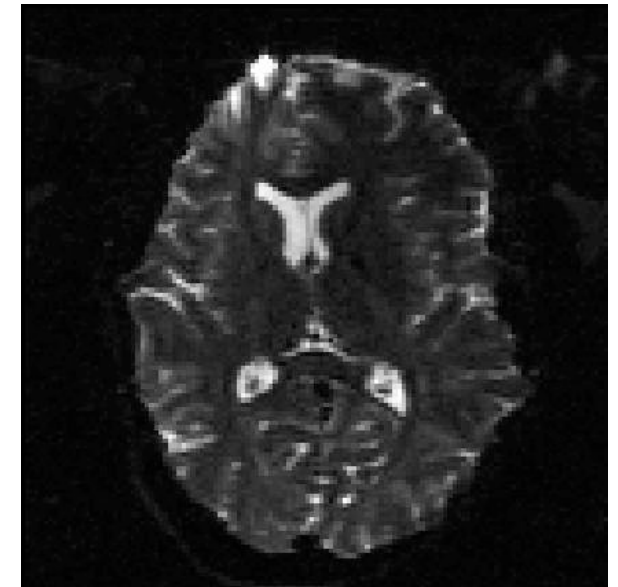
But this object



scanned in
this field

or this

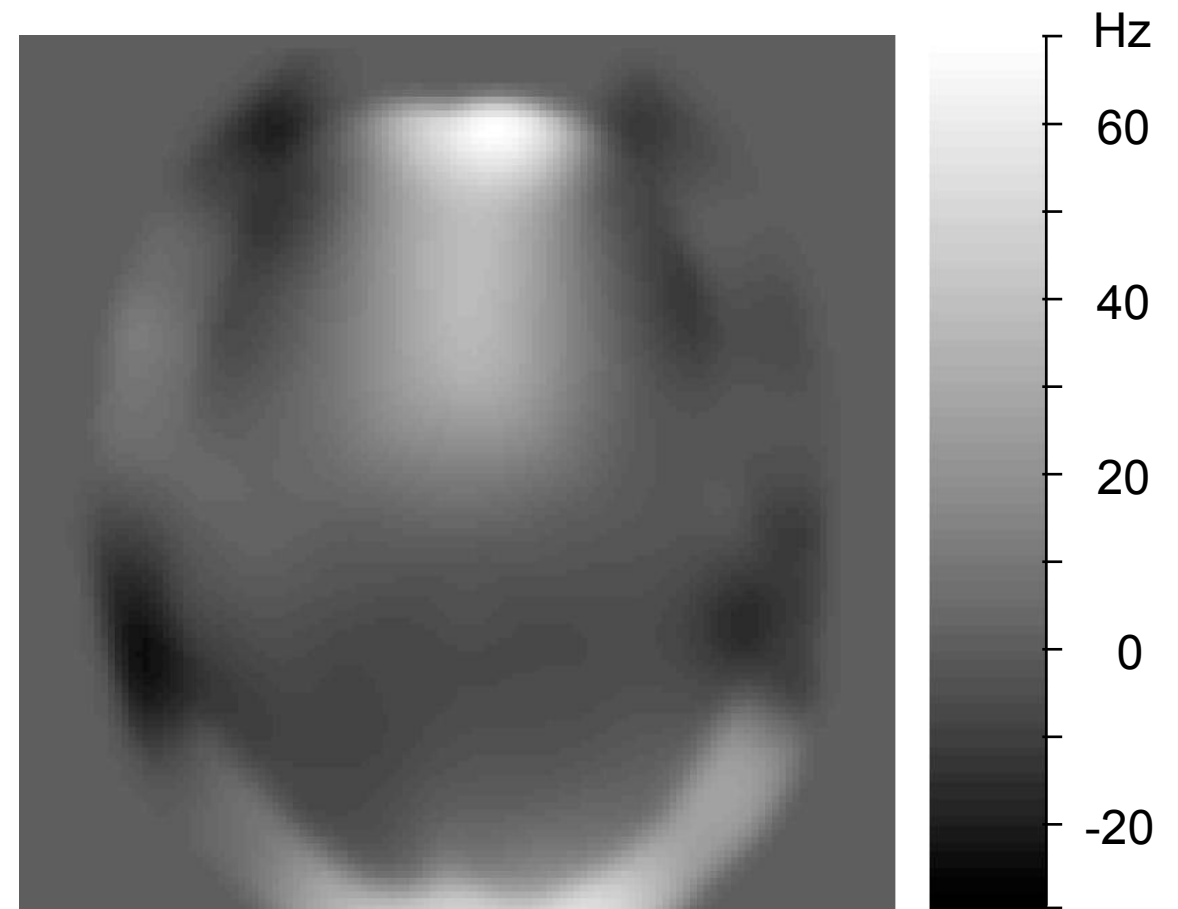
Can yield this



So there is clearly more to this story...



Off-resonance field $\Rightarrow$ Distortions

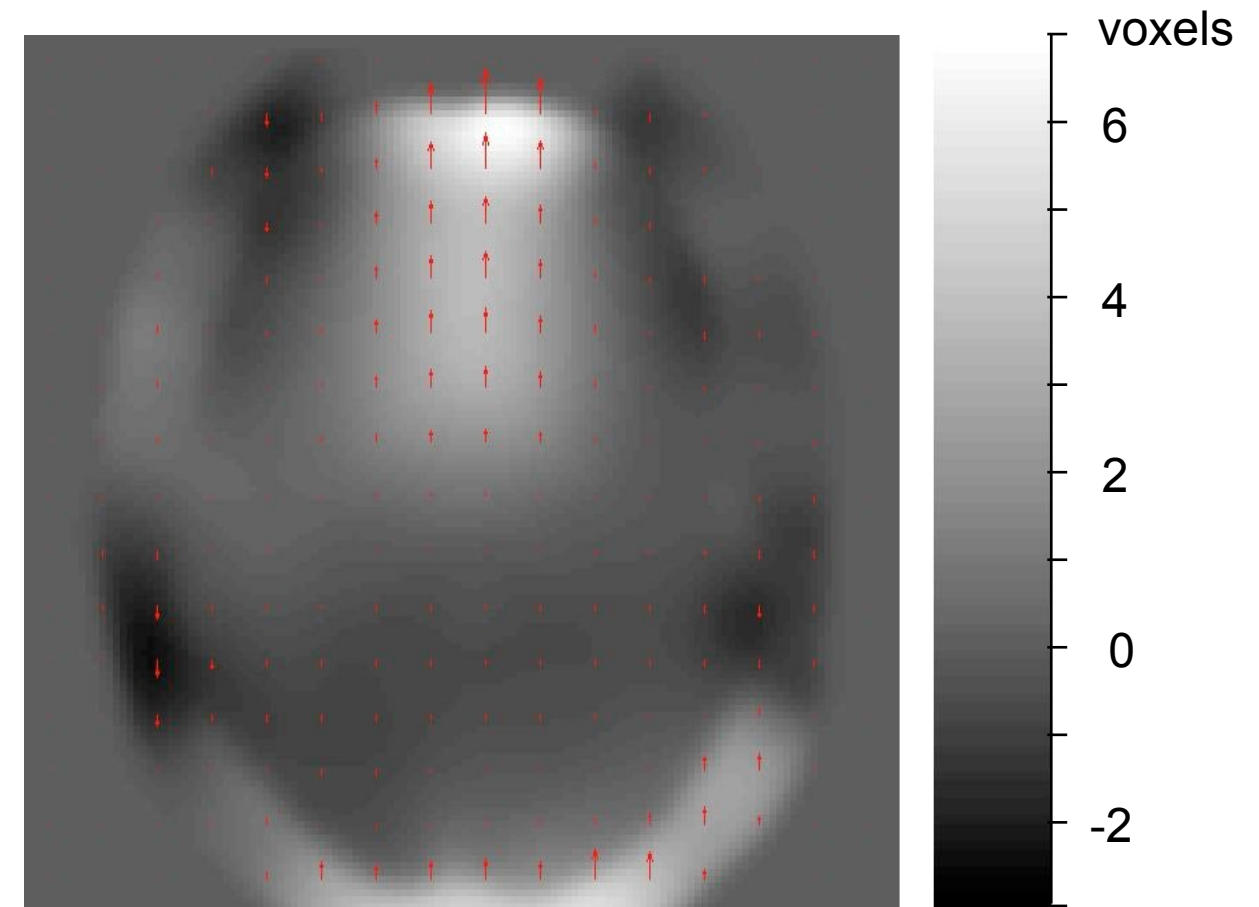
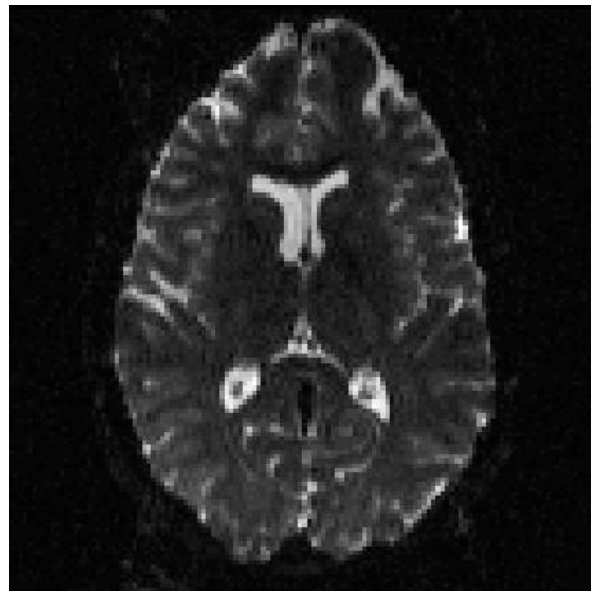


An off-resonance field is effectively a scaled voxel-displacement map.

If we know the imaging parameters we can do the translation.



Off-resonance field $\Rightarrow$ Distortions



And know what to expect

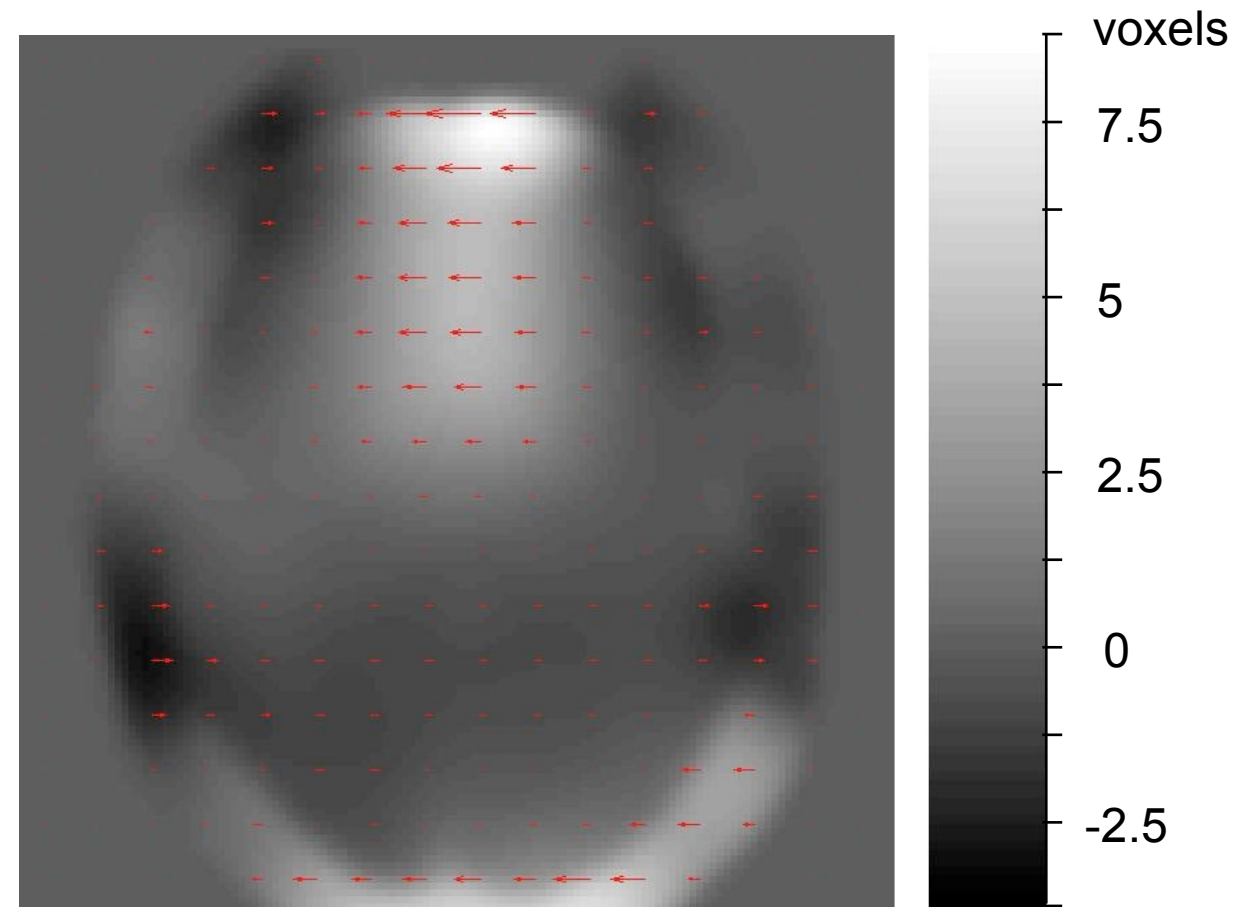
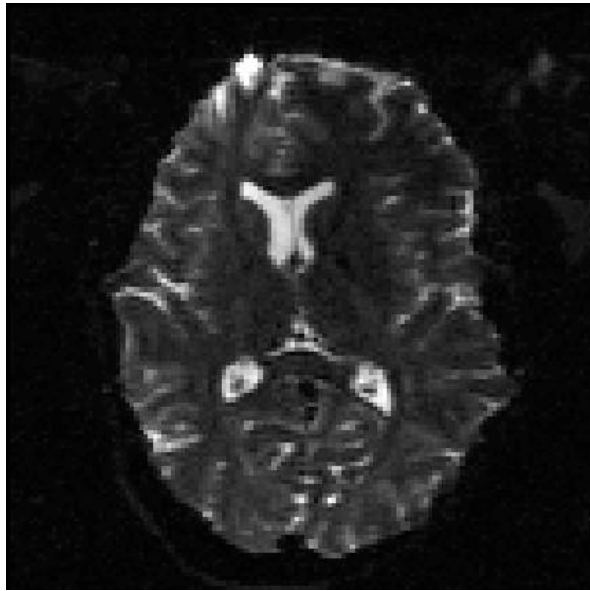
An off-resonance field is effectively a scaled voxel-displacement map.

If we know the imaging parameters we can do the translation.

$$\text{BW/voxel} = 10\text{Hz}, \mathbf{p} = [0 \ 1 \ 0]$$



Off-resonance field $\Rightarrow$ Distortions



And know what to expect

So, an off-resonance field is effectively a scaled voxel-displacement map.

And if we know the imaging parameters we can do the translation.

$$BW/\text{voxel} = 8\text{Hz}, \mathbf{p} = [-1 \ 0 \ 0]$$



Outline of the talk

- What is the problem with diffusion data?
- Off-resonance field
 - How does it cause distortions?
 - **Where does it come from?**
- Registering diffusion data
 - How topup works
 - How eddy works
- Practicalities
- Some results
- New eddy features



Where does the off-resonance field come from?

- There are two sources
- The first is the object (head) itself.

(CT of) Human head

$B_0 \odot$



Resulting field



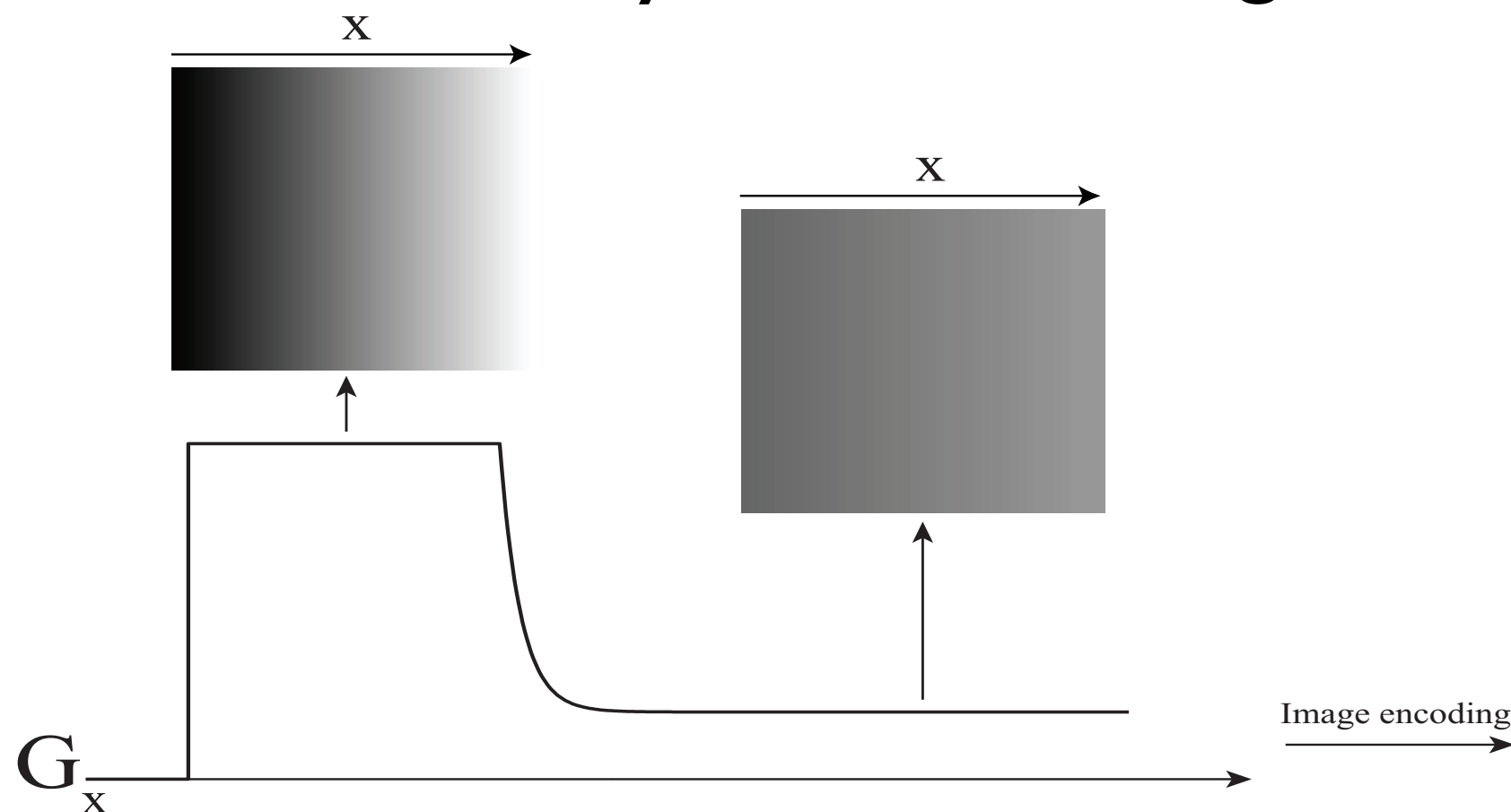
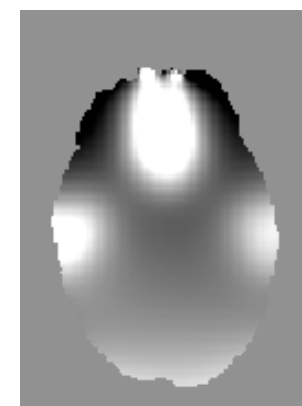
PPMs

Must fulfil $\begin{cases} \nabla \times \mathbf{H} = 0 \\ \nabla \cdot \mathbf{B} = 0 \end{cases}$ (still)



Where does the off-resonance field come from?

- There are two sources
- The first is the object (head) itself.
- The second is caused by the diffusion gradient

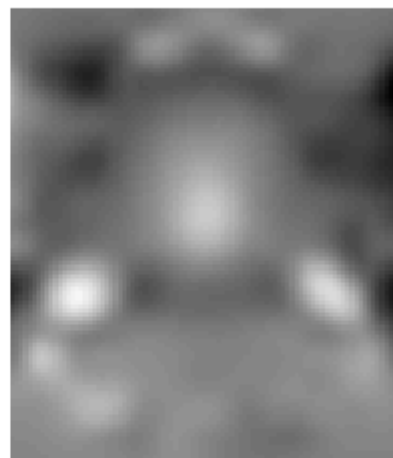




Where does the off-resonance field come from?

So for any diffusion weighted volume the off-resonance field is the sum of these two contributions

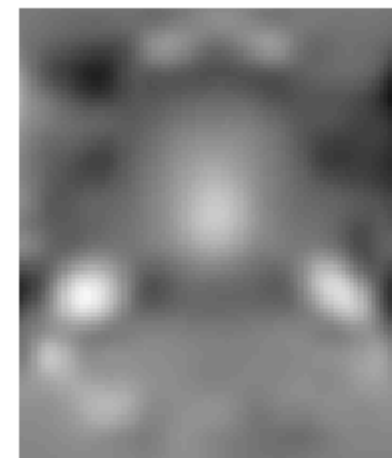
Susceptibility



Eddy currents

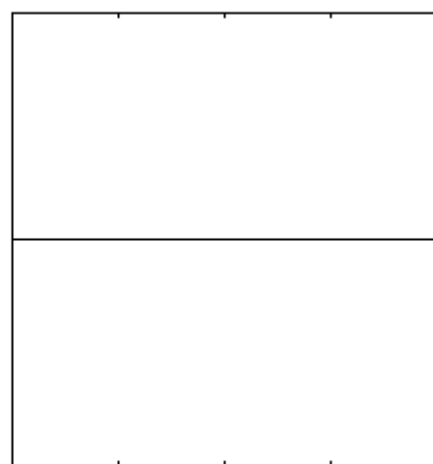


Total

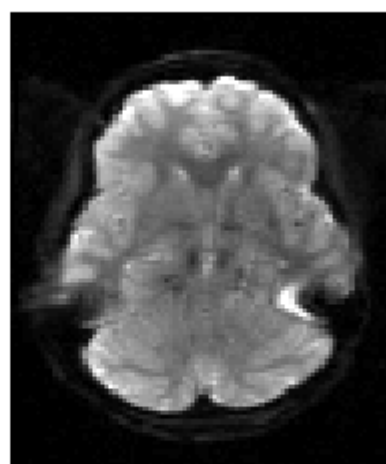


+

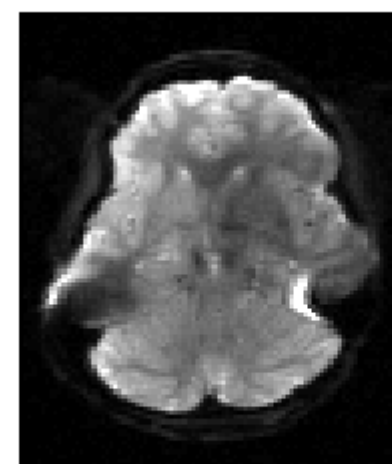
=



Diffusion gradient



"True" object



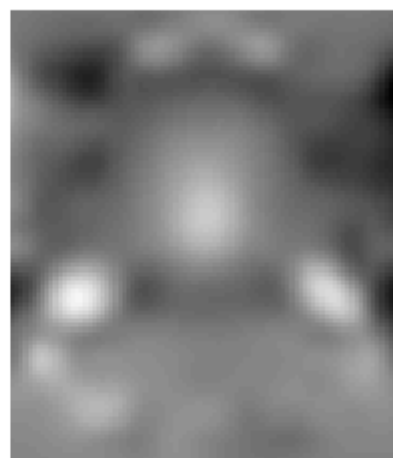
Observed image



Where does the off-resonance field come from?

So for any diffusion weighted volume the off-resonance field is the sum of these two contributions

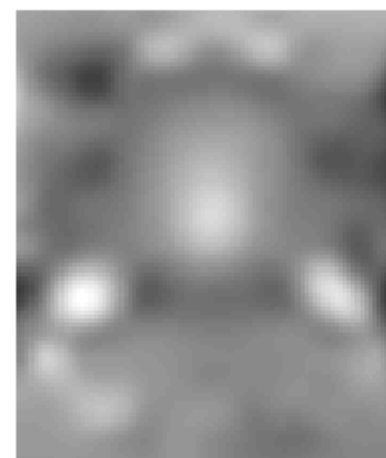
Susceptibility



Eddy currents

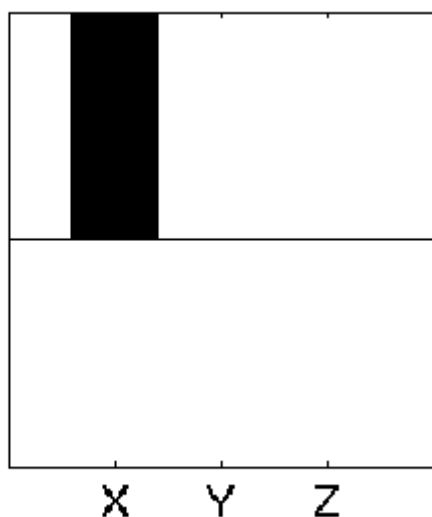


Total

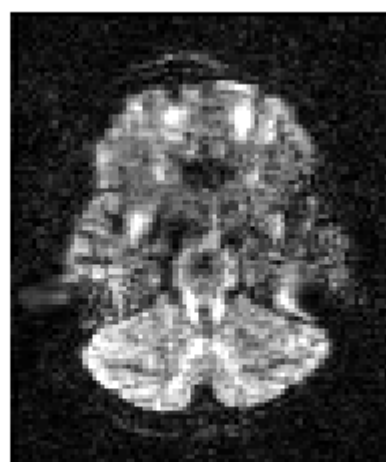


+

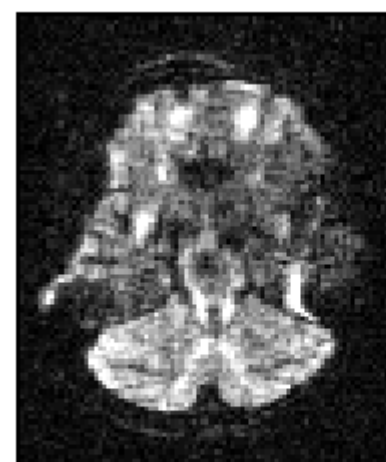
=



Diffusion gradient



"True" object



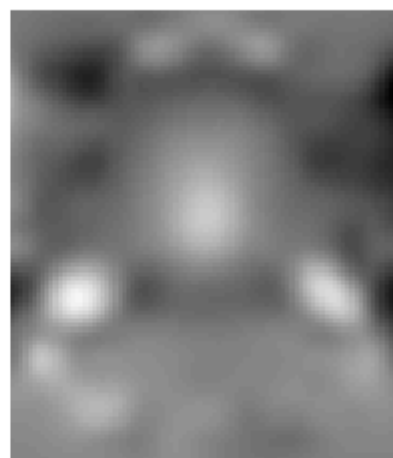
Observed image



Where does the off-resonance field come from?

So for any diffusion weighted volume the off-resonance field is the sum of these two contributions

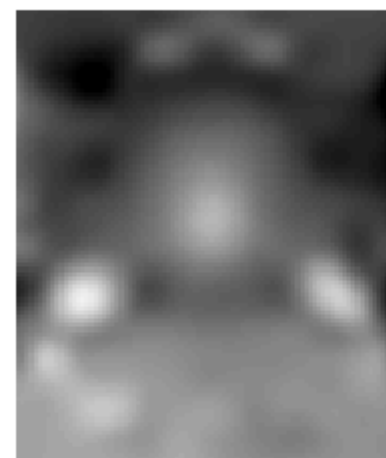
Susceptibility



Eddy currents

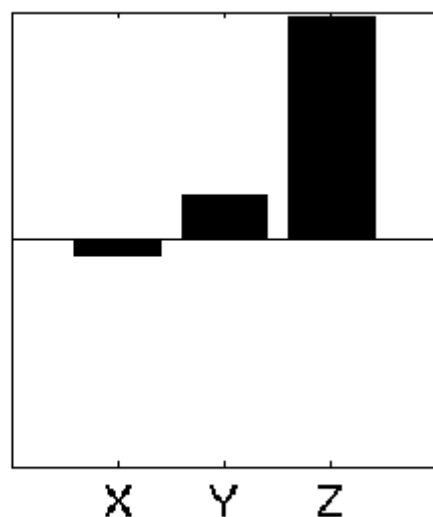


Total

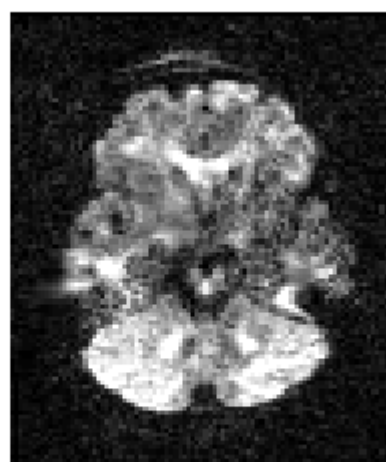


+

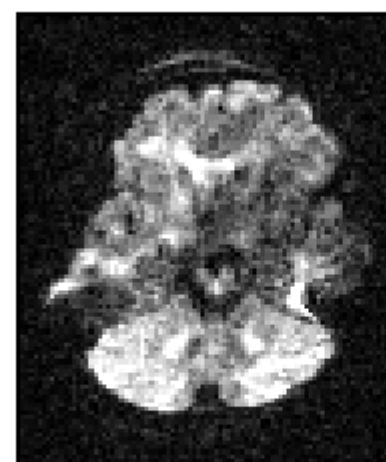
=



Diffusion gradient



"True" object



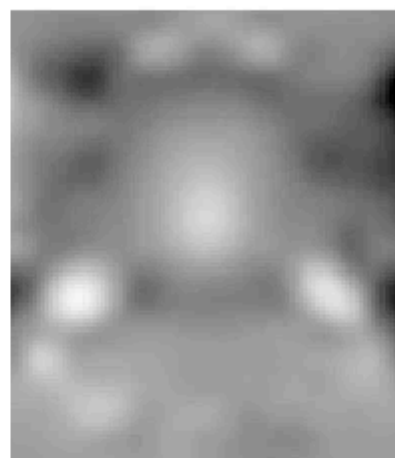
Observed image



Where does the off-resonance field come from?

So for any diffusion weighted volume the off-resonance field is the sum of these two contributions

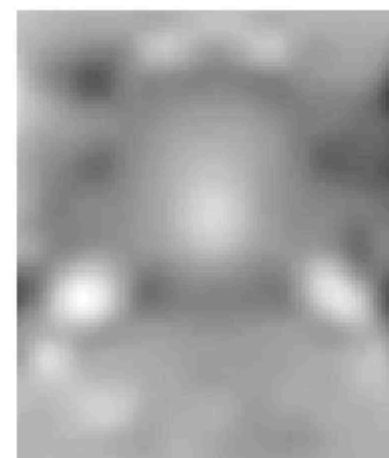
Susceptibility



Eddy currents

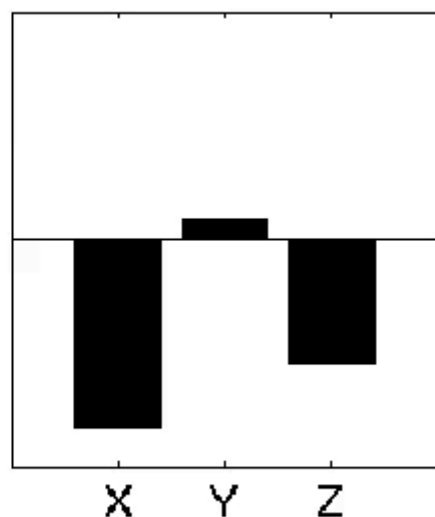


Total

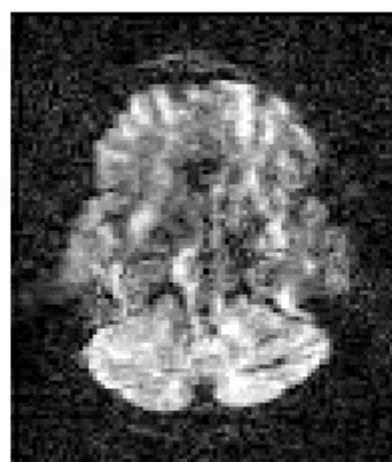


+

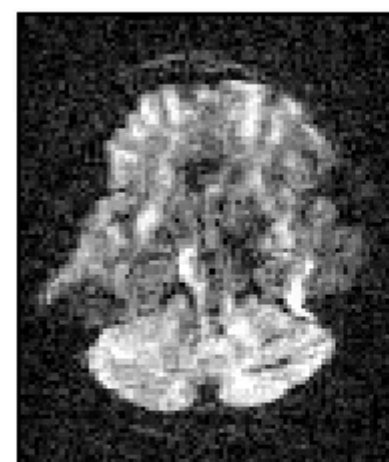
=



Diffusion gradient



"True" object



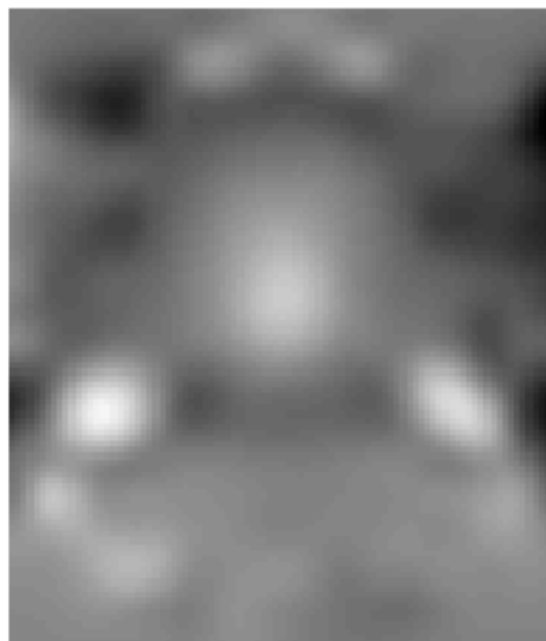
Observed image



Separate estimation of susceptibility- and eddy current-fields

So, what we need to estimate is

One of these per
subject



One of these per
volume



FSL-tools:

topup

eddy

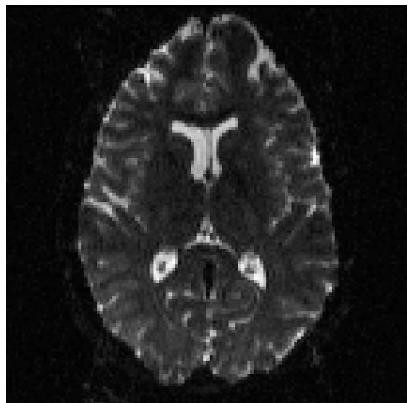


Outline of the talk

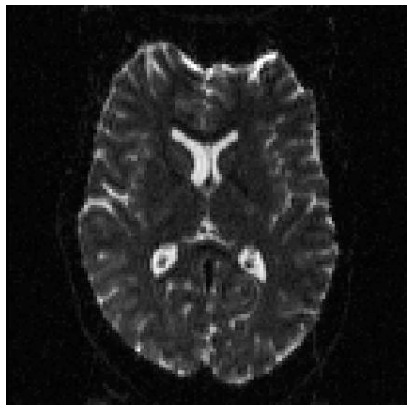
- What is the problem with diffusion data?
- Off-resonance field
 - How does it cause distortions?
 - Where does it come from?
- Registering diffusion data
 - How topup works
 - How eddy works
- Practicalities
- Some results
- Quality control
- New eddy features



How topup works (very briefly)



$p=[0 \ 1 \ 0]$

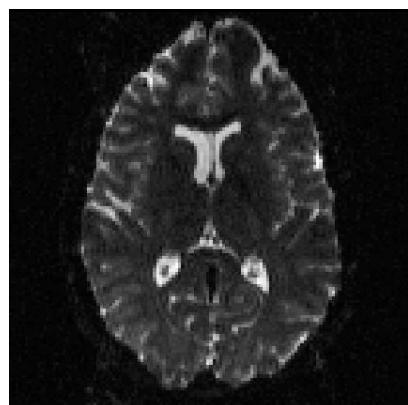


$p=[0 \ -1 \ 0]$

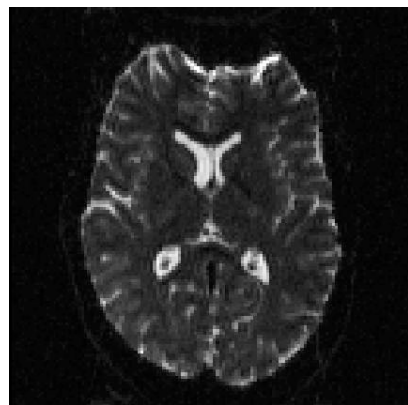
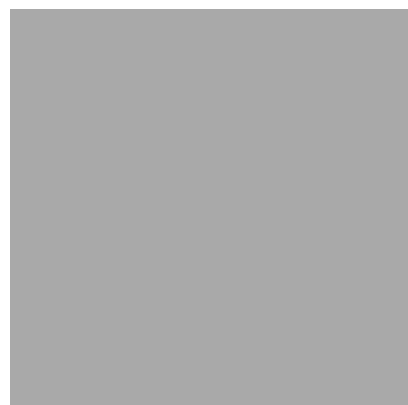
Given two images acquired with
different phase-encoding



How topup works (very briefly)



$p=[0 \ 1 \ 0]$

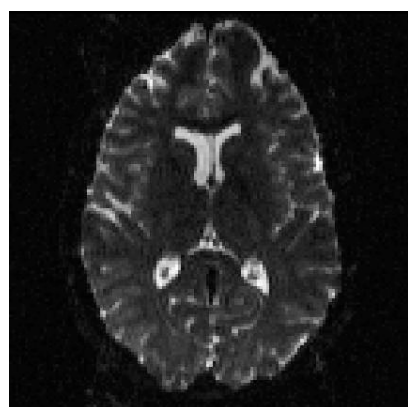


$p=[0 \ -1 \ 0]$

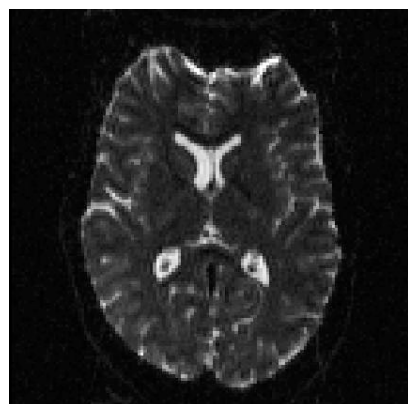
topup “guesses” a field...



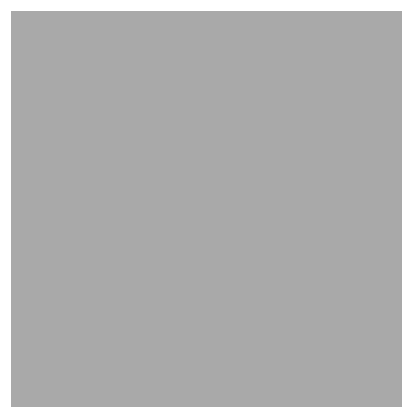
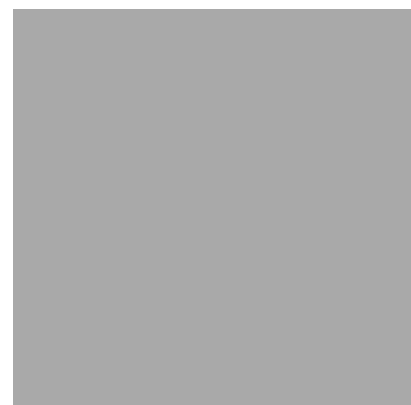
How topup works (very briefly)



$p=[0 \ 1 \ 0]$



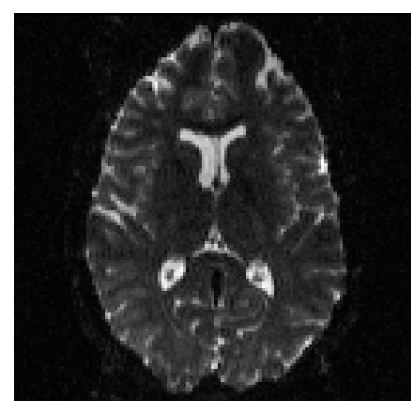
$p=[0 \ -1 \ 0]$



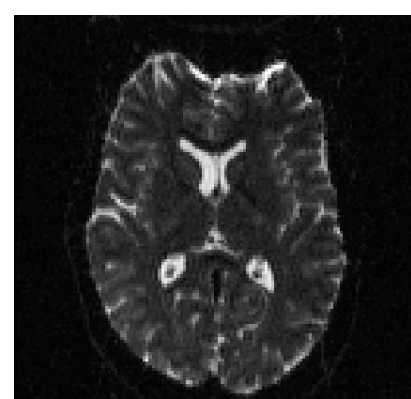
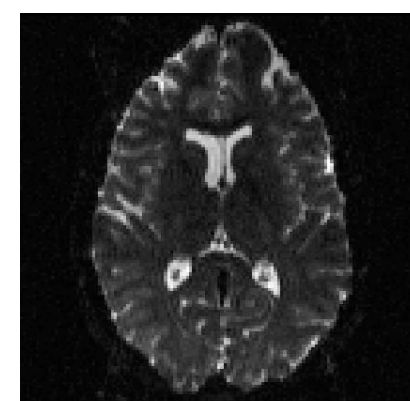
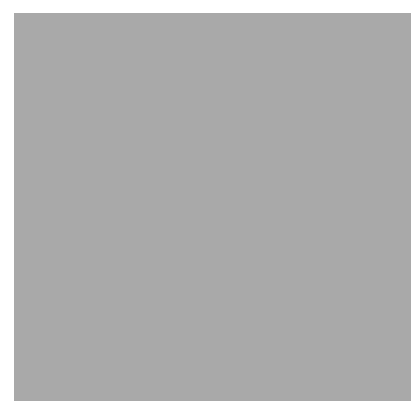
...calculates the displacement maps...



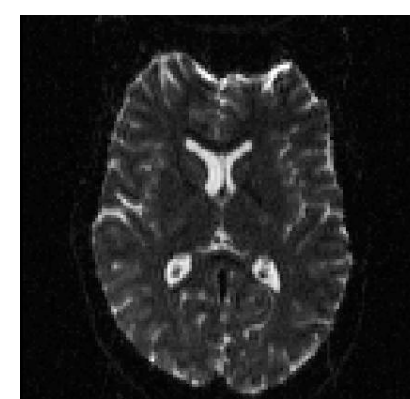
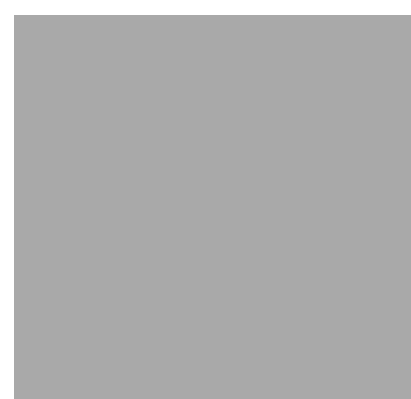
How topup works (very briefly)



$p=[0 \ 1 \ 0]$



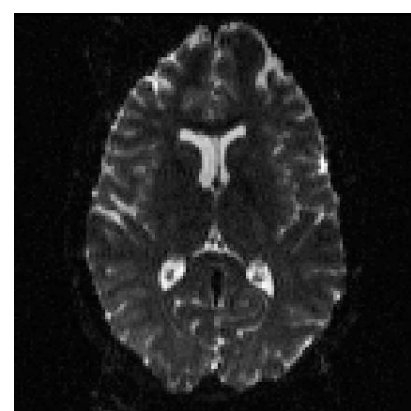
$p=[0 \ -1 \ 0]$



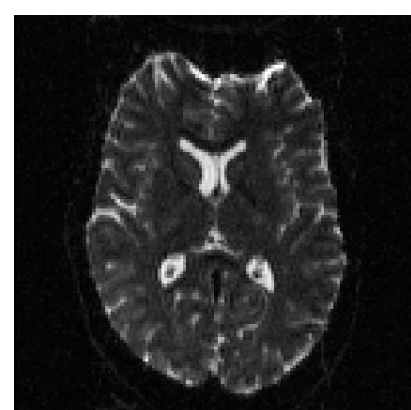
...”corrects” the images...



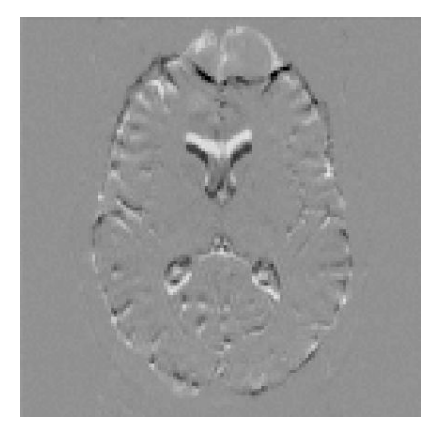
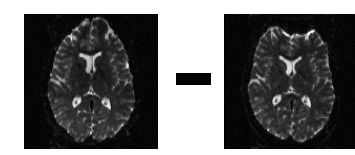
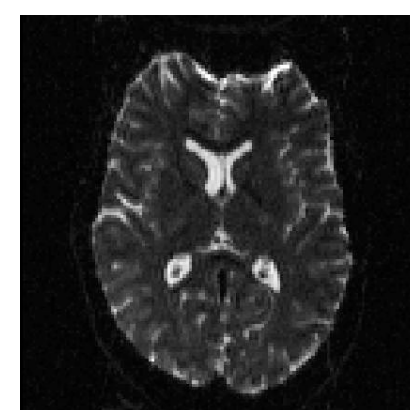
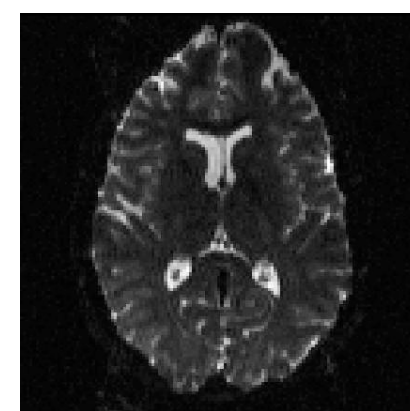
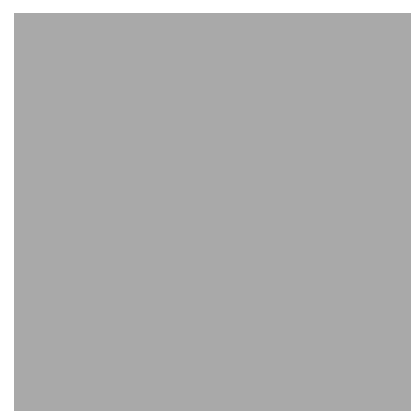
How topup works (very briefly)



$p=[0 \ 1 \ 0]$



$p=[0 \ -1 \ 0]$

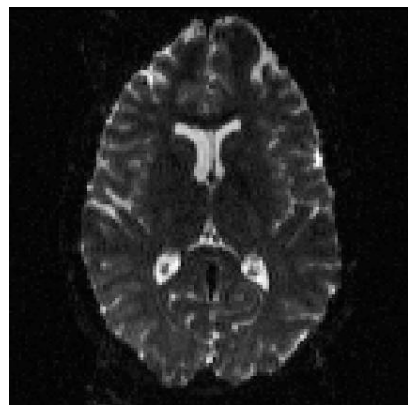


BAD!

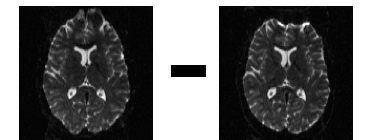
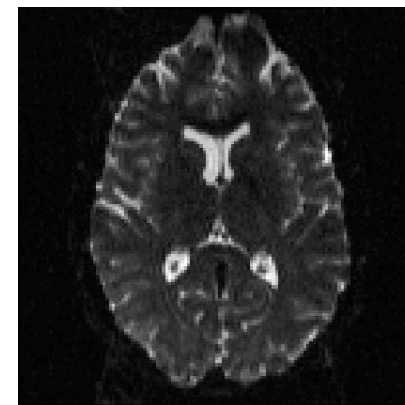
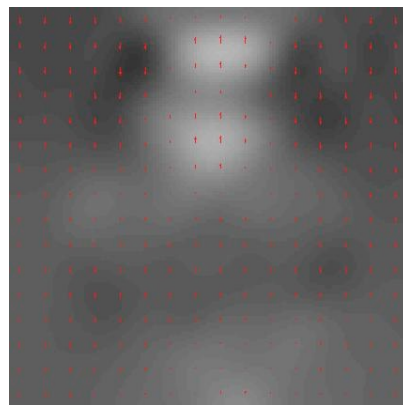
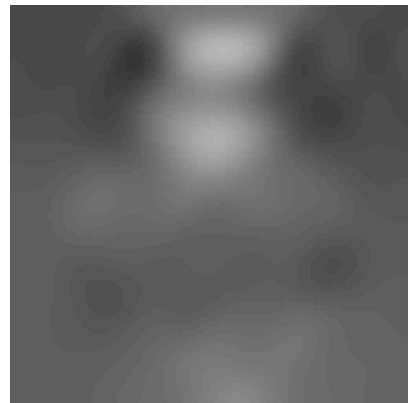
...and evaluates the results...
And **this** is the crucial bit.



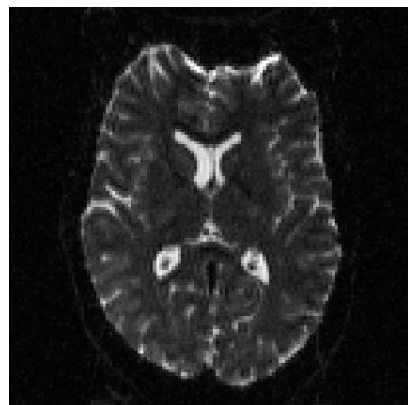
How topup works (very briefly)



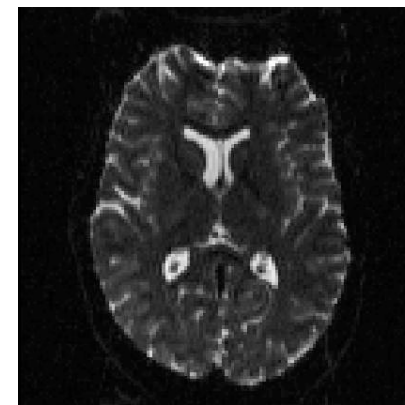
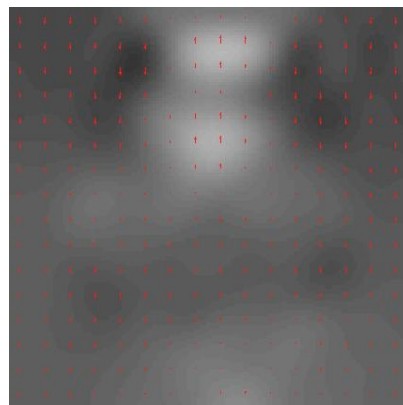
$p=[0 \ 1 \ 0]$



better



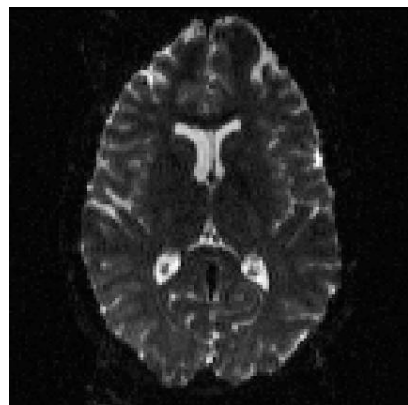
$p=[0 \ -1 \ 0]$



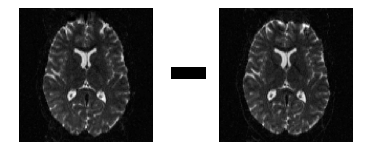
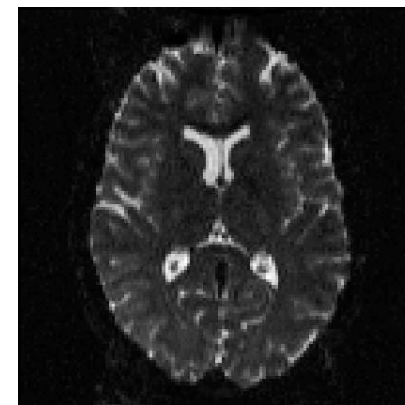
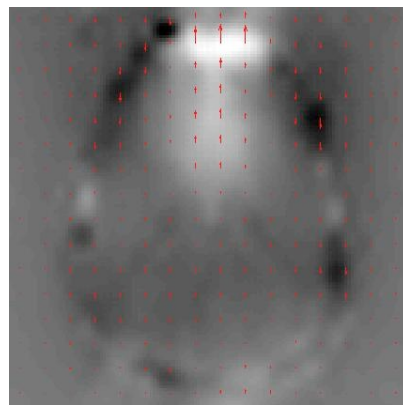
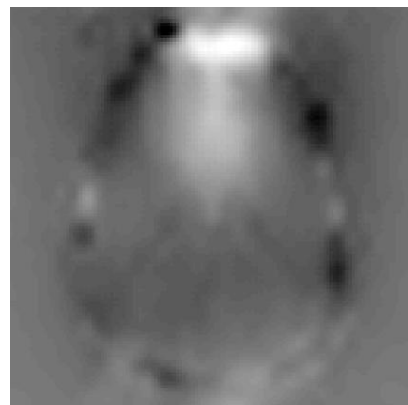
Because topup can then “guess”
another field



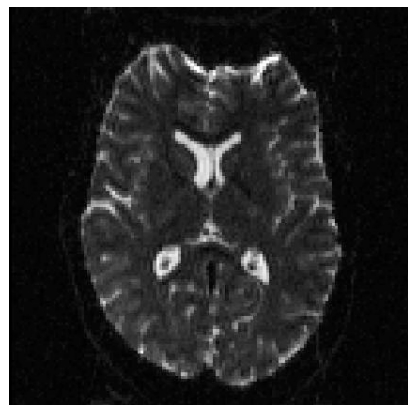
How topup works (very briefly)



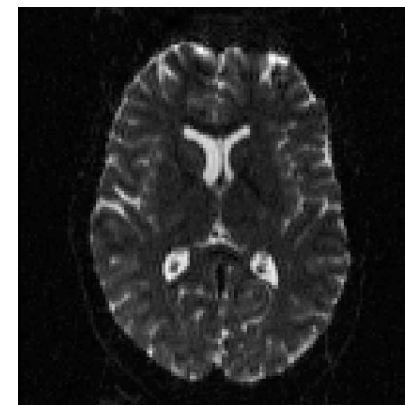
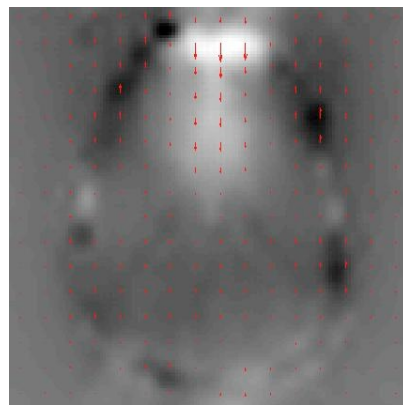
$p=[0 \ 1 \ 0]$



even
better



$p=[0 \ -1 \ 0]$



...and another...until it is happy,
and then it “knows” the field

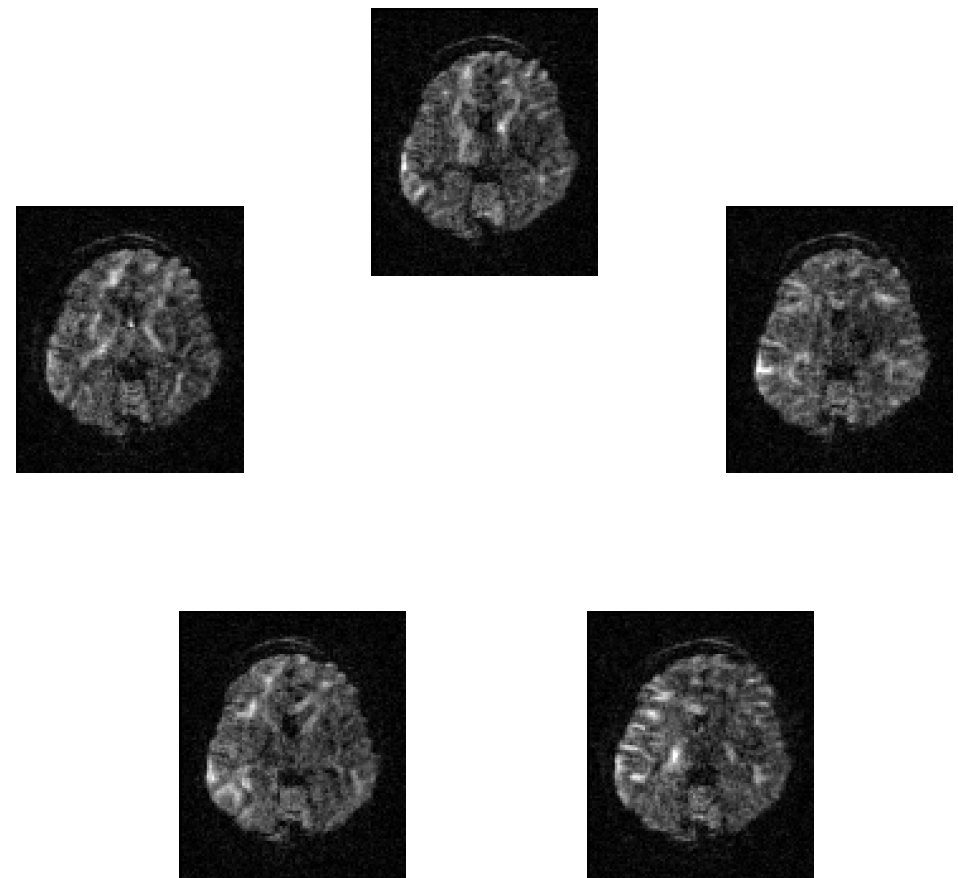


Outline of the talk

- What is the problem with diffusion data?
- Off-resonance field
 - How does it cause distortions?
 - Where does it come from?
- Registering diffusion data
 - How topup works
 - **How eddy works**
- Practicalities
- Some results
- Quality control
- New eddy features



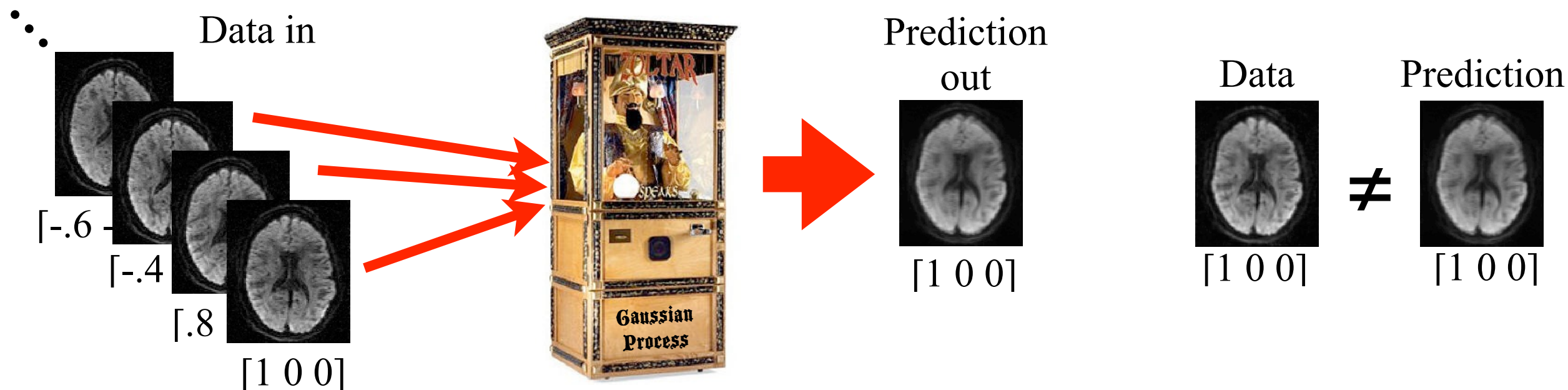
But it is not easy to register diffusion weighted images



- Each image has different distortions -> non-linear registration
- What is the reference image?



Zoltar -- The prediction maker



Given some data in, Zoltar will make a prediction what the data "should" be.

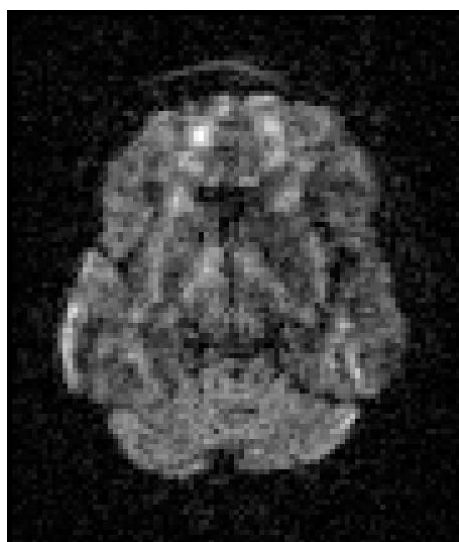
The prediction for a given dwi will not be identical to the "input" for that dwi

I know this sounds crazy, but please trust me on this.
(Zoltar is actually a Gaussian Process)



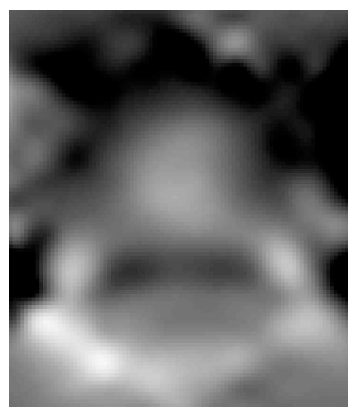
How eddy works: Loading step

Pick the first dwi

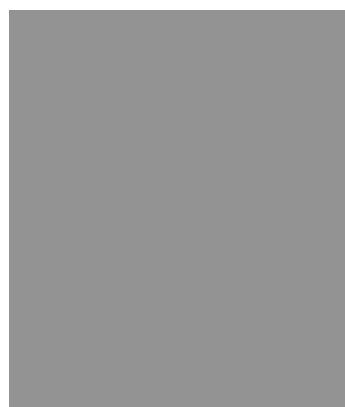


Use current estimates of

Susc



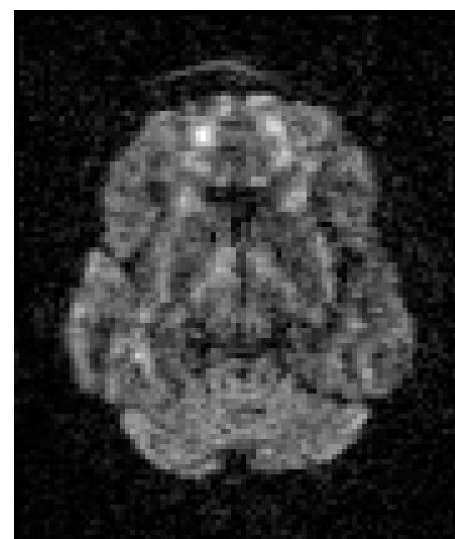
EC



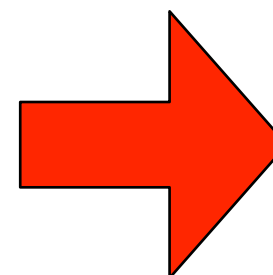
MP

$$\begin{bmatrix} 0 \\ 0 \\ \vdots \\ 0 \end{bmatrix}$$

To correct
image



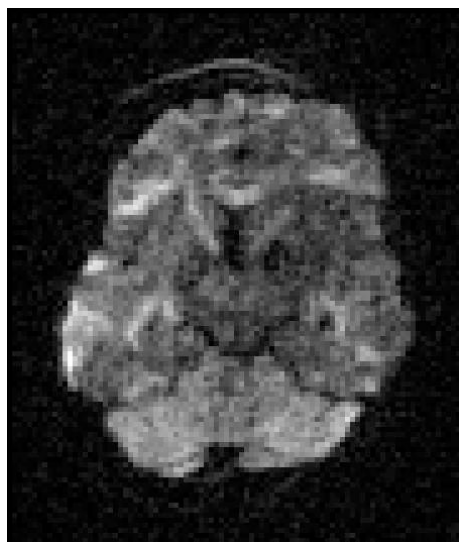
And load into
prediction
maker





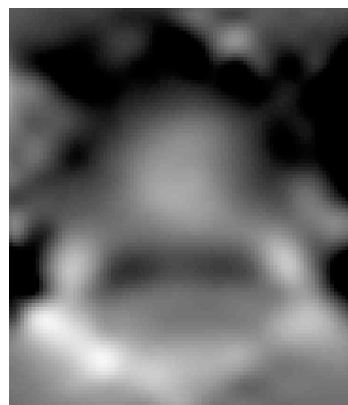
How eddy works: Loading step

then the 2nd dwi

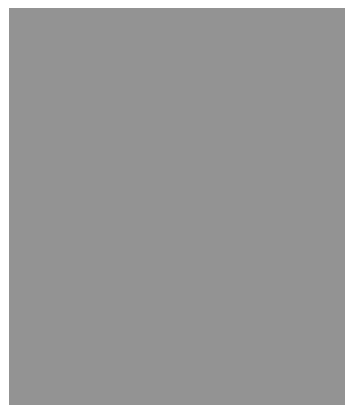


Use current estimates of

Susc



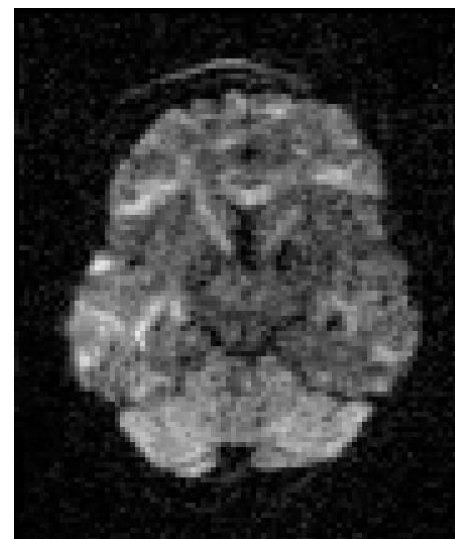
EC



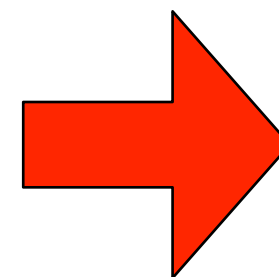
MP

$$\begin{bmatrix} 0 \\ 0 \\ \vdots \\ 0 \end{bmatrix}$$

To correct
2nd image



And load into
prediction
maker

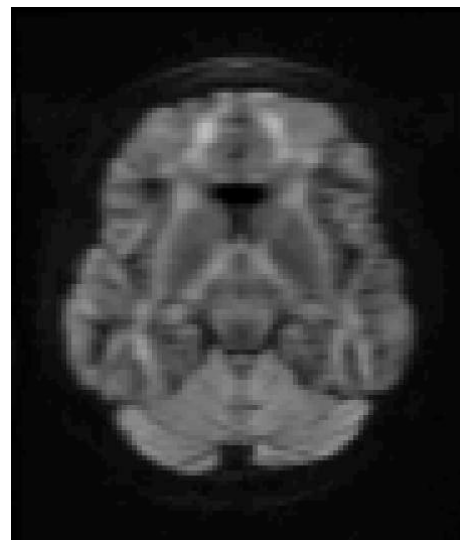
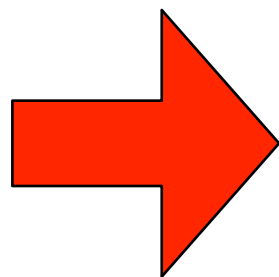


Until we have
loaded all dwis

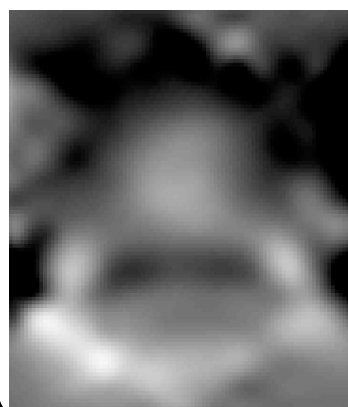


How eddy works: Estimation step

Draw a prediction
for first dwi

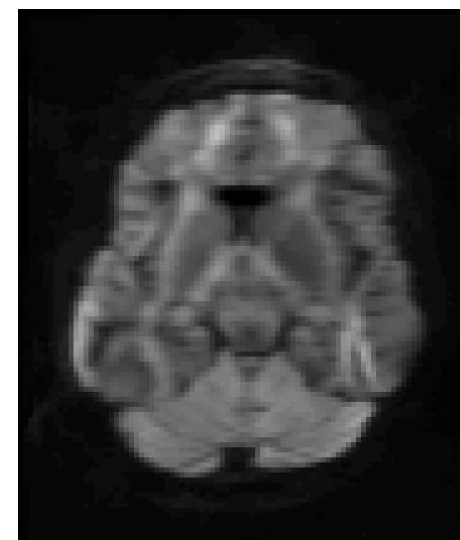


Use current estimates of
Susc EC MP

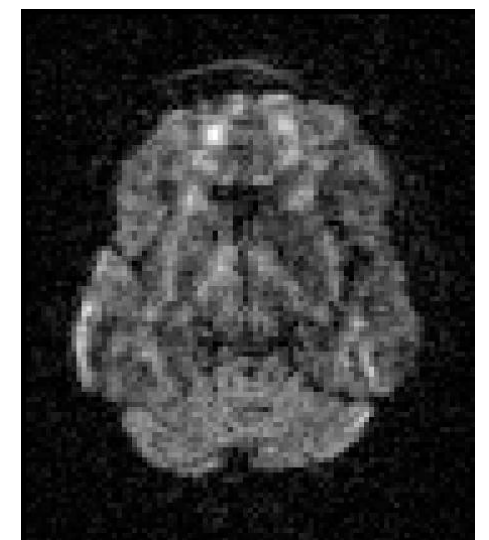


$$\begin{bmatrix} 0 \\ 0 \\ \vdots \\ 0 \end{bmatrix}$$

Invert



To get
prediction in
“observation
space”

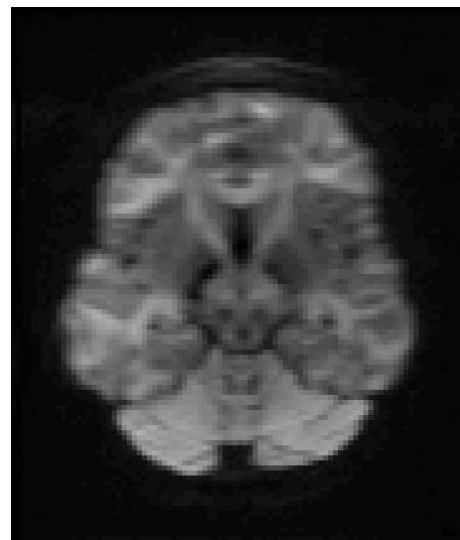
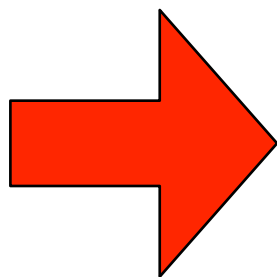


And compare
to actual
observation

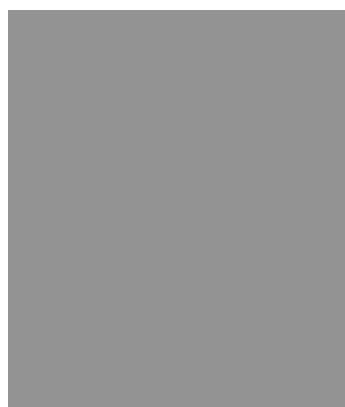
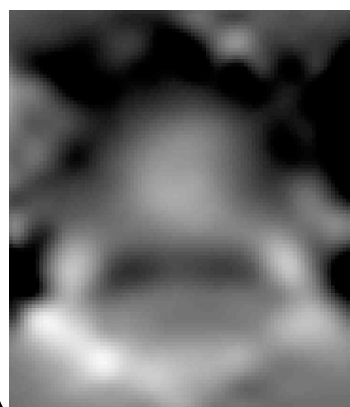


How eddy works: Estimation step

Draw a prediction
for 2nd dwi

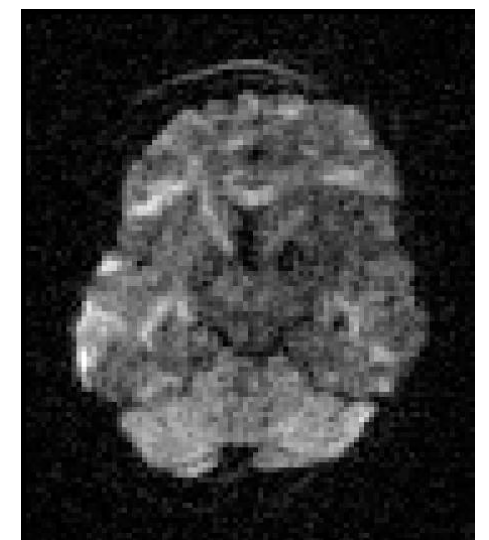
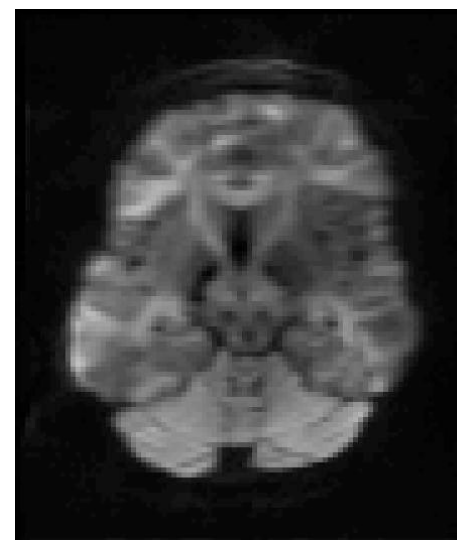


Use current estimates of
Susc EC MP



$$\begin{bmatrix} 0 \\ 0 \\ \vdots \\ 0 \end{bmatrix}$$

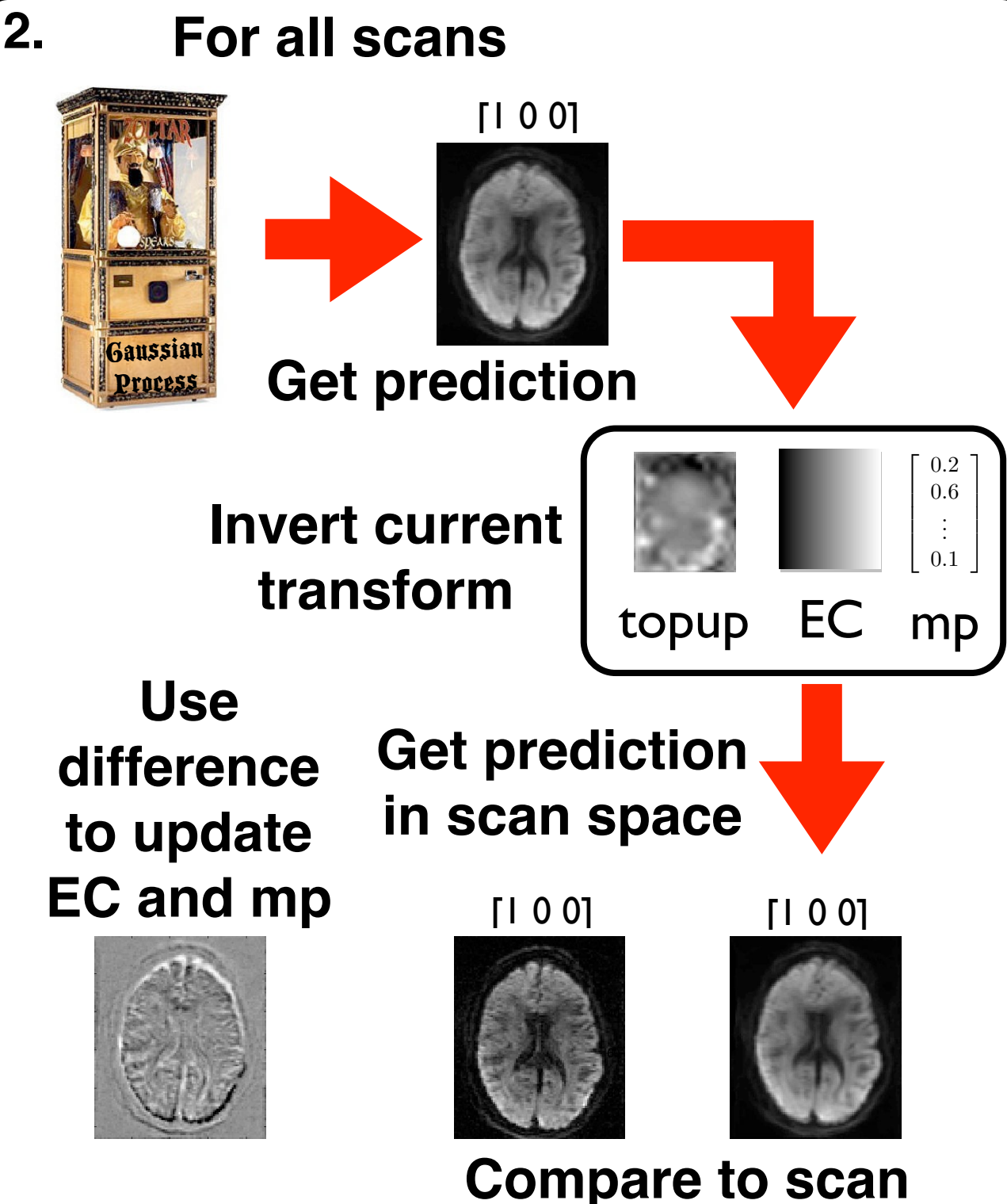
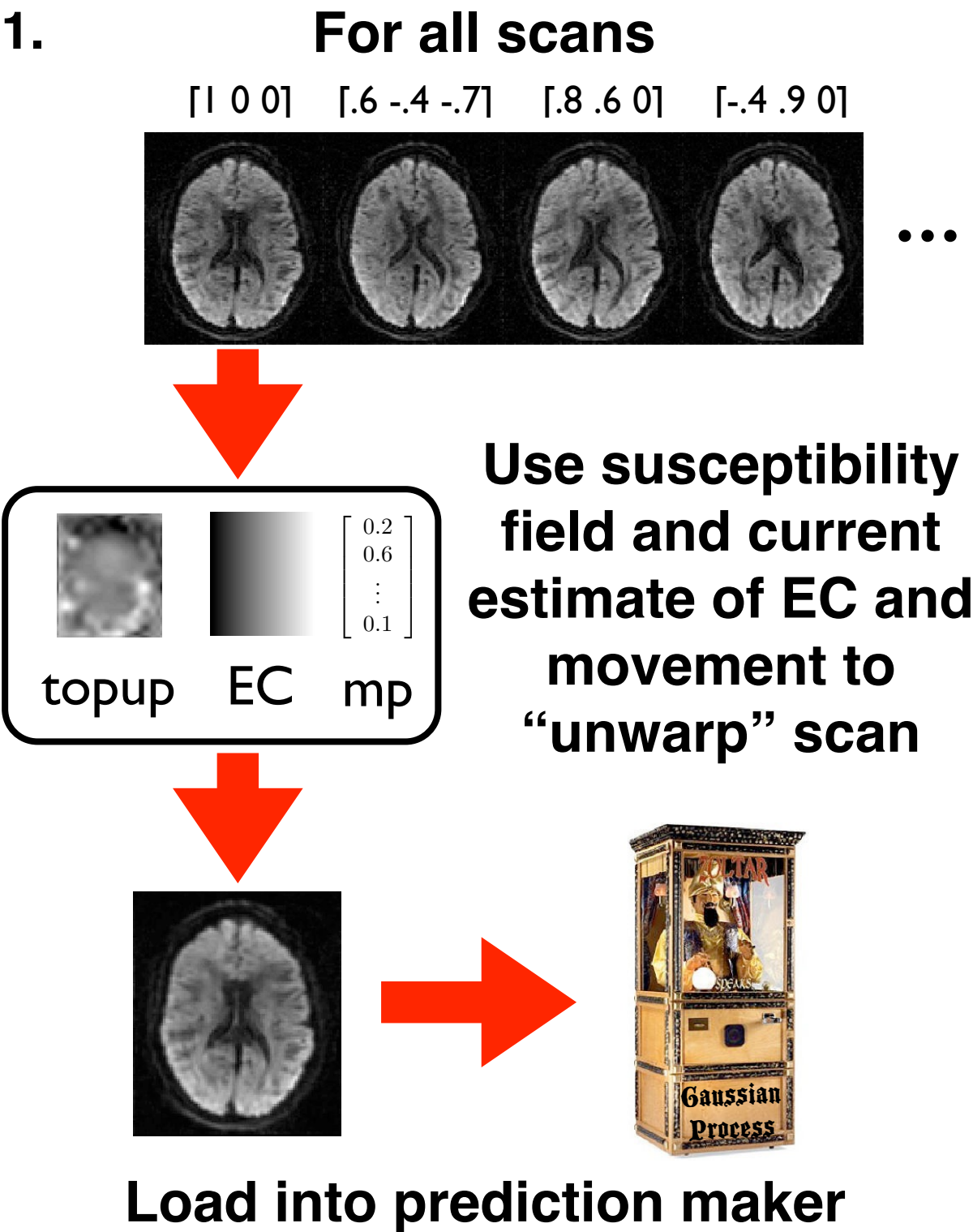
Invert



And then we repeat
the procedure for the
next dwi ...

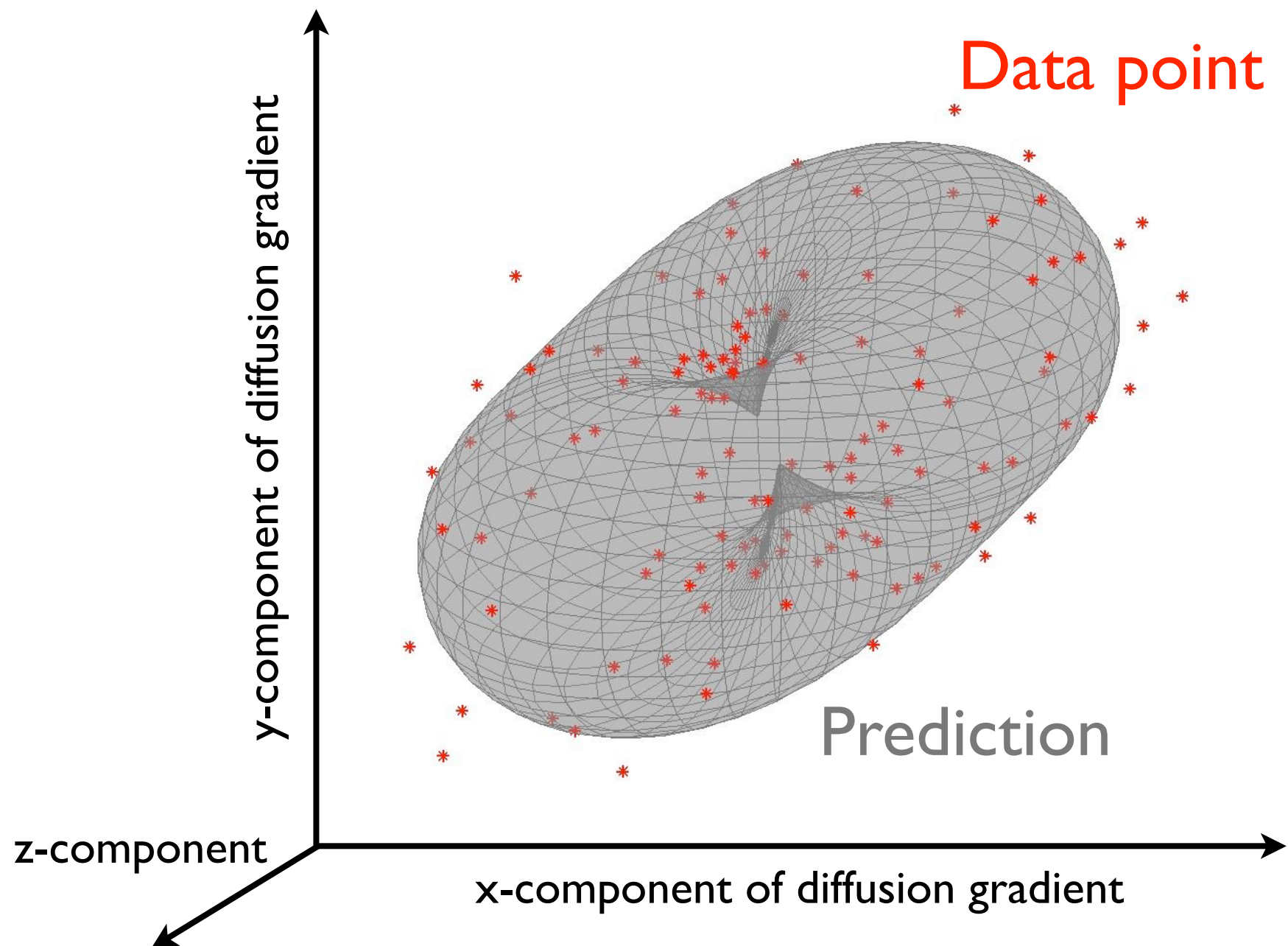


How eddy works

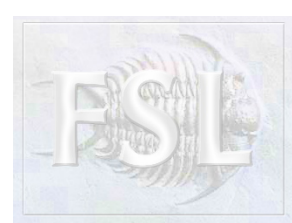




Under the hood of Zoltar

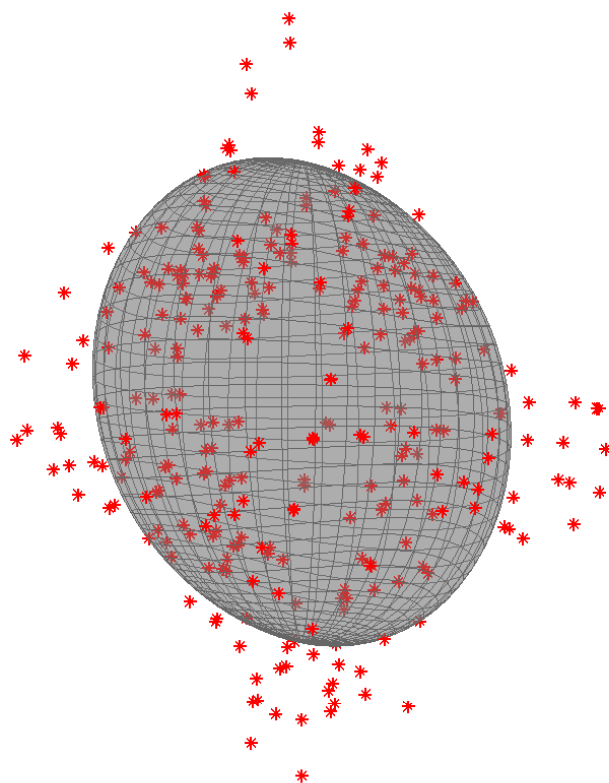


The signal is “modelled” in a data-driven fashion assuming that points close together on the unit sphere have similar signal.

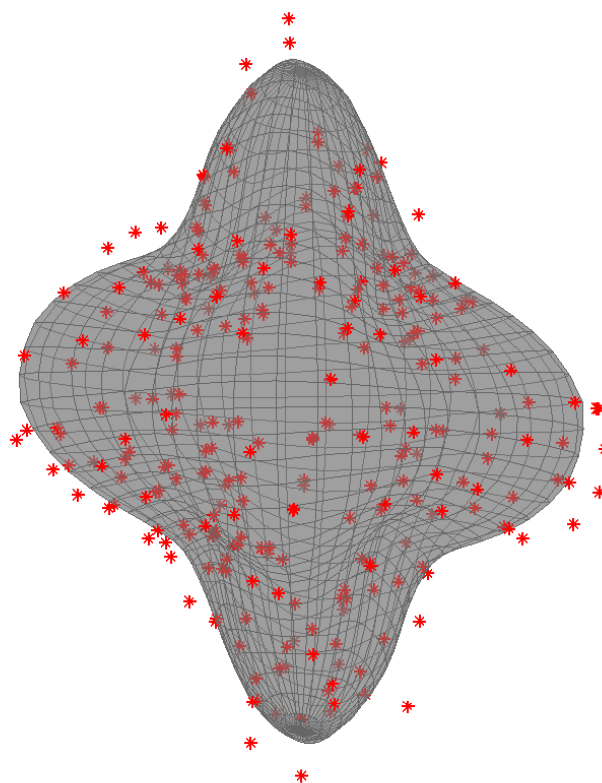


Under the hood of Zoltar

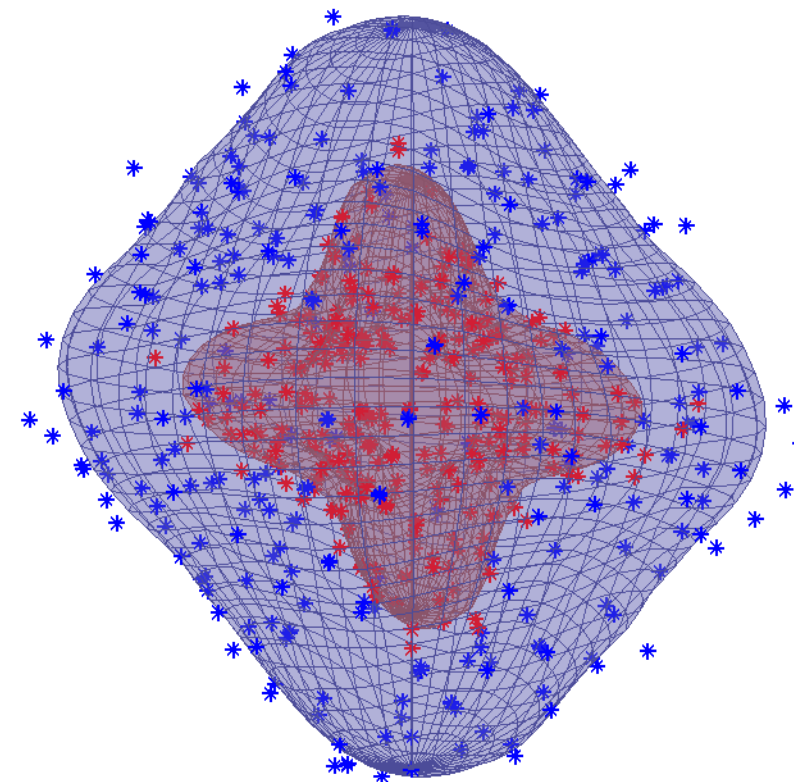
Tensor



Gaussian Process



Multi-shell predictions



The GP can model voxels with complicated anatomy while still being computationally convenient.

Shells with strong signal can help inform predictions in shells with poor signal

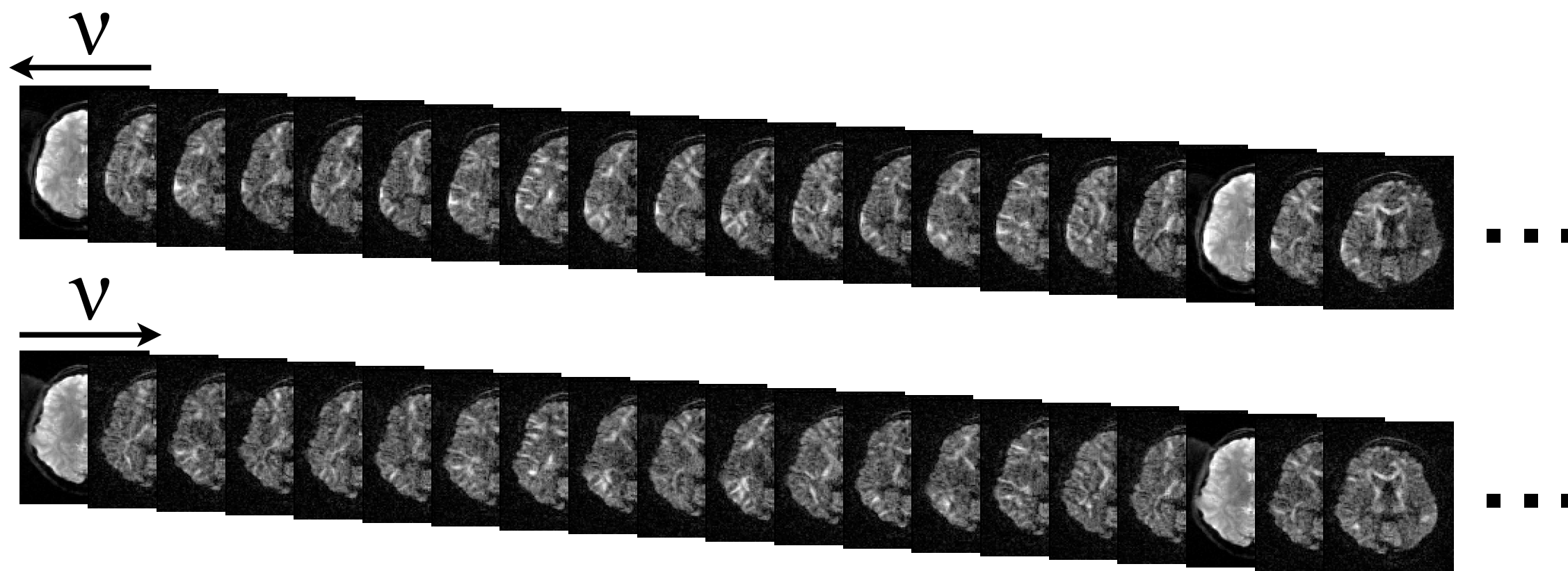


Outline of the talk

- What is the problem with diffusion data?
- Off-resonance field
 - How does it cause distortions?
 - Where does it come from?
- Registering diffusion data
 - How topup works
 - How eddy works
- **Practicalities**
- Some results
- Quality control
- New eddy features



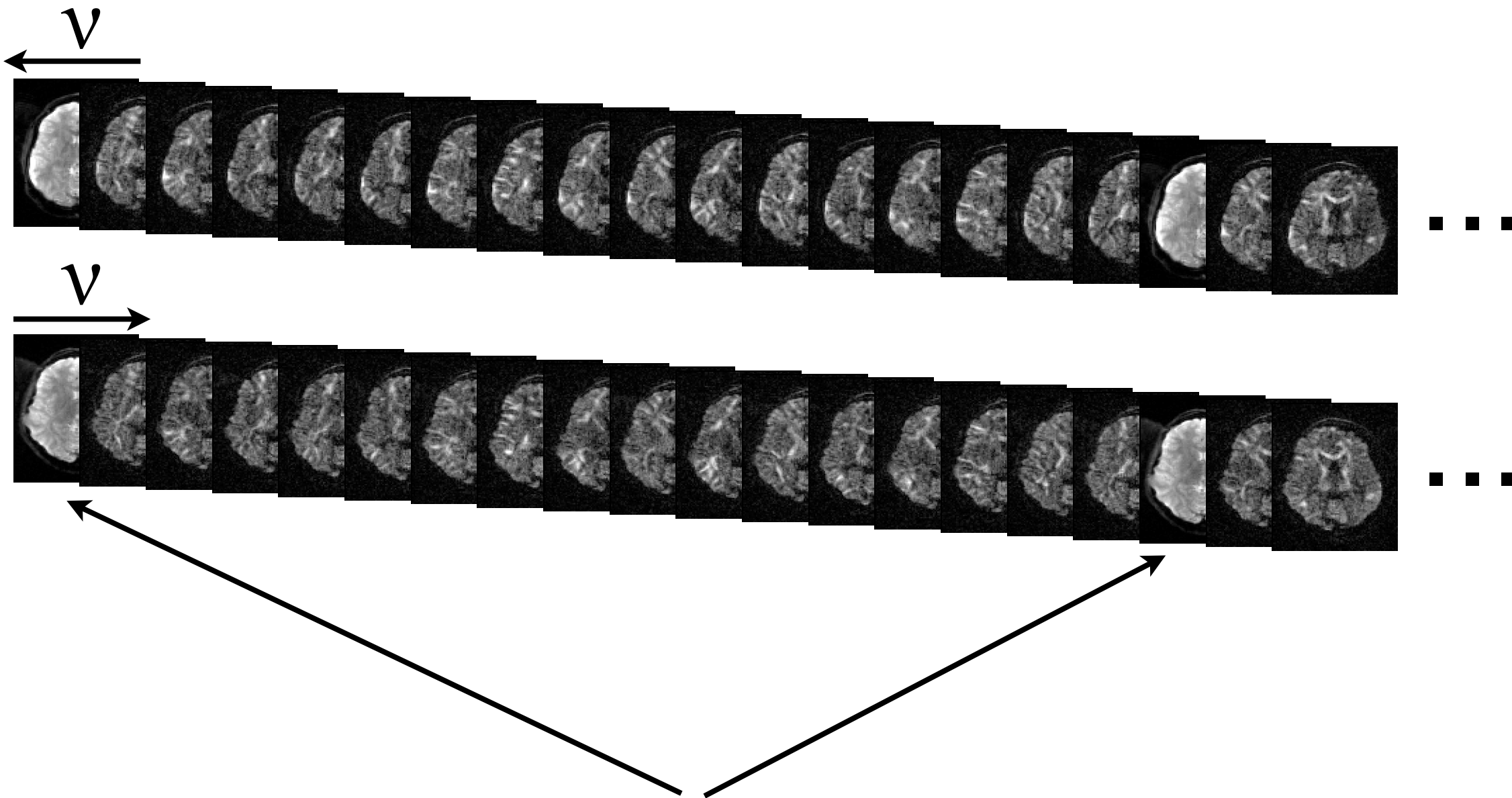
Practicalities



- Our example data consists of:
 - N diffusion weighted volumes and n $b=0$ volumes
 - $b=0$ volumes interspersed
 - Two repetitions, phase-encode $L \rightarrow R$ and $R \rightarrow L$
 - Same diffusion table for both repetitions



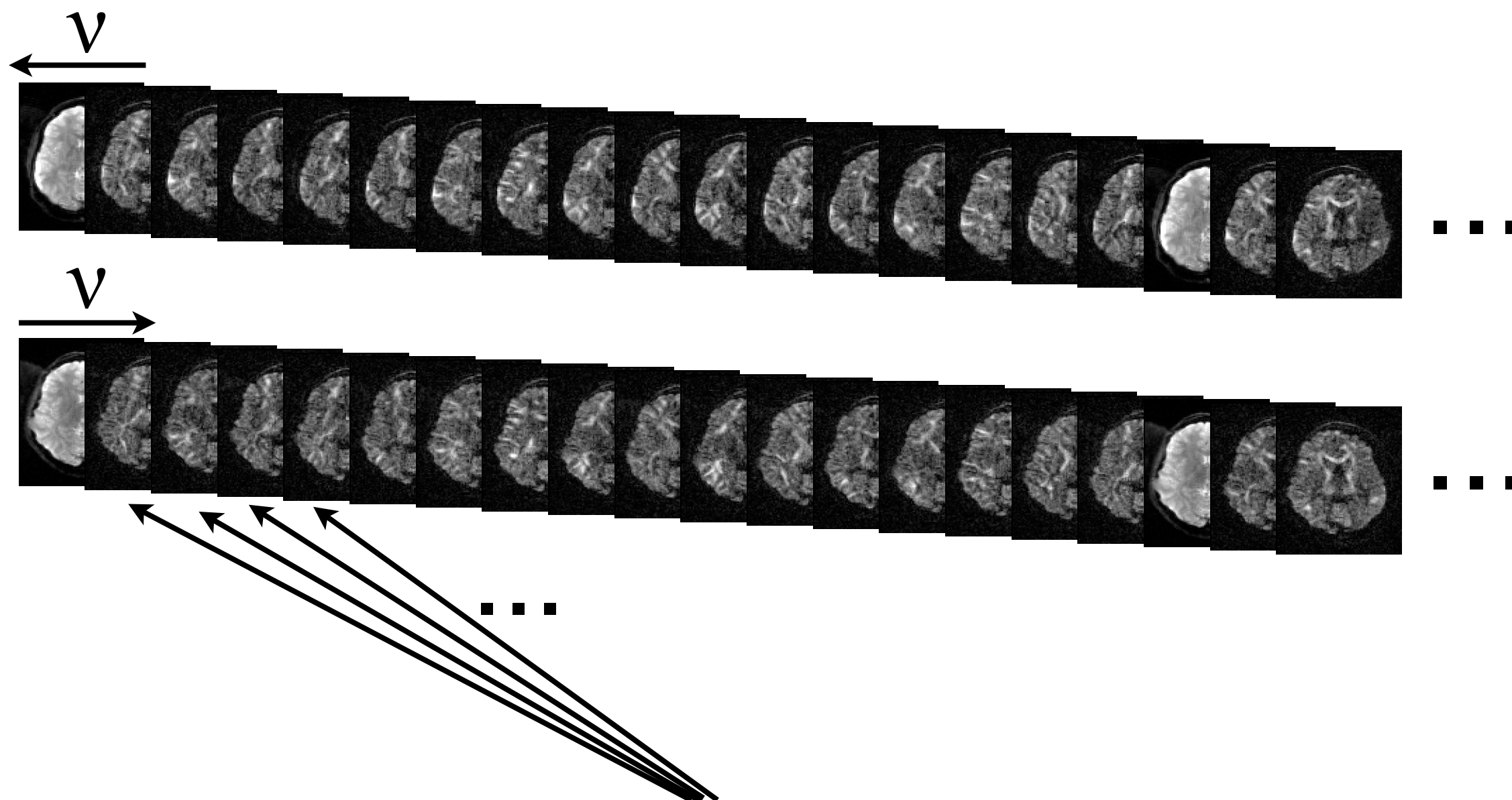
Practicalities



Affected by susceptibility distortions



Practicalities

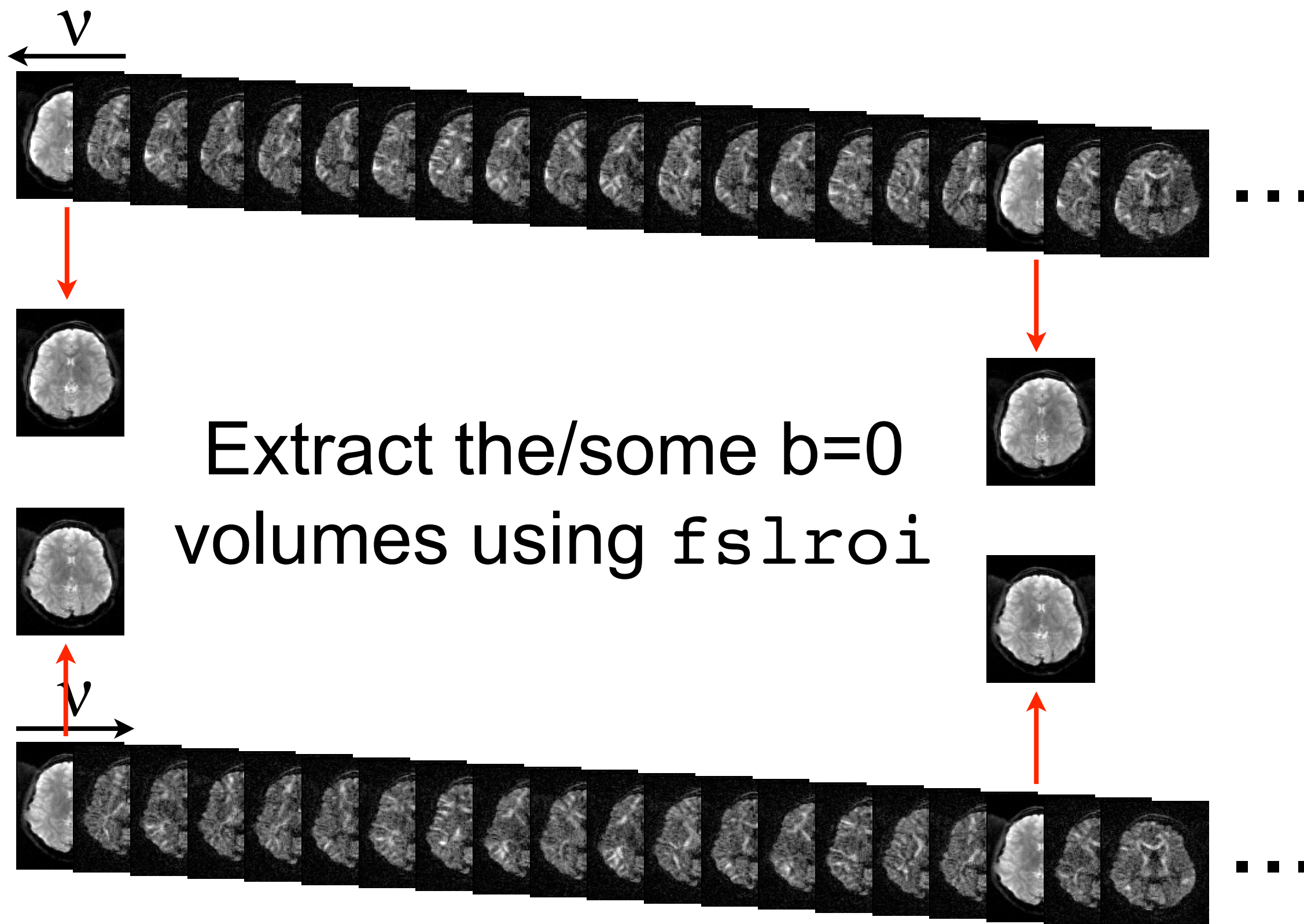


Affected by susceptibility distortions
AND eddy current distortions

And everything is of course affected by subject
movement.

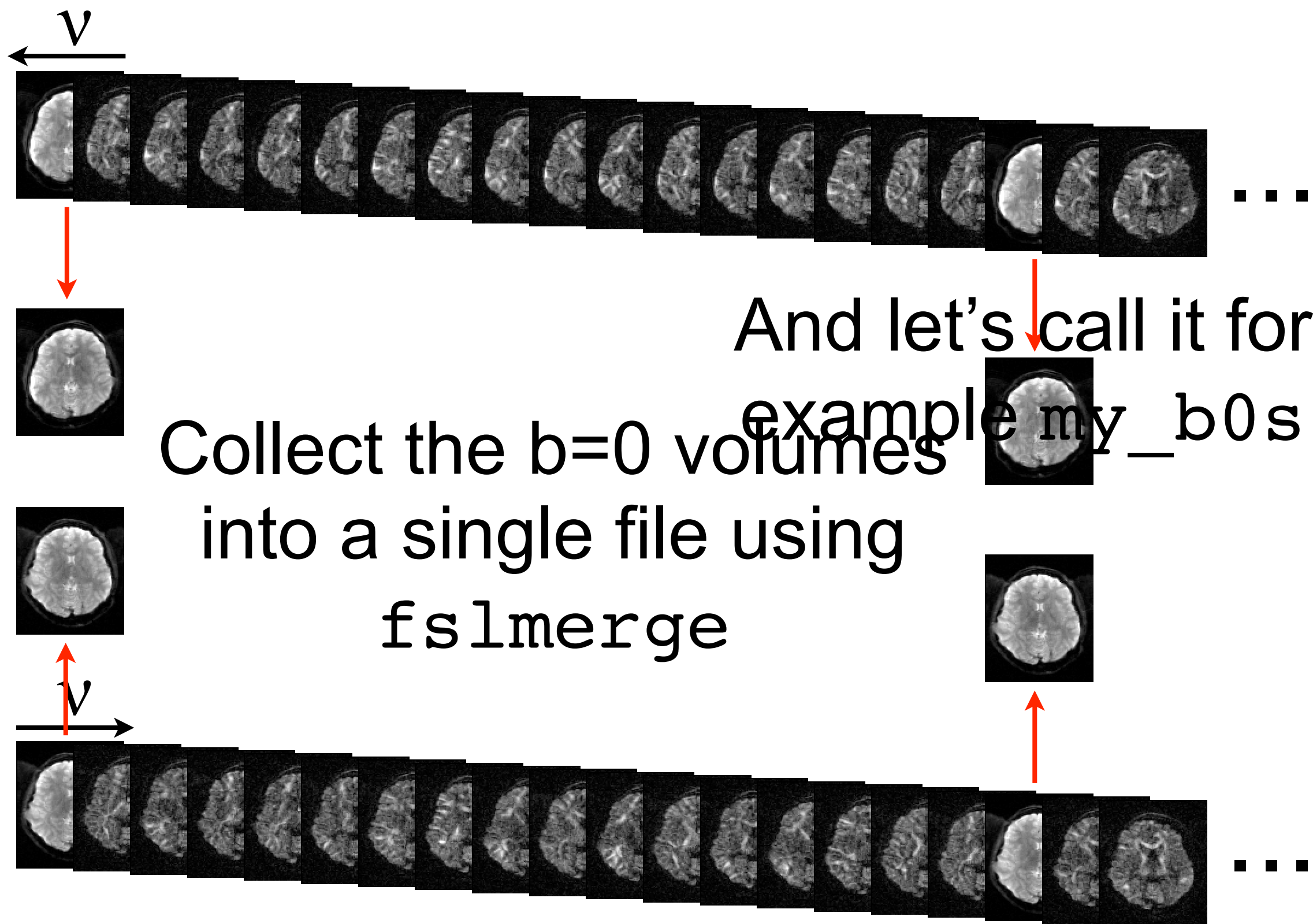


So, let's start with susceptibility





So, let's start with susceptibility





And the tool for that is `topup`

`topup -i main=my_b0s`

The diagram shows four axial brain scan images arranged horizontally. Above the first two images, the word 'topup' is written. Above the last two images, the text '-i main=my_b0s' is written. Four arrows point from the text 'topup' and '-i main=my_b0s' down to the four images respectively. A long double-headed arrow is positioned below the four images, spanning their entire width.

But we also need to inform `topup` about the acquisition parameters



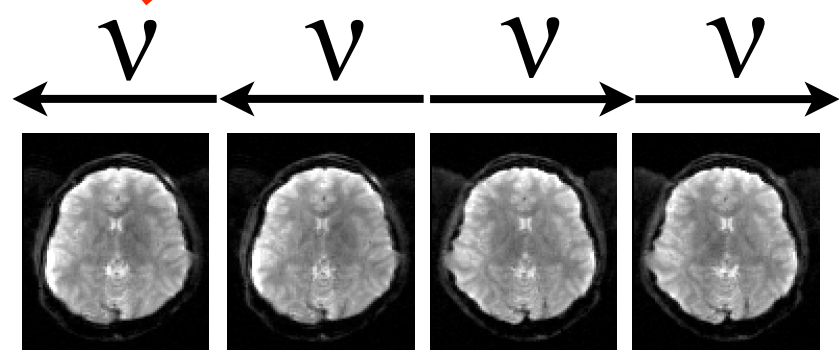
And the tool for that is `topup`

```
topup --imain=my_b0s
```

Means PE in x-direction, L→R

`-1 0 0 0.051`

Total readout time
(in seconds)



`my_b0s`

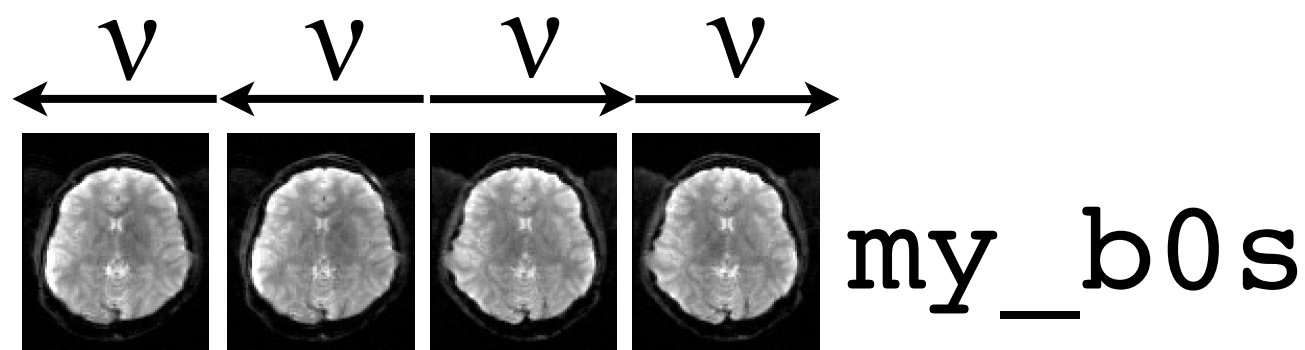


And the tool for that is `topup`

```
topup --imain=my_b0s --datain=acqparams.txt
```

```
-1 0 0 0.051  
-1 0 0 0.051  
1 0 0 0.051  
1 0 0 0.051
```

Text file that we can
call for example
`acqparams.txt`



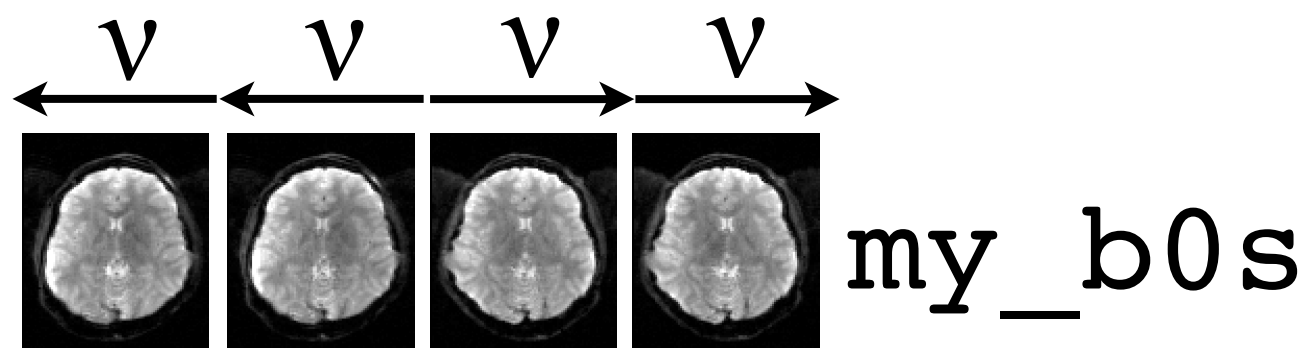


And the tool for that is `topup`

```
topup --imain=my_b0s --datain=acqparams.txt --config=b02b0.cnf
```



And then some
technical details



```
-1 0 0 0.051  
-1 0 0 0.051  
1 0 0 0.051  
1 0 0 0.051
```

`acqparams.txt`



And the tool for that is `topup`

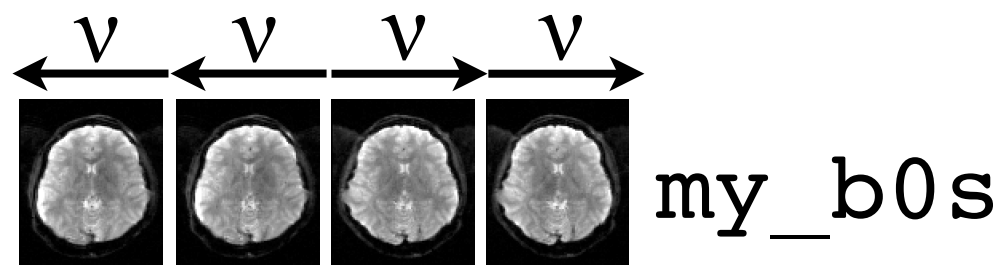
And finally we need to tell it where to put the results

```
topup --imain=my_b0s --datain=acqparams.txt --config=b02b0.cnf --out=my_topup
```

Tells position of 2nd b=0 scan relative the first

`my_topup_movpar.txt`

```
0 0 0 0 0 0
0.72 -0.02 -0.07 0.002 0.000 0.002
0 -0.11 -0.33 0.002 0.013 -0.004
-0.70 -0.12 -0.43 0.002 0.014 -0.004
```



```
-1 0 0 0.051
-1 0 0 0.051
1 0 0 0.051
1 0 0 0.051
```

`acqparams.txt`

`b02b0.cnf`

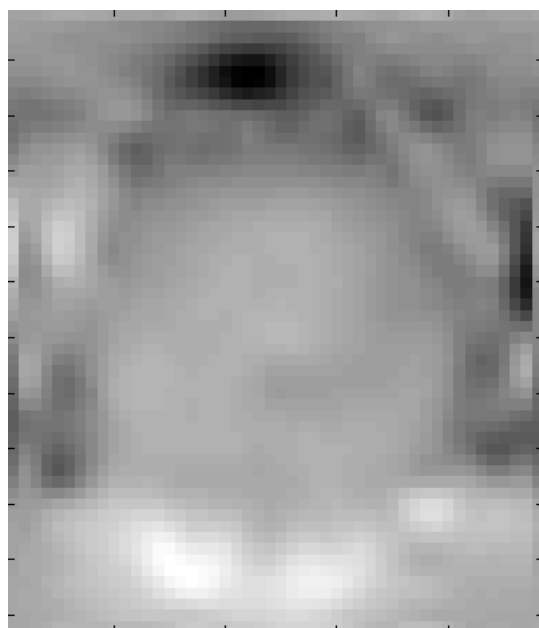


And the tool for that is `topup`

And finally we need to tell it where to put the results

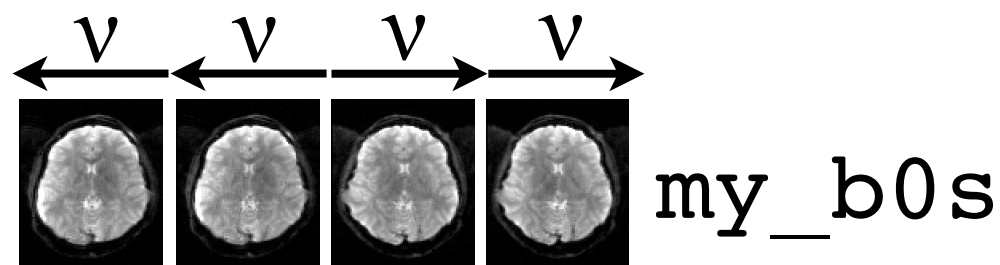
```
topup --imain=my_b0s --datain=acqparams.txt --config=b02b0.cnf --out=my_topup
```

`my_topup_fieldcoef.nii`



`my_topup_movpar.txt`

```
0 0 0 0 0 0
0.72 -0.02 -0.07 0.002 0.000 0.002
0 -0.11 -0.33 0.002 0.013 -0.004
-0.70 -0.12 -0.43 0.002 0.014 -0.004
```



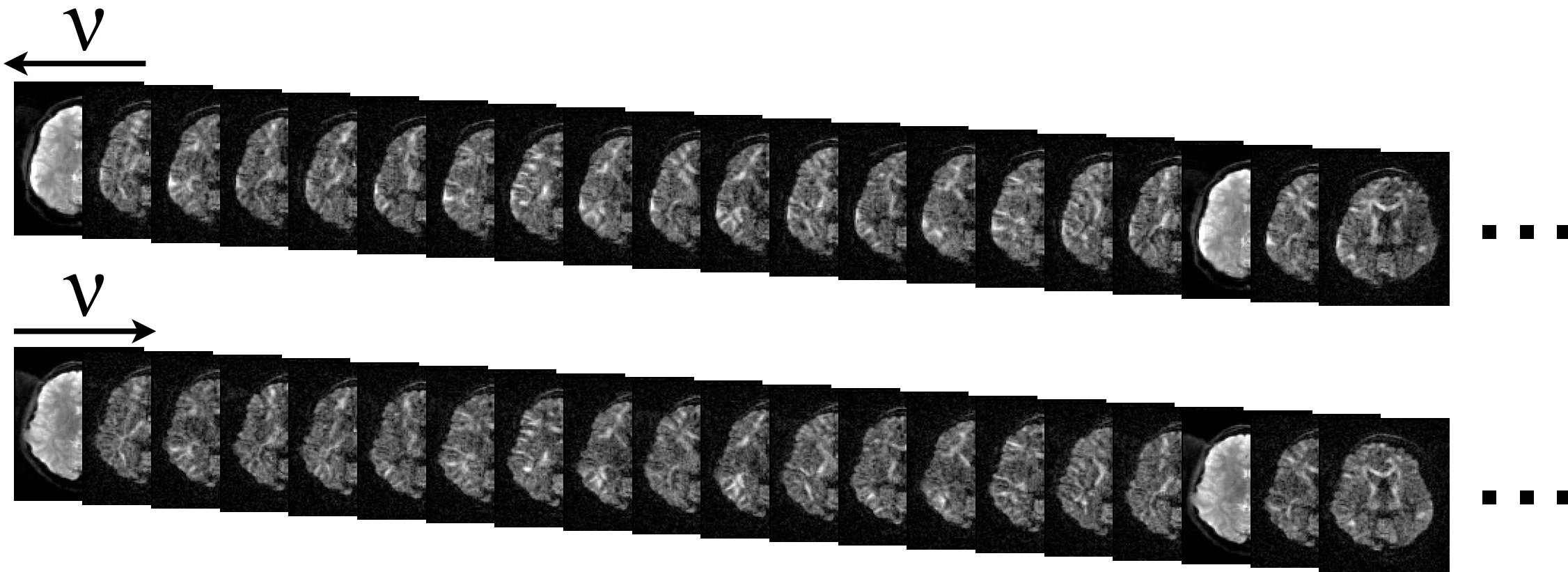
```
-1 0 0 0.051
-1 0 0 0.051
1 0 0 0.051
1 0 0 0.051
```

`acqparams.txt`

`b02b0.cnf`

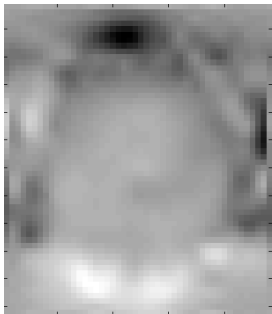


Back to the full data-set



Now we want to correct the eddy current-distortions and subject movement in the whole data set.

my_topup_fieldcoef.nii

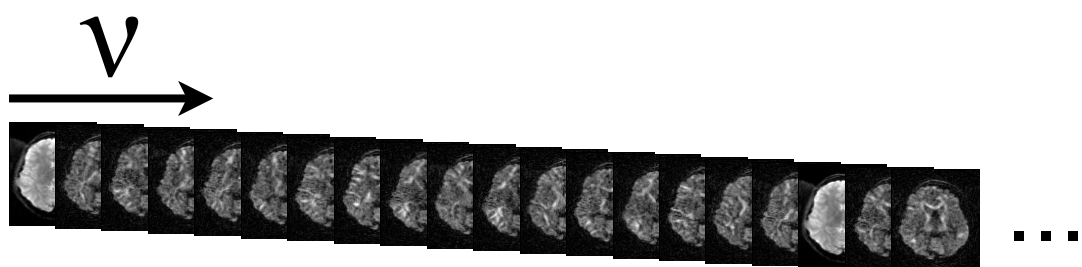
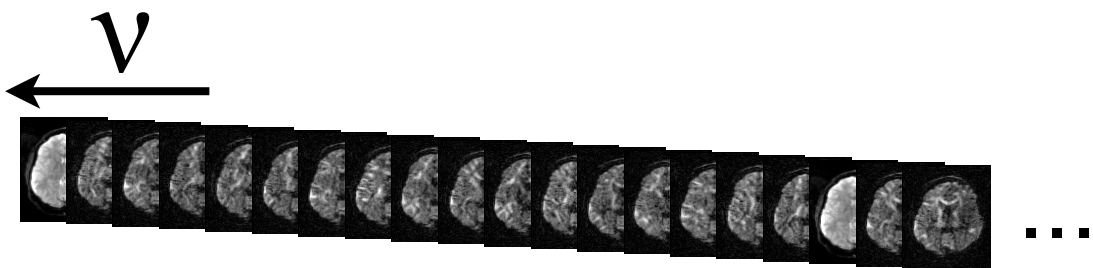


acqparams.txt

my_topup_movpar.txt



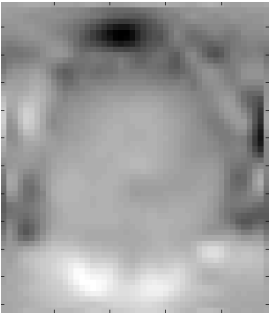
Collect all data in one file



LR_RL

The first thing we do is to collect all data in a single file using `fslmerge` and call it for example LR_RL

`my_topup_fieldcoef.nii`



`acqparams.txt`

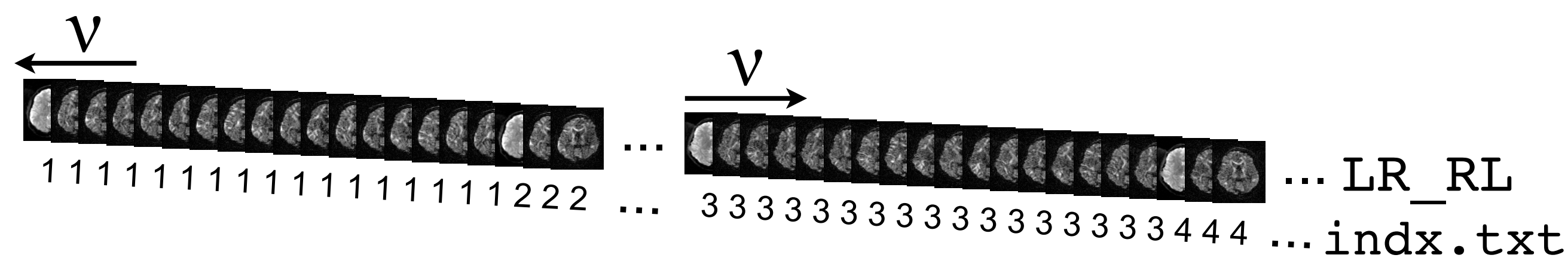
```
-1 0 0 0.051
-1 0 0 0.051
1 0 0 0.051
1 0 0 0.051
```

```
0 0 0 0 0 0
0.72 -0.02 -0.07 0.002 0.000 0.002
0 -0.11 -0.33 0.002 0.013 -0.004
-0.70 -0.12 -0.43 0.002 0.014 -0.004
```

`my_topup_movpar.txt`



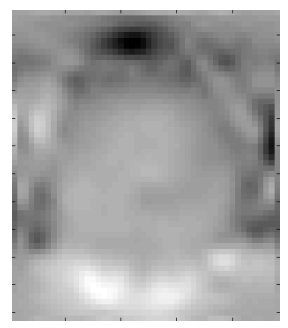
Inform eddy of acquisition parameters



Then we make a text file with one index for each volume, and call it for example `indx.txt`

`my_topup_fieldcoef.nii`

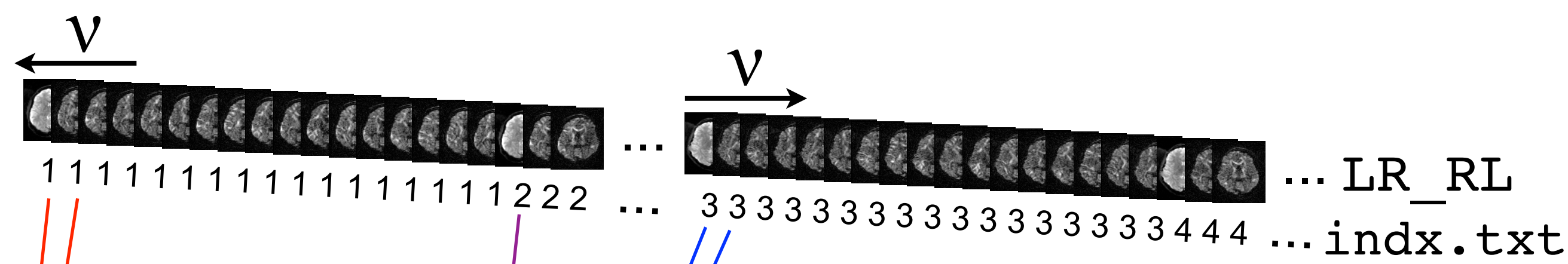
`acqparams.txt`



`my_topup_movpar.txt`



Inform eddy of acquisition parameters

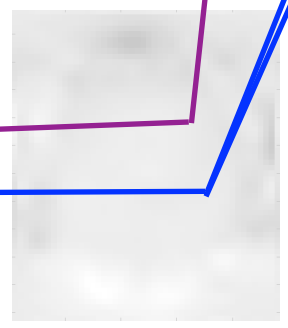


By referring into `acqparams.txt`
this file specifies how every
volume was acquired

`my_topup_fielddef.nii`

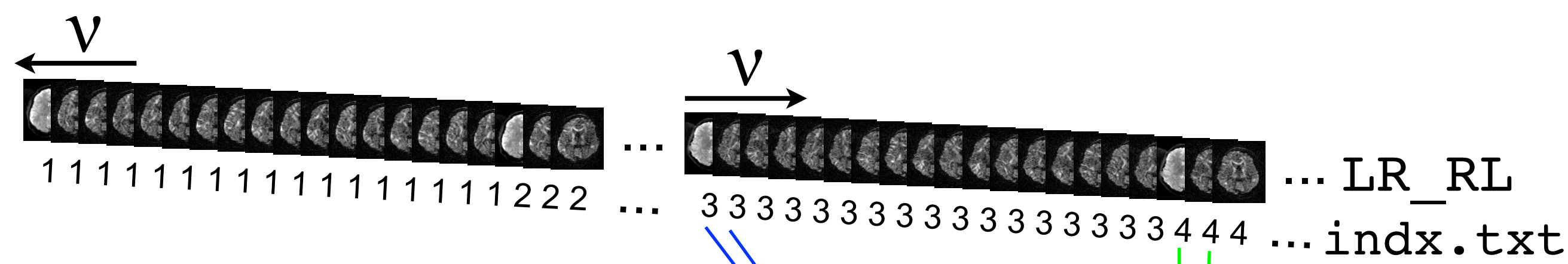
`-1 0 0 0.051`
`-1 0 0 0.051`
`1 0 0 0.051`
`1 0 0 0.051`
`acqparams.txt`

`0 0 0 0 0 0`
`0.72 -0.02 -0.07 0.002 0.000 0.002`
`0 -0.11 -0.33 0.002 0.013 -0.004`
`-0.70 -0.12 -0.43 0.002 0.014 -0.004`
`my_topup_movpar.txt`





Inform eddy of acquisition parameters



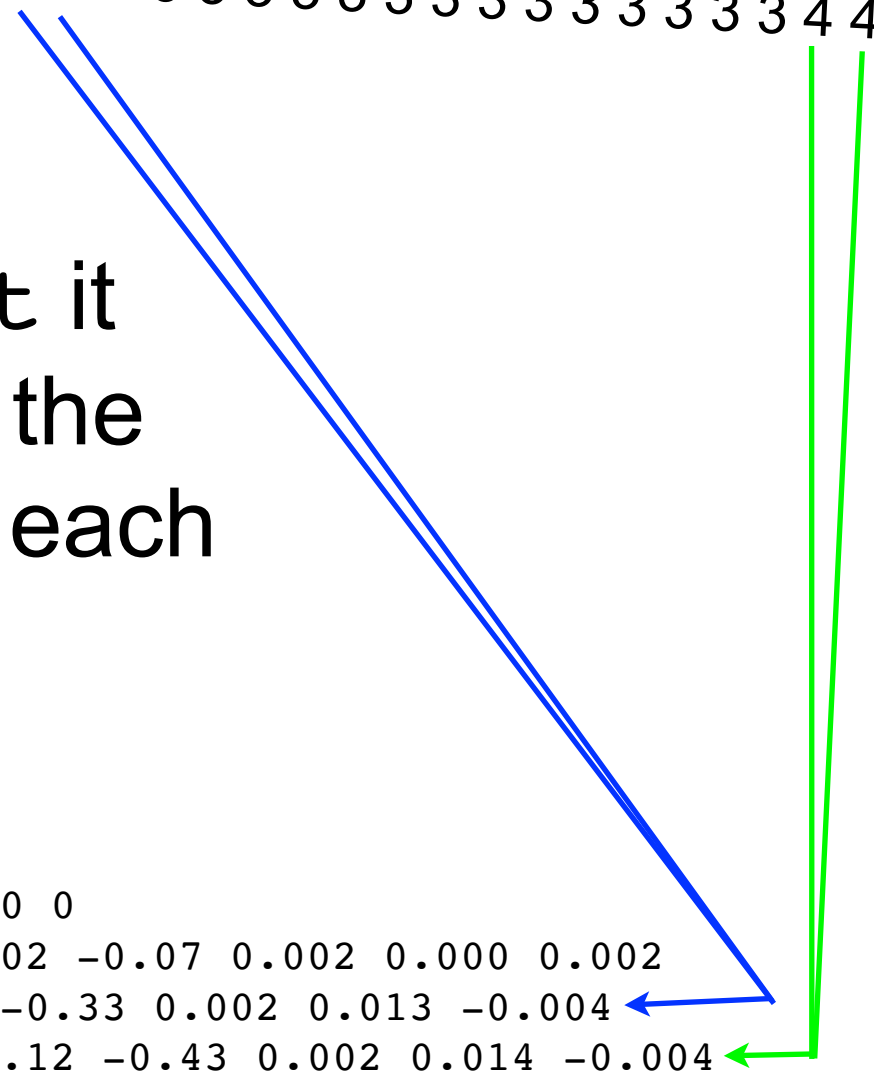
And by referring into
my_topup_movpar.txt it
gives a starting guess for the
relative subject position for each
volume

my_topup_fieldcoef.nii



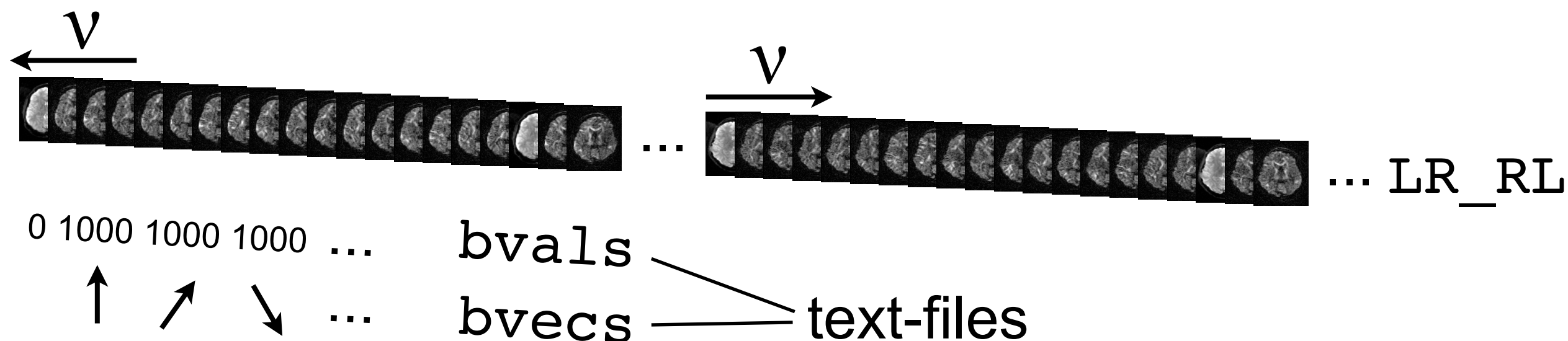
-1 0 0 0.051
-1 0 0 0.051
1 0 0 0.051
1 0 0 0.051
acqparams.txt

0 0 0 0 0 0
0.72 -0.02 -0.07 0.002 0.000 0.002
0 -0.11 -0.33 0.002 0.013 -0.004
-0.70 -0.12 -0.43 0.002 0.014 -0.004
my_topup_movpar.txt





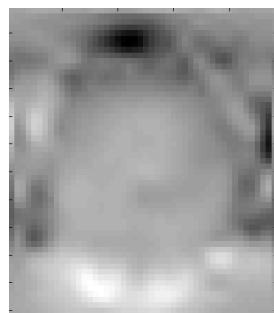
And of diffusion parameters



And we also need to know the b-value and b-vector for each volume (same as for `dtifit` or `bedpost`).

my_topup_fieldcoef.nii

acqparams.txt

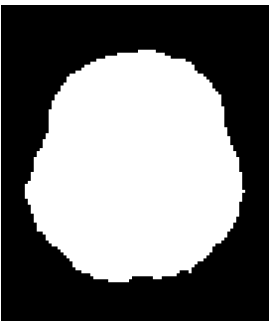
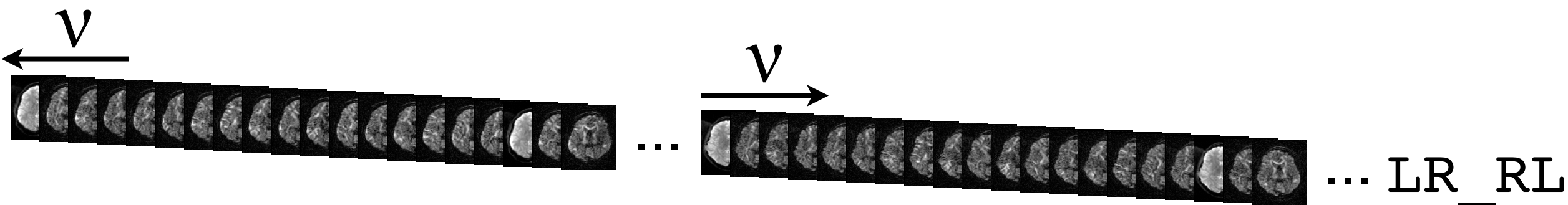


my_topup_movpar.txt

indx.txt



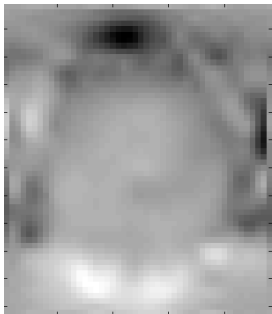
And where the brain is



brain_mask.nii

And finally a binary mask that tells eddy which voxels are brain. Also the same that is used for dtifit/bedpost.

my_topup_fieldcoef.nii



acqparams.txt

```
-1 0 0 0.051
-1 0 0 0.051
1 0 0 0.051
1 0 0 0.051
```

my_topup_movpar.txt

```
0 0 0 0 0 0
0.72 -0.02 -0.07 0.002 0.000 0.002
0 -0.11 -0.33 0.002 0.013 -0.004
-0.70 -0.12 -0.43 0.002 0.014 -0.004
```

indx.txt

```
1111...
```

bvals

0 1000 1000 1000 ...

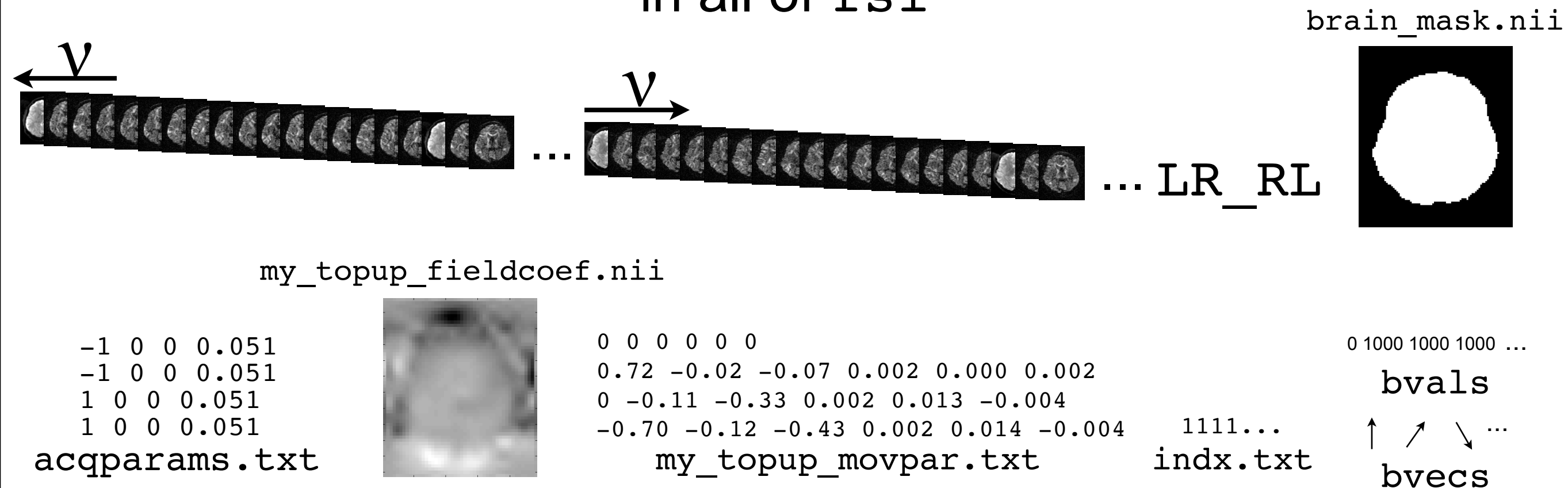
bvecs

↑ ↗ ↘ ...

And now we can run eddy

```
eddy --imain=LR_RL --acqp=acqparams.txt
--index=indx.txt --bvecs=bvecs
--bvals=bvals --mask=brain_mask
--topup=my_topup --out=my_eddy
```

And now we are ready for the most horrible command line
in all of `fsl`



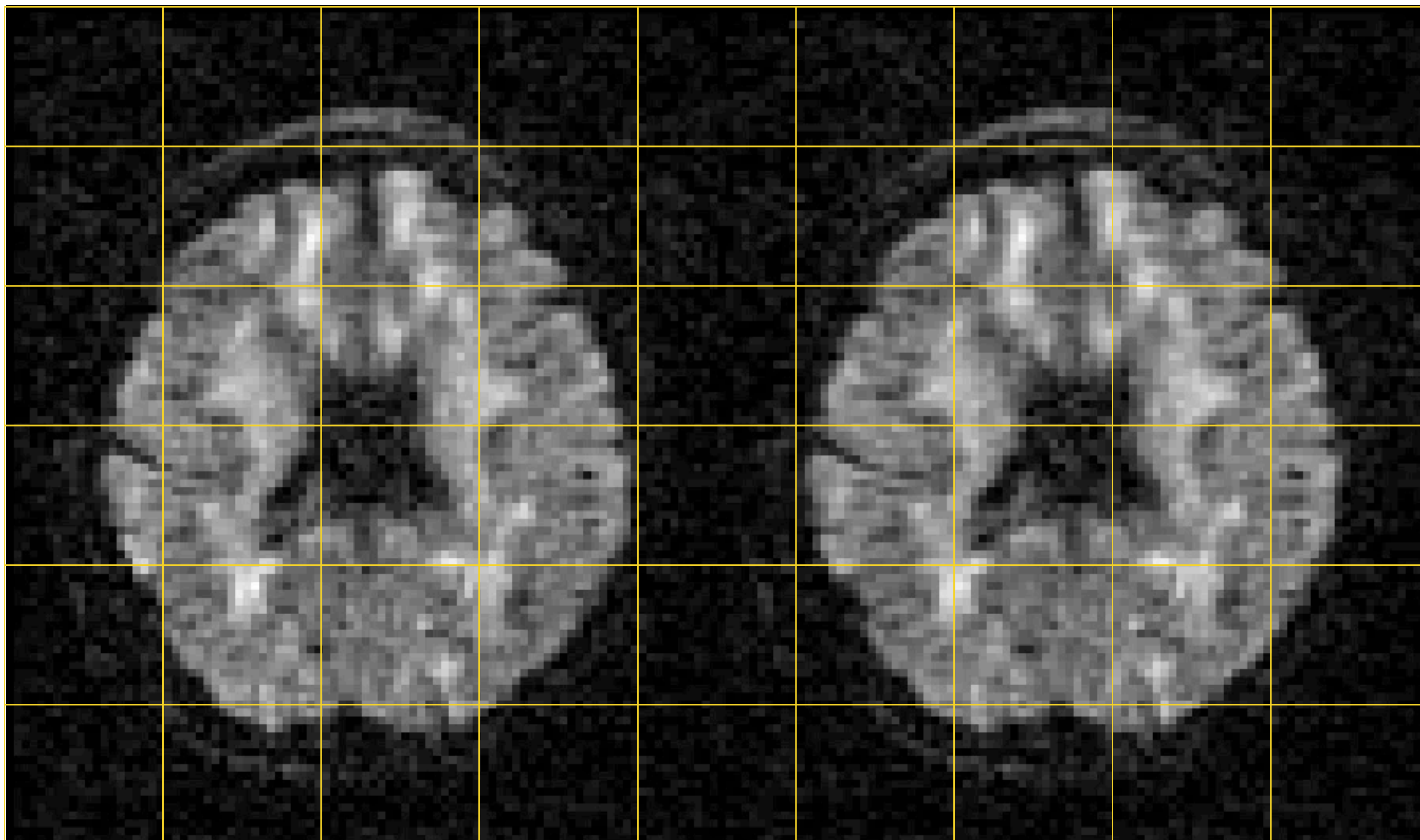


Outline of the talk

- What is the problem with diffusion data?
- Off-resonance field
 - How does it cause distortions?
 - Where does it come from?
- Registering diffusion data
 - How topup works
 - How eddy works
- Practicalities
- **Some results**
- Quality control
- New eddy features

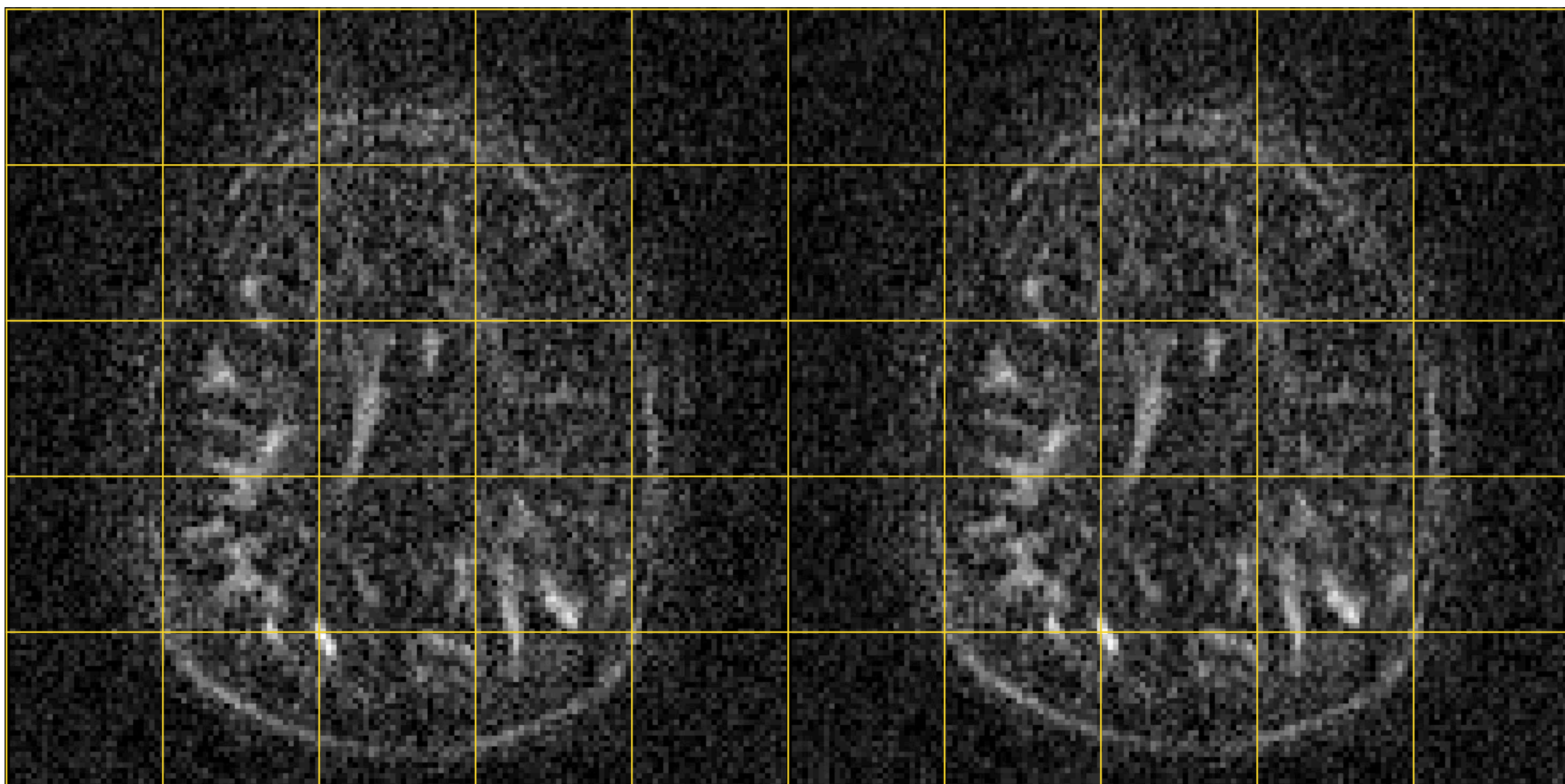


HCP-data, 150 directions, b=3000, blip-up-blip-down



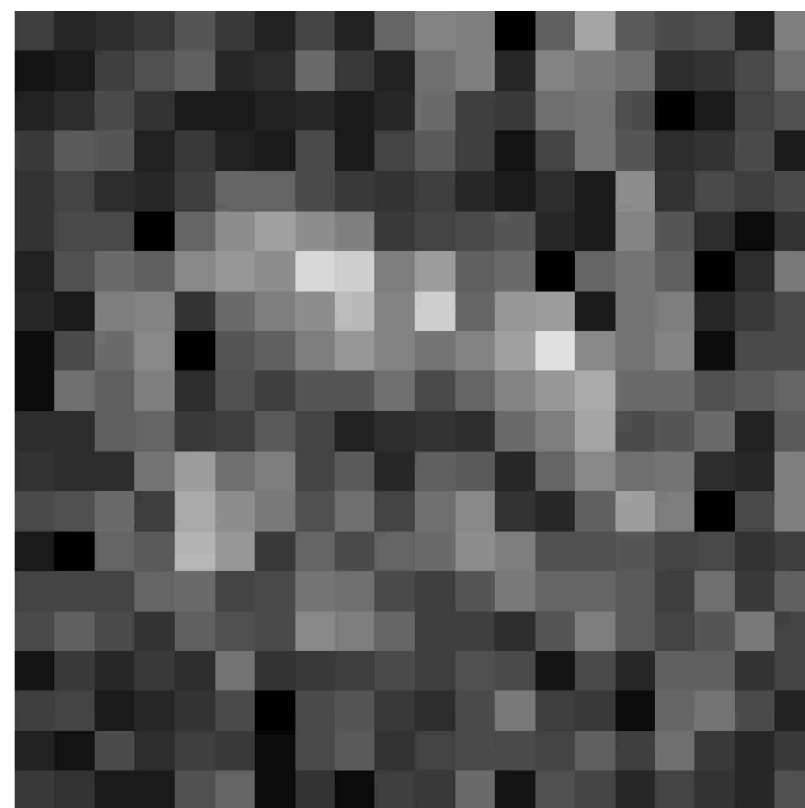
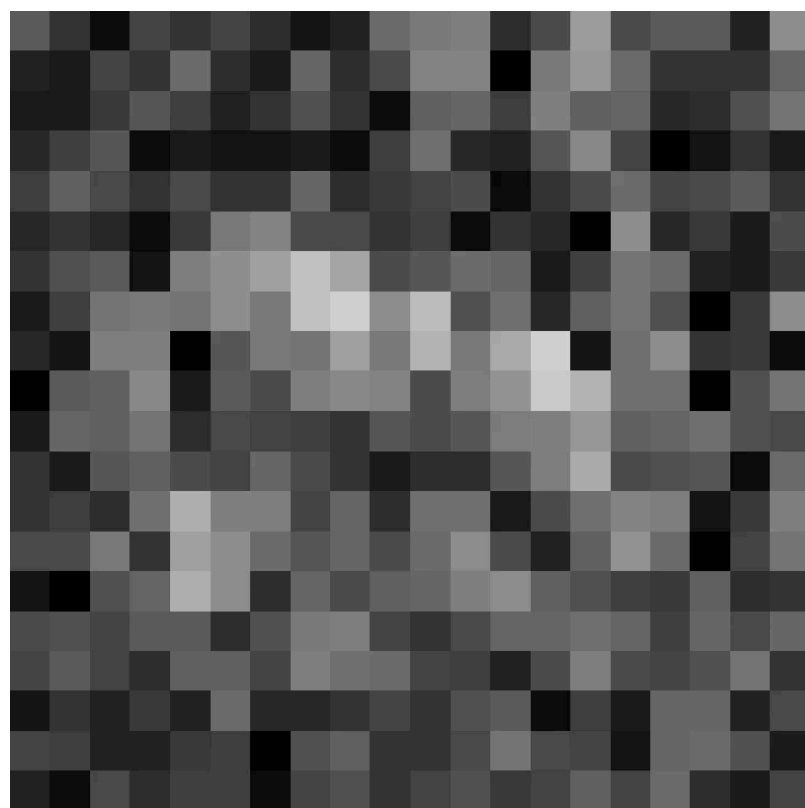
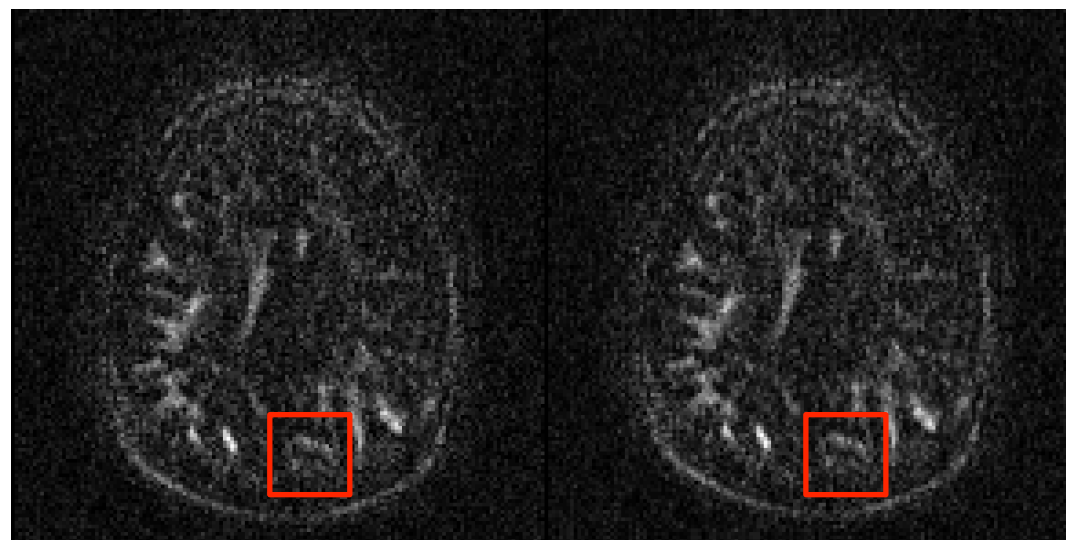


MGH-data, 198 directions, b=10000!





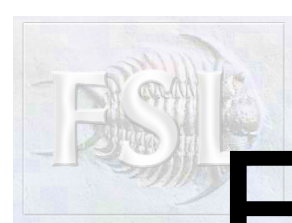
MGH-data, 198 directions, $b=10000!$





Outline of the talk

- What is the problem with diffusion data?
- Off-resonance field
 - How does it cause distortions?
 - Where does it come from?
- Registering diffusion data
 - How topup works
 - How eddy works
- Practicalities
- Some results
- **Quality control**
- New eddy features



EDDY QC: data quality summary

QUAD
(subject)

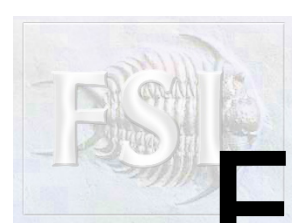
 S1/qc.json
 S2/qc.json
 S3/qc.json
.
.
.
 S_n/qc.json

SQUAD
(study)

 qc_group.pdf

 qc_group.json

 P1/qc.json
 P2/qc.json
 P3/qc.json
...



EDDY QC: single-subject reports

Biobank subject A

Volume-to-volume motion

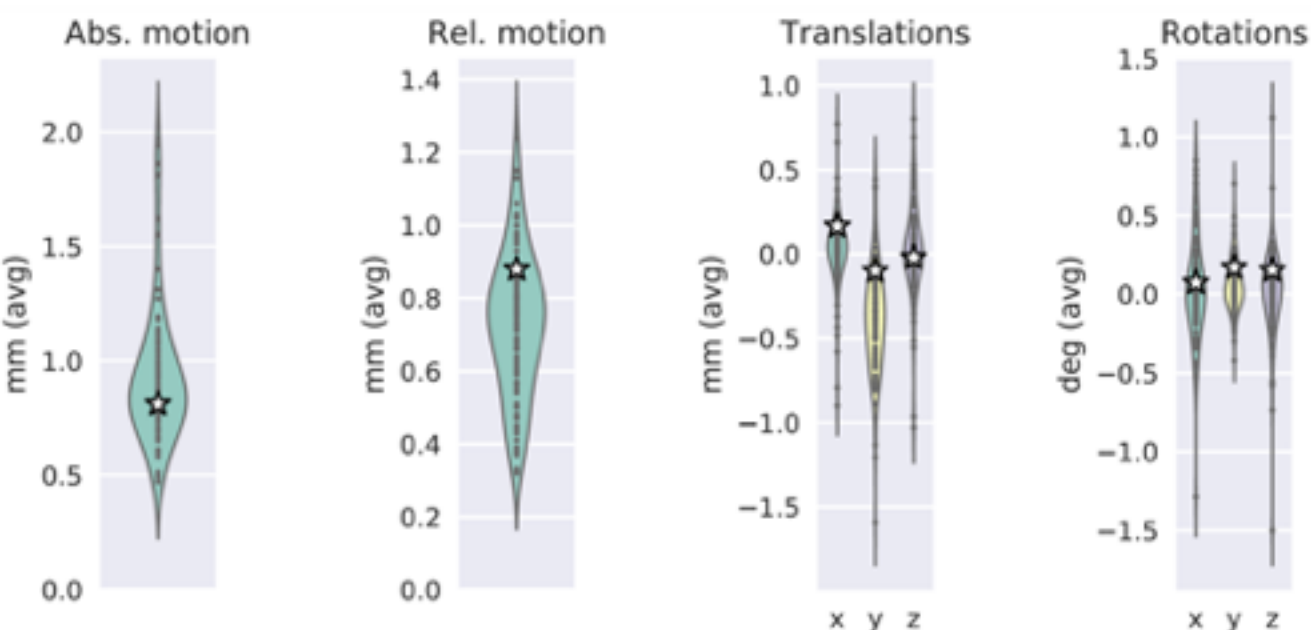
Average abs. motion (mm)	0.81
Average rel. motion (mm)	0.88
Average x translation (mm)	0.17
Average y translation (mm)	-0.10
Average z translation (mm)	-0.02
Average x rotation (deg)	0.07
Average y rotation (deg)	0.17
Average z rotation (deg)	0.15

Within-volume motion

Avg std x translation (mm)	0.02
Avg std y translation (mm)	0.11
Avg std z translation (mm)	0.04
Avg std x rotation (deg)	0.05
Avg std y rotation (deg)	0.05
Avg std z rotation (deg)	0.06

Outliers

Total outliers (%)	0.11
Outliers (b=1000 s/mm ²)	0.22
Outliers (b=2000 s/mm ²)	0.00
Outliers (PE dir=[0. 1. 0.])	0.00
Outliers (PE dir=[0. -1. 0.])	0.11



Biobank subject B

Volume-to-volume motion

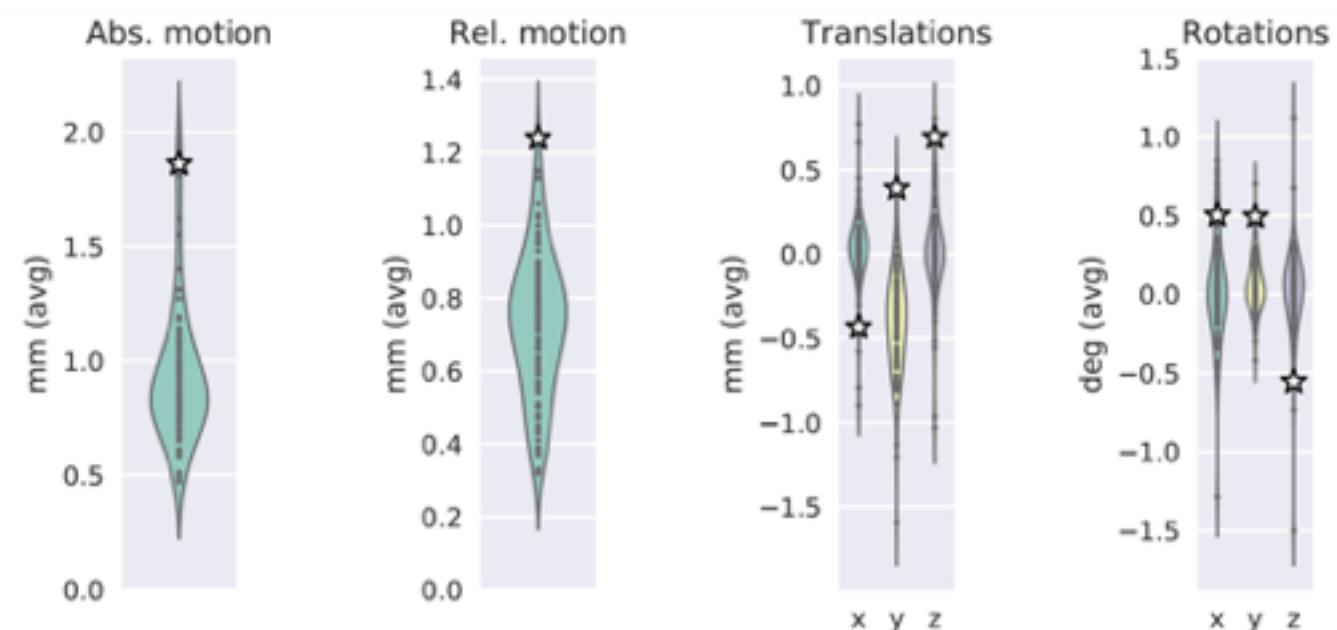
Average abs. motion (mm)	1.86
Average rel. motion (mm)	1.24
Average x translation (mm)	-0.43
Average y translation (mm)	0.39
Average z translation (mm)	0.69
Average x rotation (deg)	0.50
Average y rotation (deg)	0.49
Average z rotation (deg)	-0.55

Within-volume motion

Avg std x translation (mm)	0.08
Avg std y translation (mm)	0.22
Avg std z translation (mm)	0.13
Avg std x rotation (deg)	0.15
Avg std y rotation (deg)	0.09
Avg std z rotation (deg)	0.11

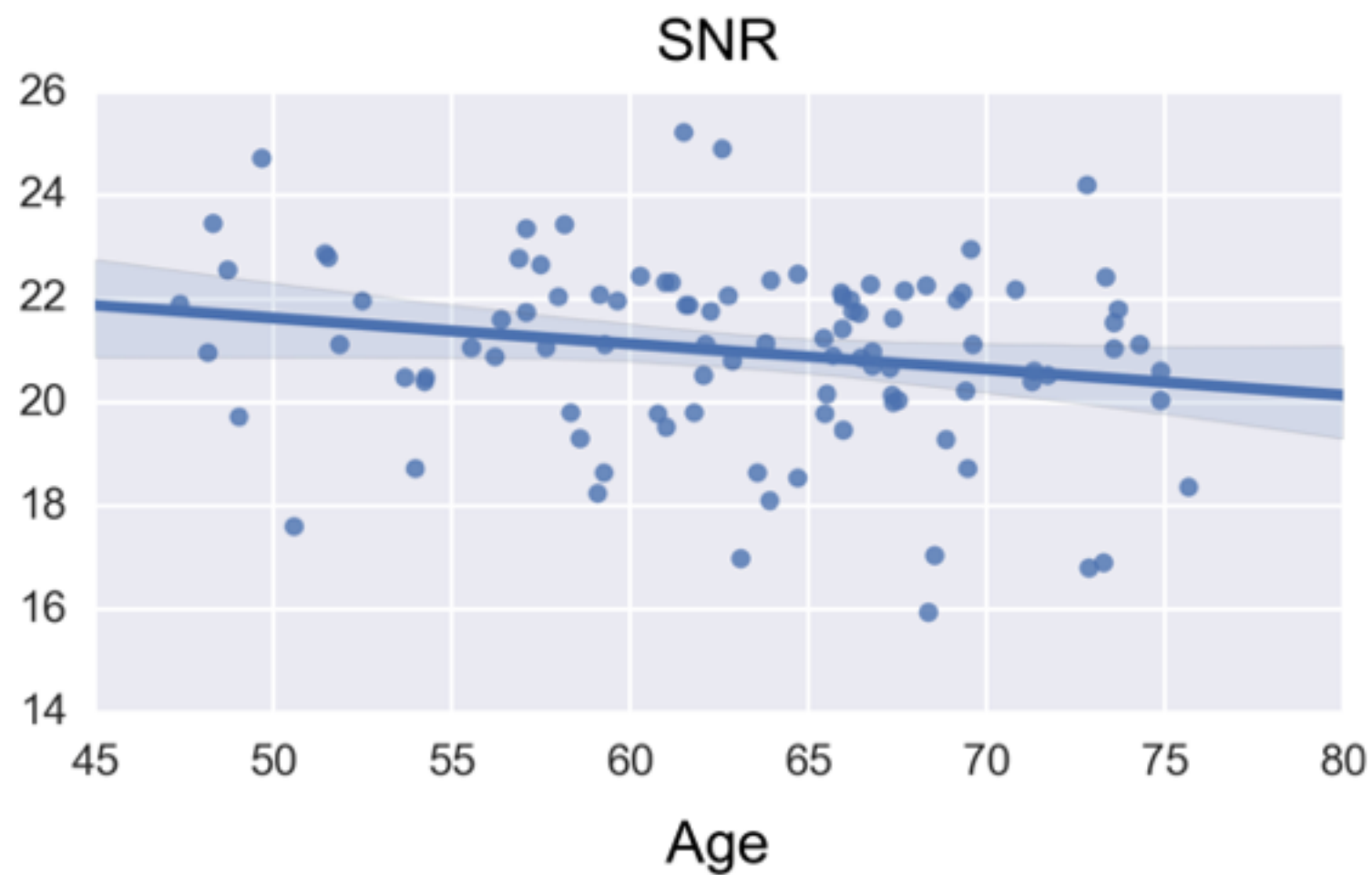
Outliers

Total outliers (%)	2.86
Outliers (b=1000 s/mm ²)	4.69
Outliers (b=2000 s/mm ²)	1.13
Outliers (PE dir=[0. 1. 0.])	2.55
Outliers (PE dir=[0. -1. 0.])	2.66



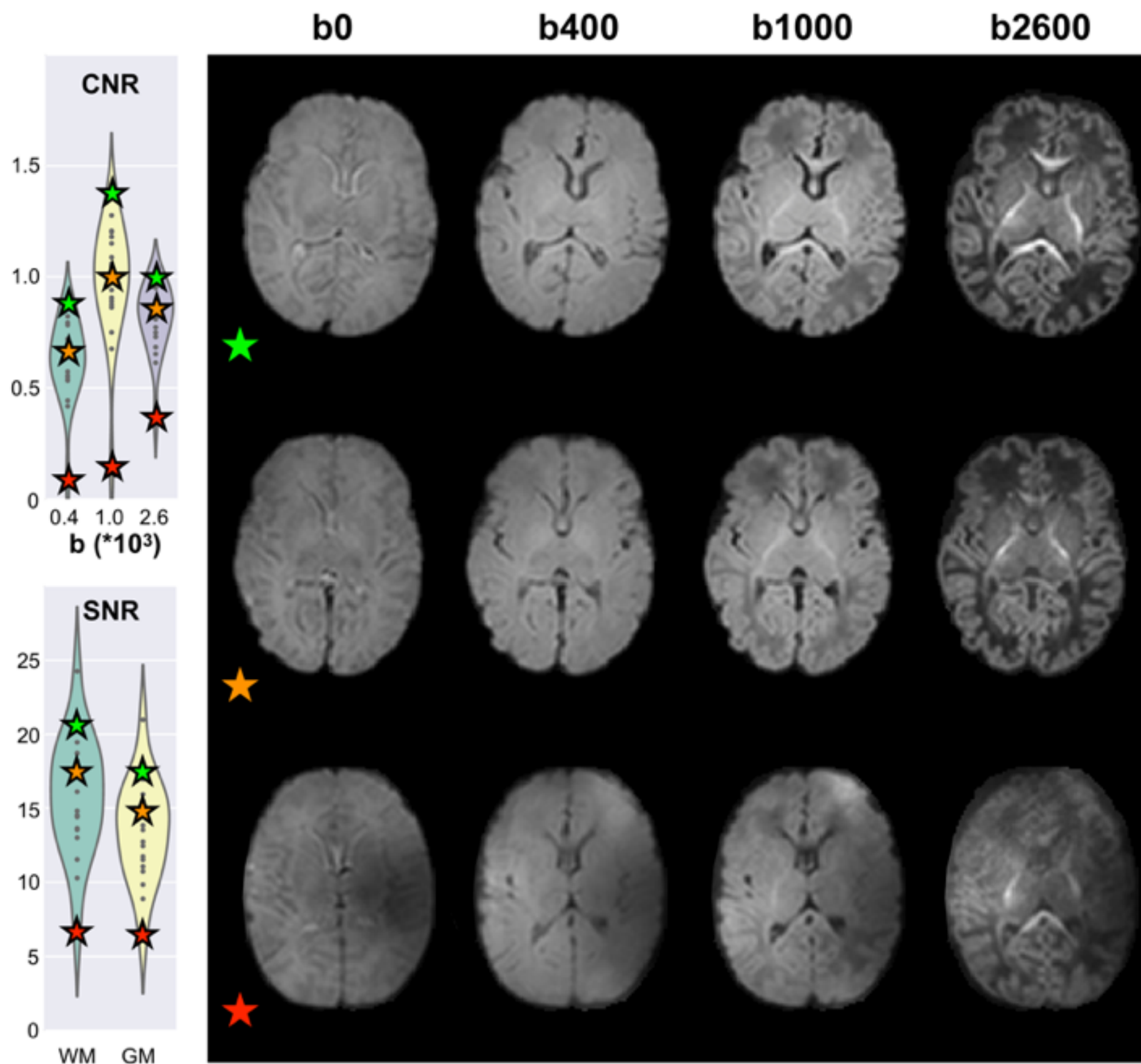


EDDY QC: group report





Data quality illustration





Outline of the talk

- What is the problem with diffusion data?
- Off-resonance field
- Registering diffusion data
- Practicalities
- Some results
- New eddy features
 - Movement-induced dropout
 - Intra-volume motion



Movement induced dropout

Diffusion encoding

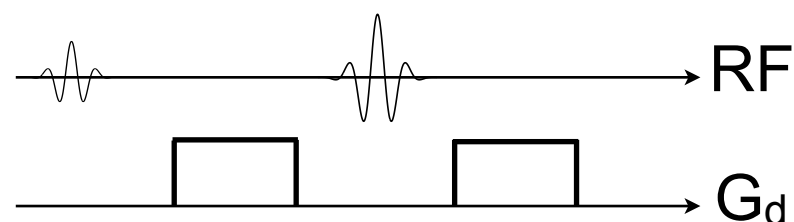
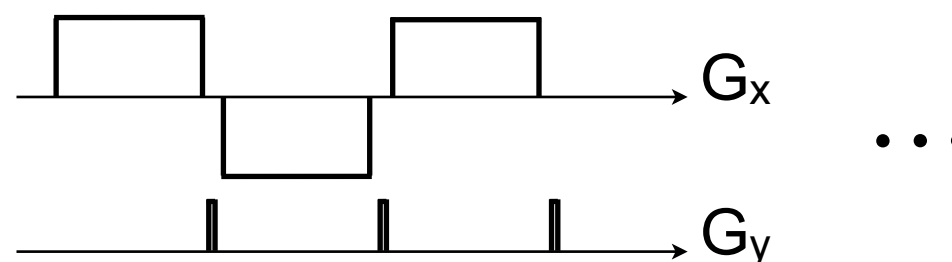
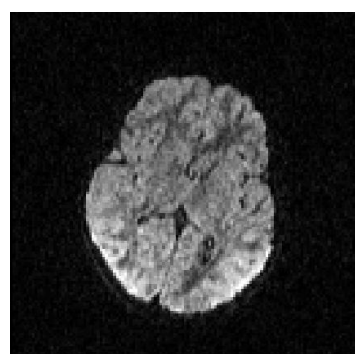


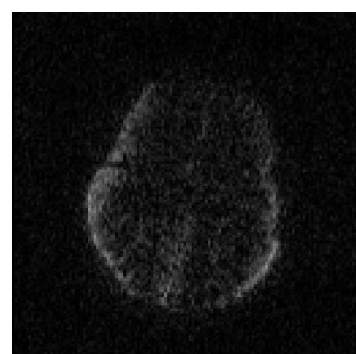
Image encoding



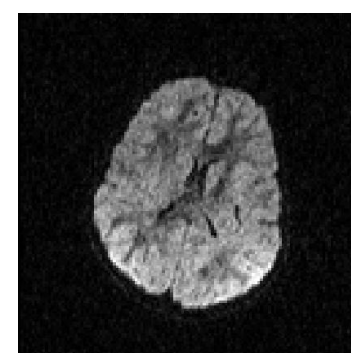
If there is movement during this part...



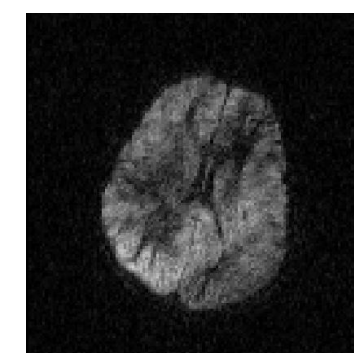
this



can turn
to this



or this

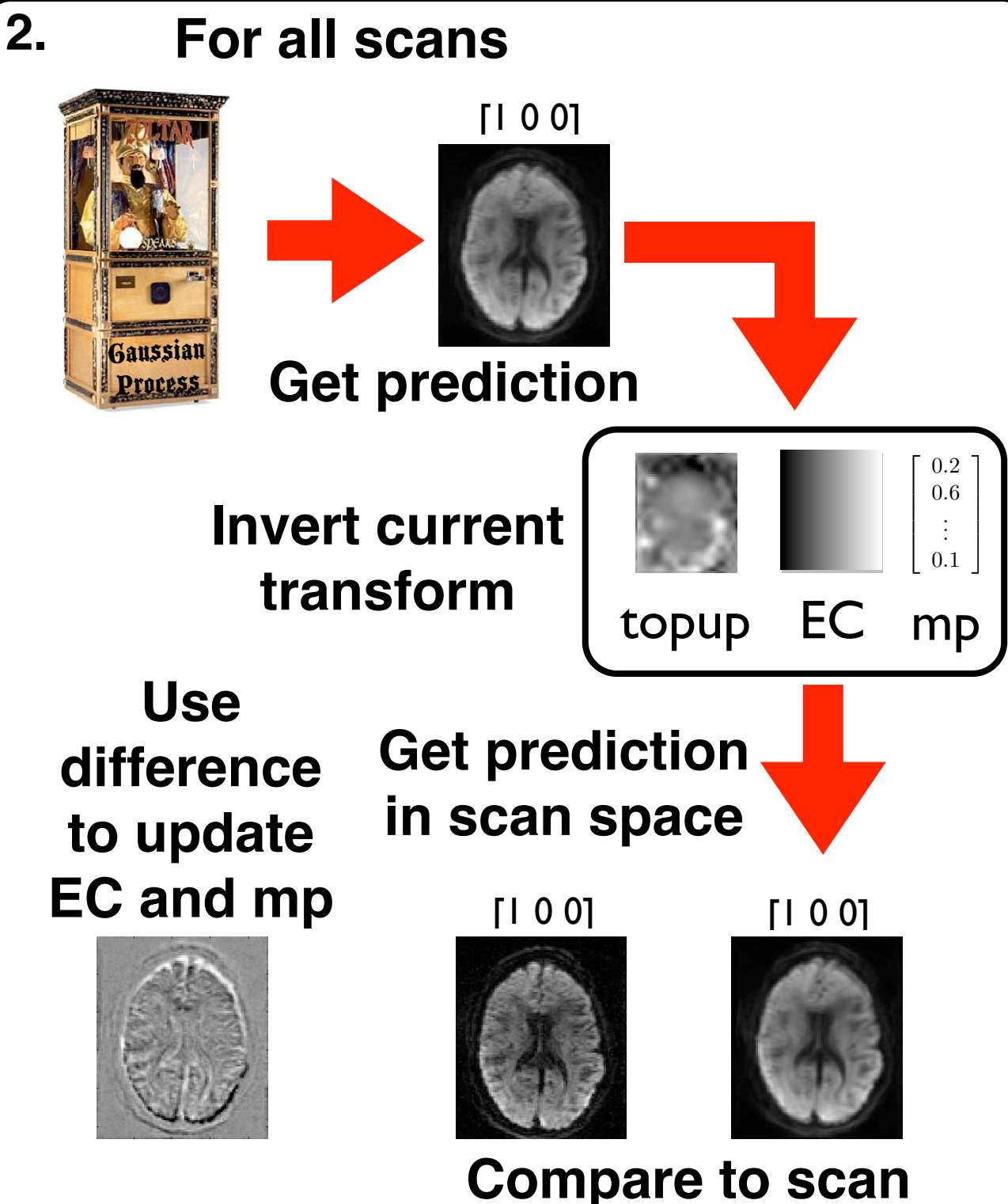
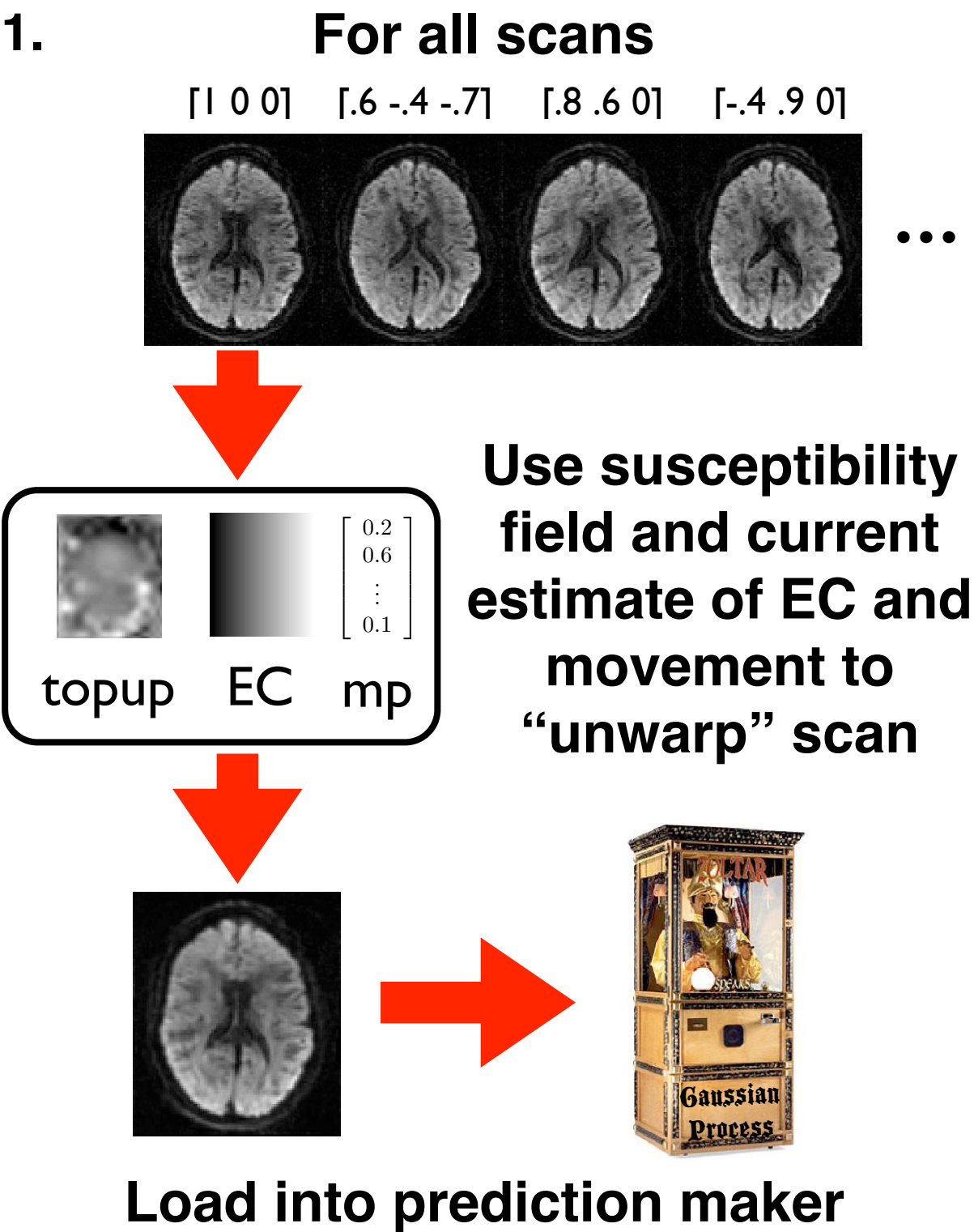


to this



What can eddy do about it?

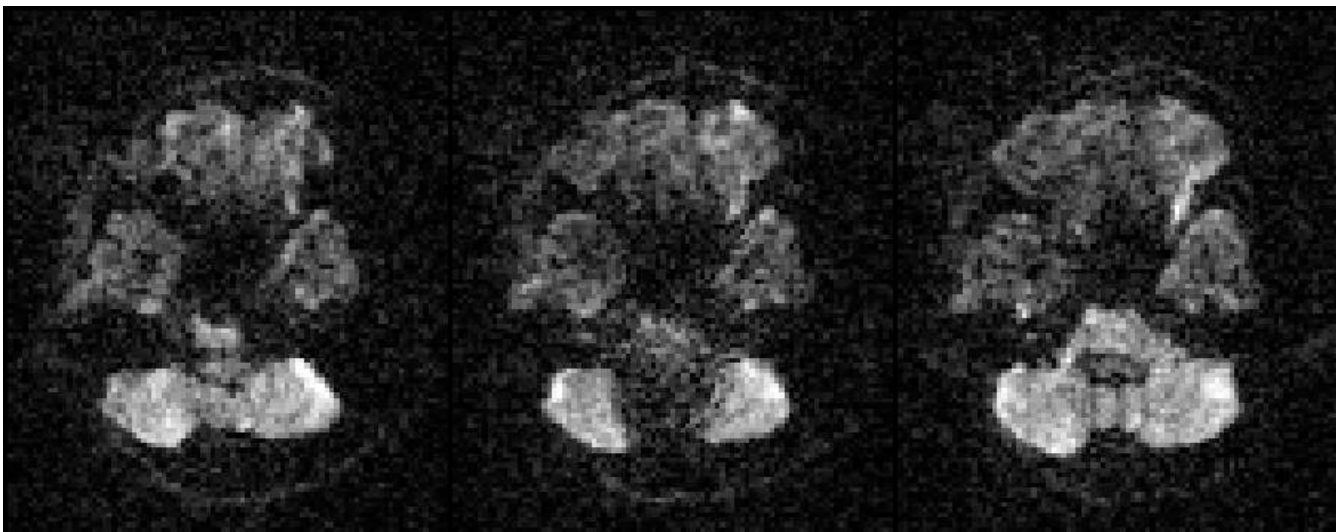
But first a little recap of eddy



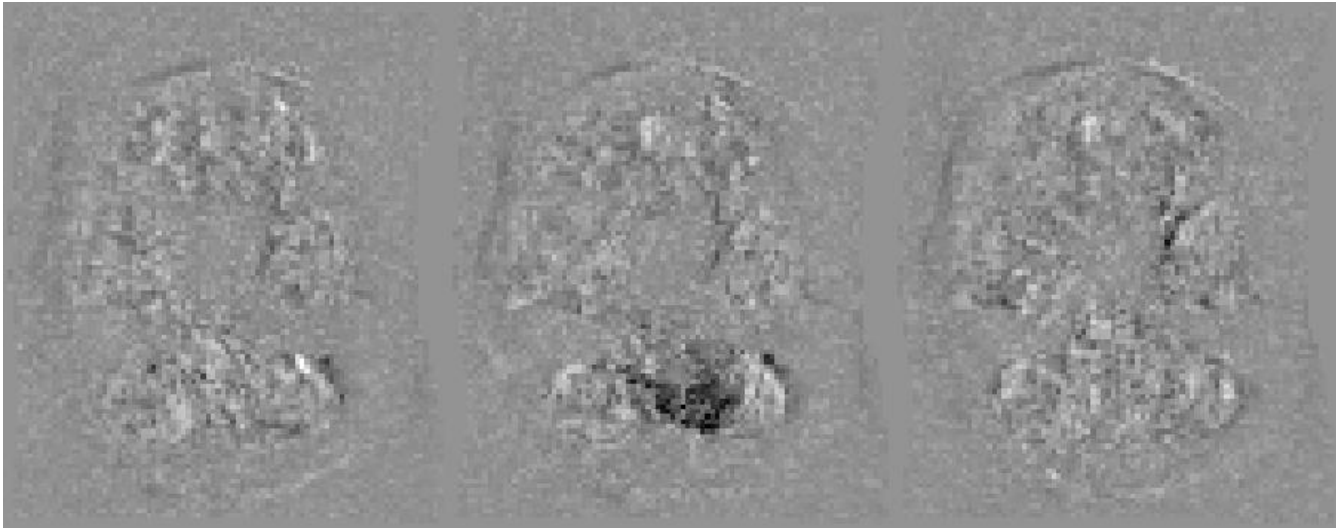


Outlier detection

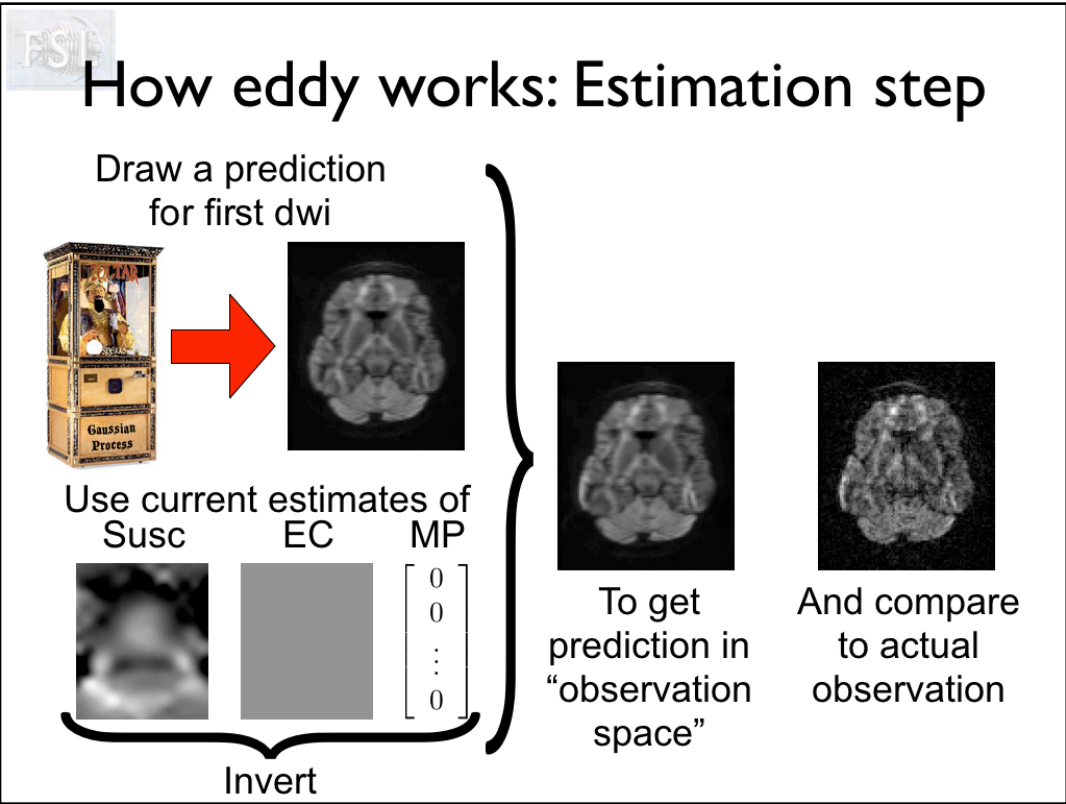
Observed data



Observed - predicted



$\bar{x} = 0.084$ $\bar{x} = -0.791$ $\bar{x} = -0.125$

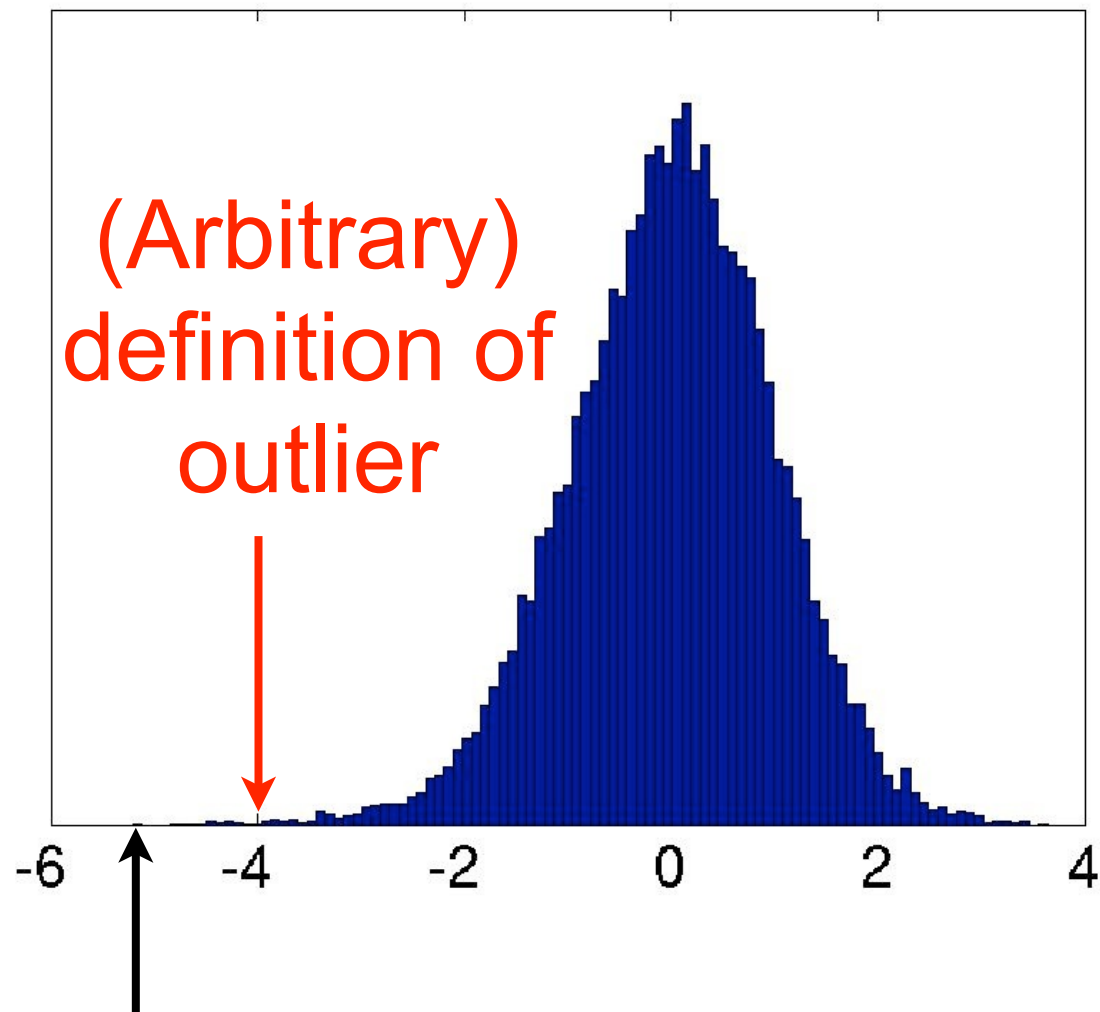


Remember that we do all comparisons in observation space.

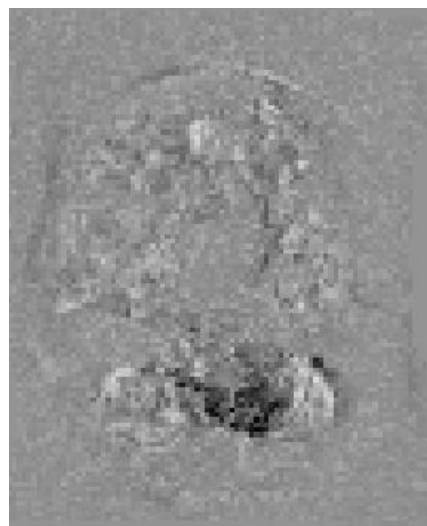
This allows us to calculate the per-slice mean difference between observation and prediction



Outlier detection



We can calculate the mean difference for every slice in every volume and get an empirical distribution that we can convert to z-scores

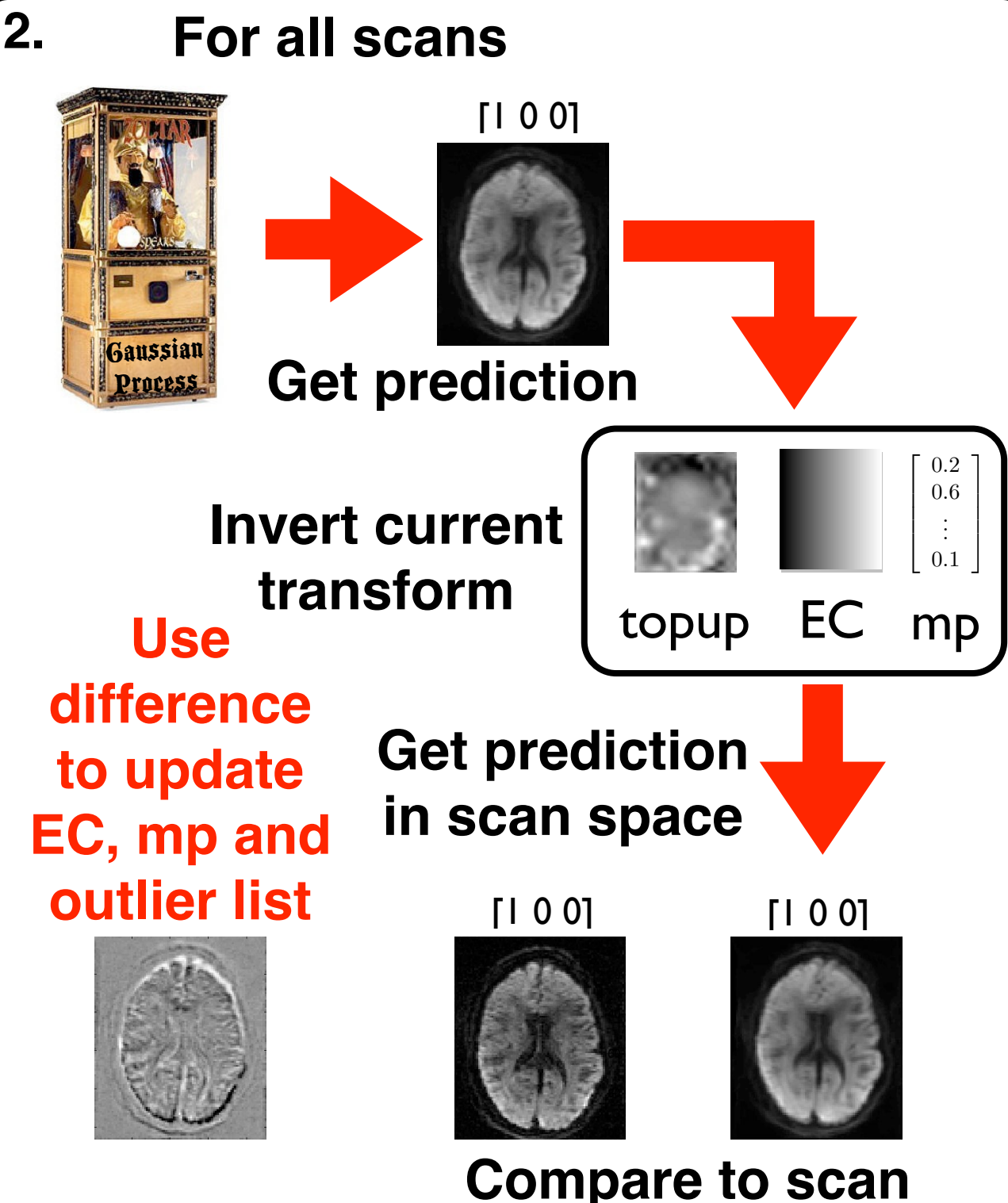
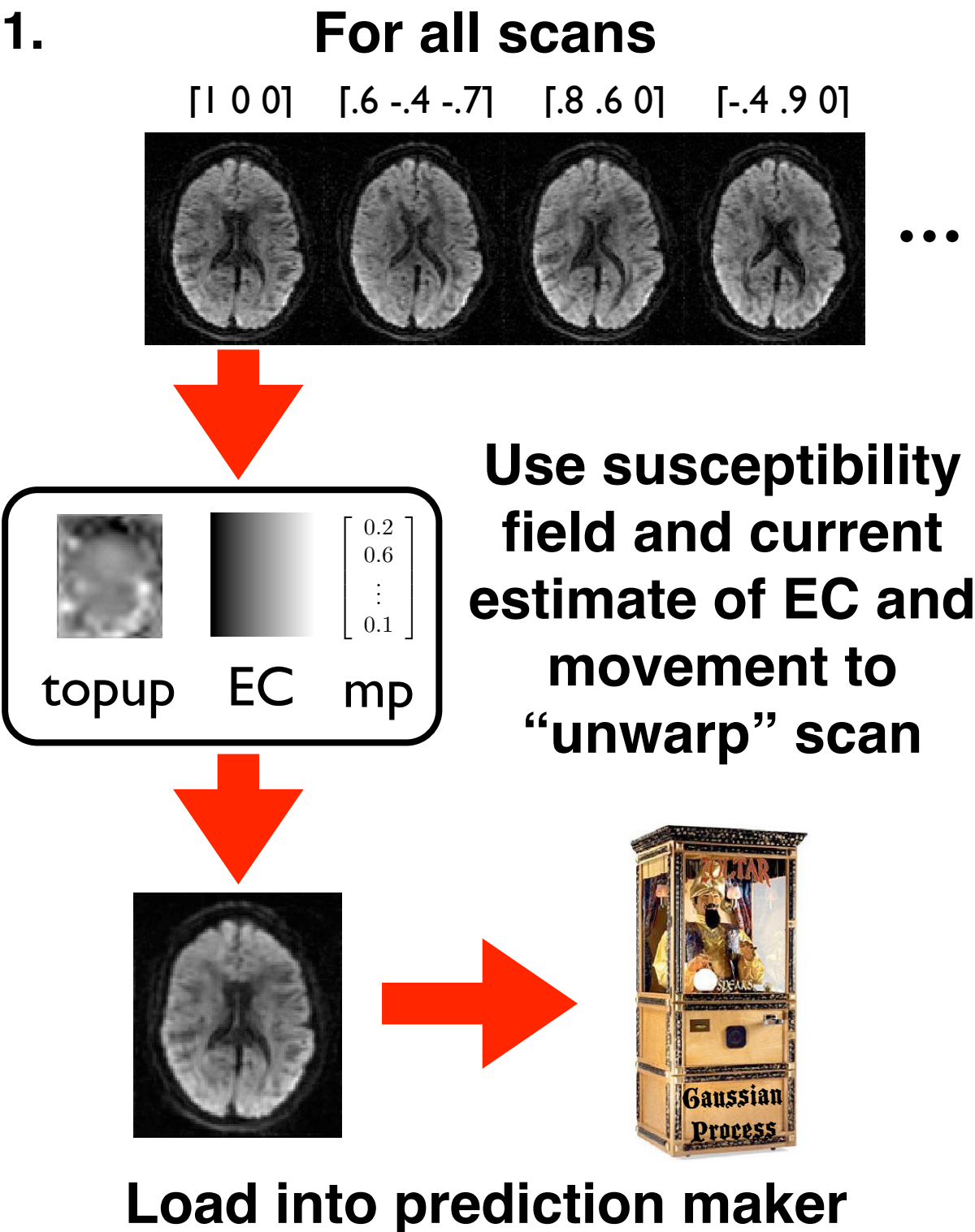


We can define an outlier slice as one with a z-score above an (arbitrary) threshold. We then have a choice of reporting outliers and/or replacing them with their predictions.

Worst slice

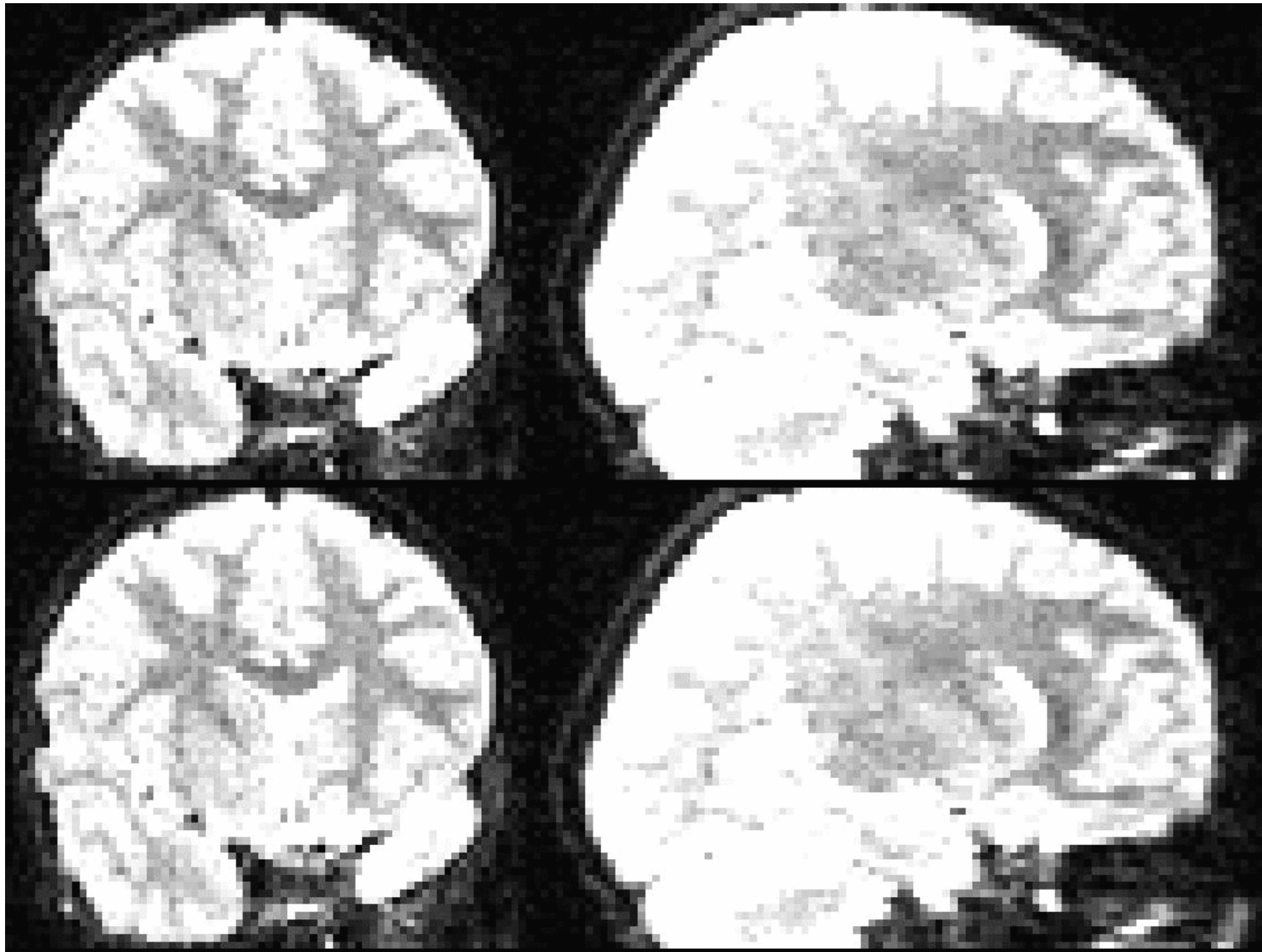


eddy revisited





Norwegian data. 32 directions. Hundreds of children.



Eight year
old who gets
tired towards
the end of
scanning

After outlier
detection
and
replacement
by eddy



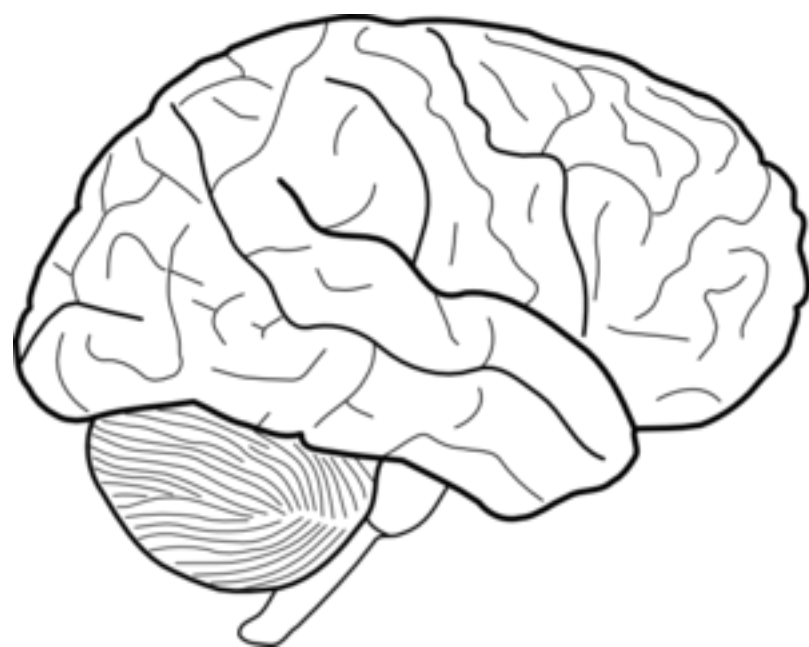
Outline of the talk

- What is the problem with diffusion data?
- Off-resonance field
- Registering diffusion data
- Practicalities
- Some results
- New eddy features
 - Movement-induced dropout
 - Intra-volume motion



Intra-volume movement

One of the (possibly naive) assumptions of most movement correction is that any movement is instantaneous and occurs between the acquisition of consecutive volumes.

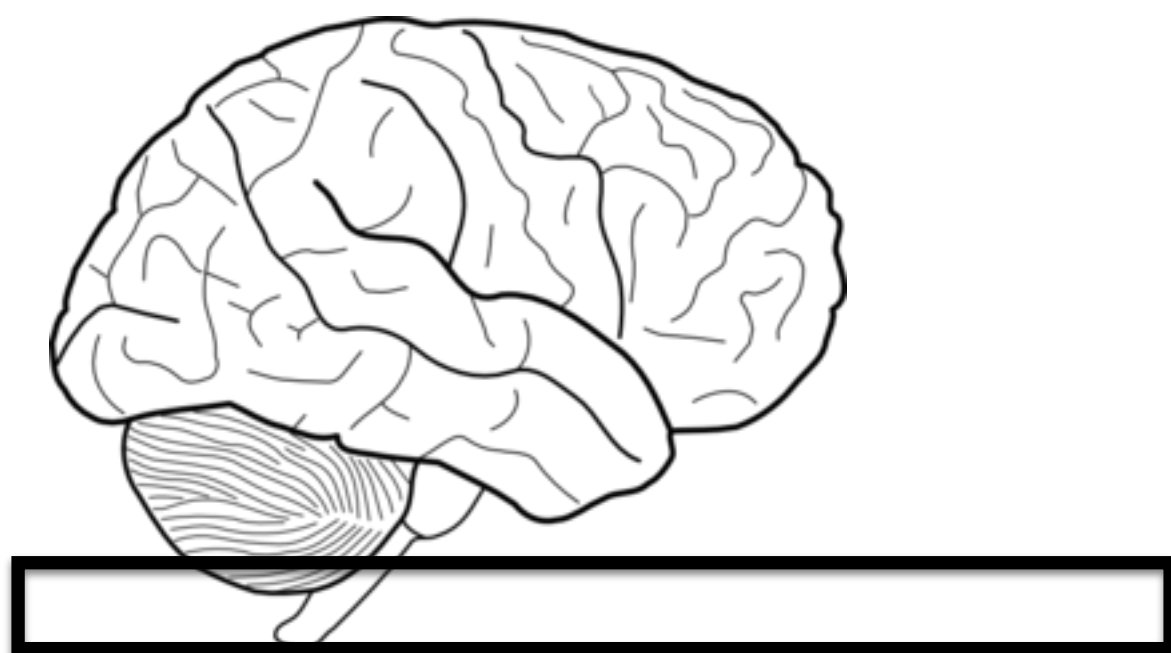


This is the brain
we set out to
image



Intra-volume movement

One of the (possibly naive) assumptions of most movement correction is that any movement is instantaneous and occurs between the acquisition of consecutive volumes.



This is the brain
we set out to
image



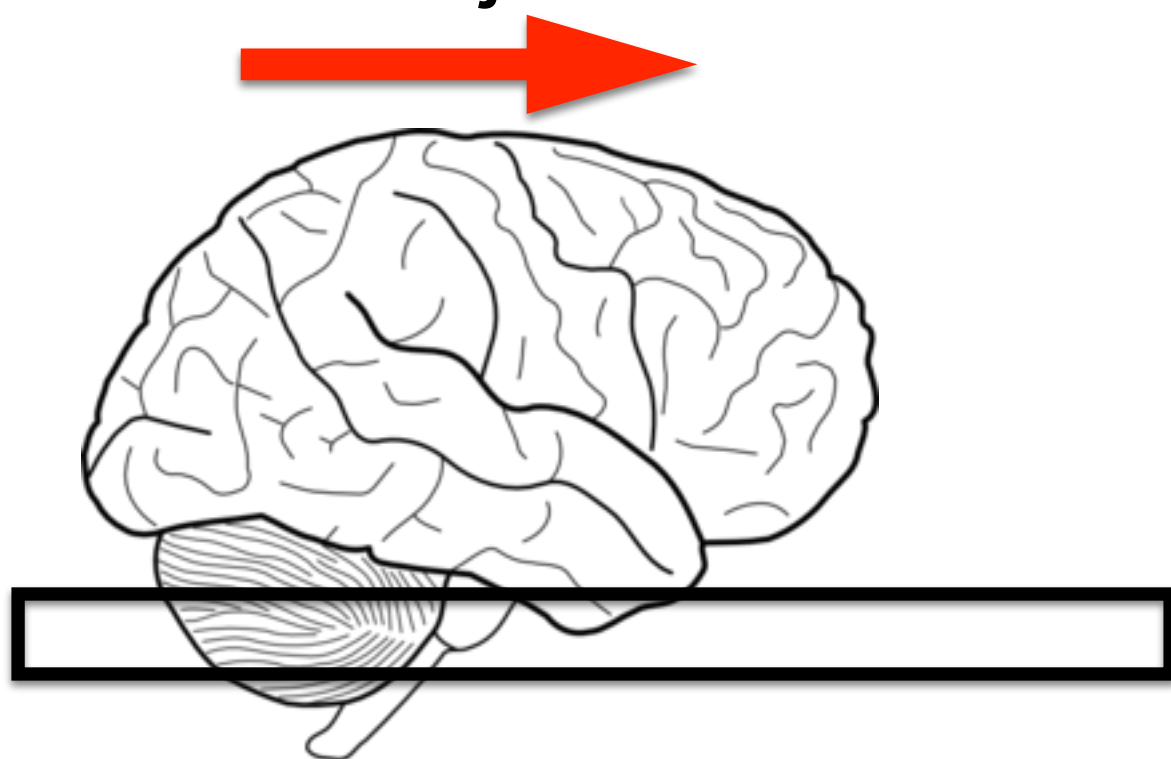
And here we have
acquired the first
slice



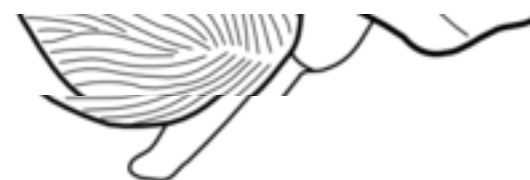
Intra-volume movement

One of the (possibly naive) assumptions of most movement correction is that any movement is instantaneous and occurs between the acquisition of consecutive volumes.

But the subject moves



This is the brain
we set out to
image



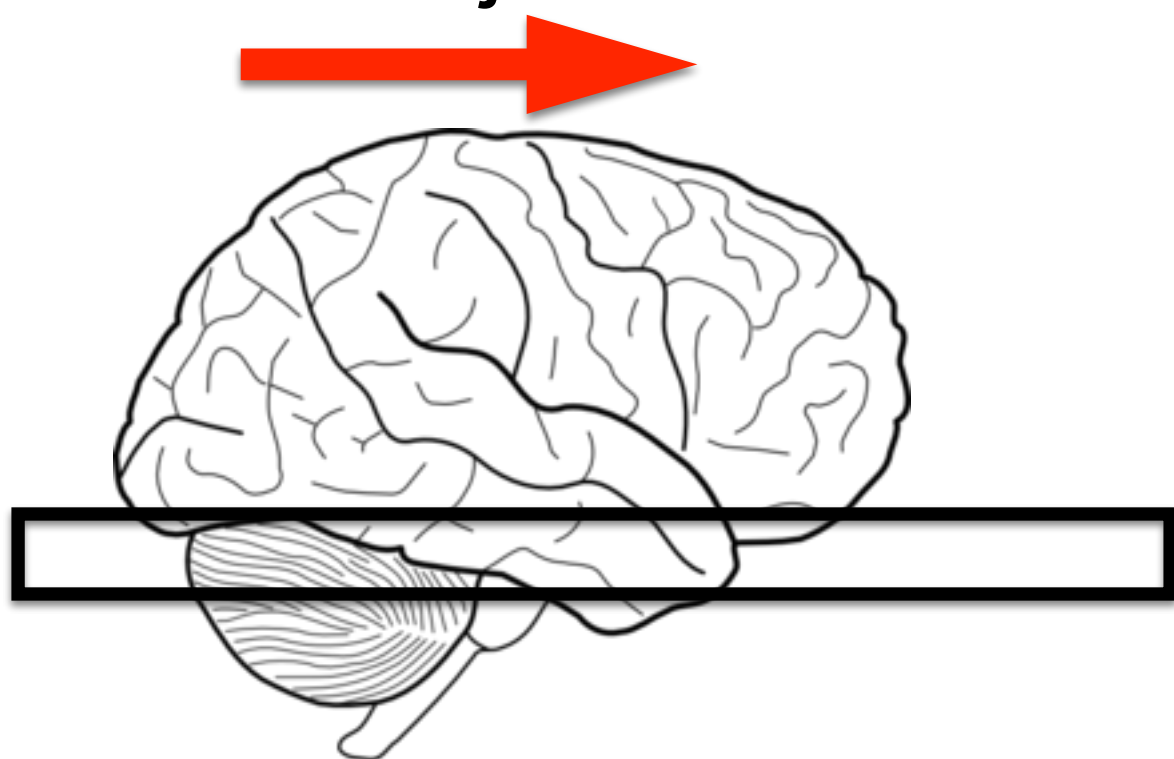
So the brain is
offset in the
second slice



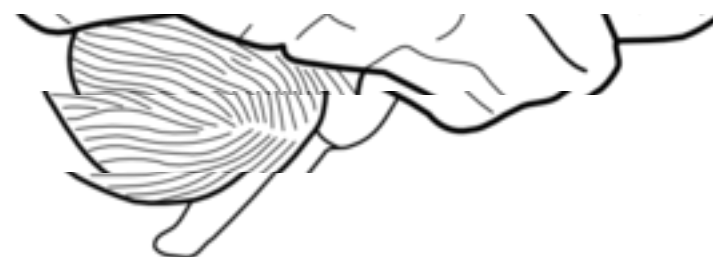
Intra-volume movement

One of the (possibly naive) assumptions of most movement correction is that any movement is instantaneous and occurs between the acquisition of consecutive volumes.

But the subject moves



This is the brain
we set out to
image



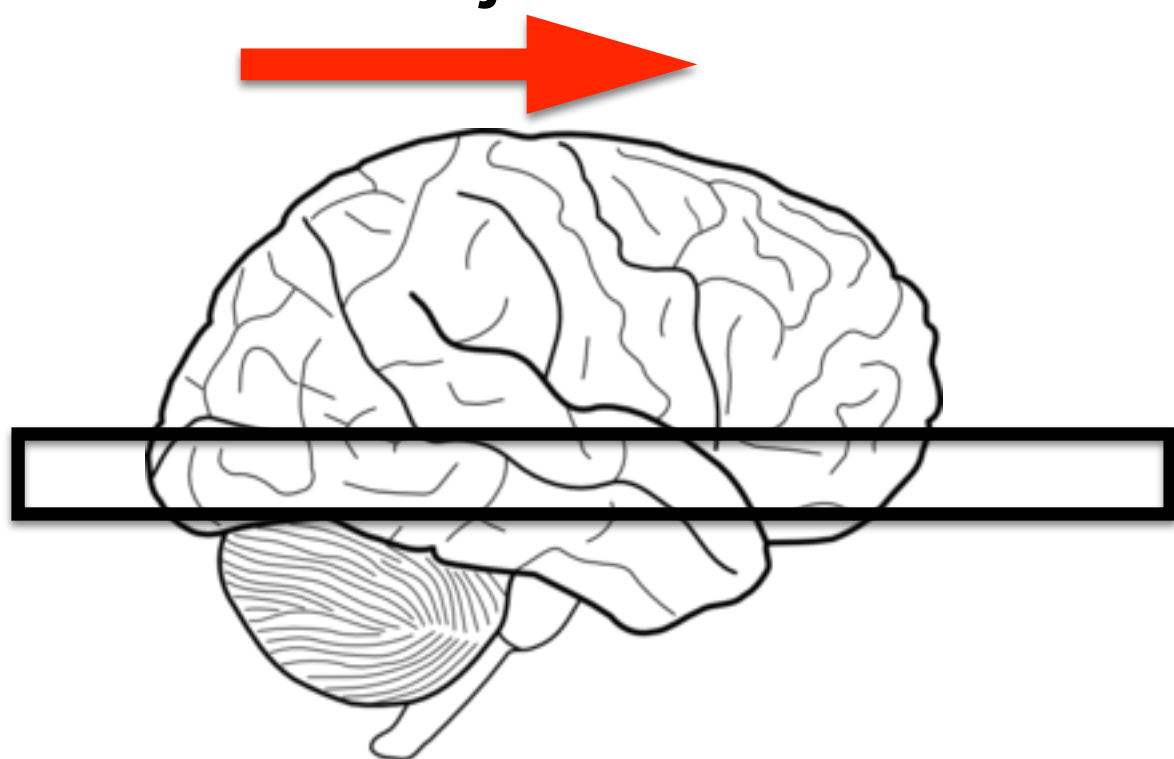
And even more so
in the third slice



Intra-volume movement

One of the (possibly naive) assumptions of most movement correction is that any movement is instantaneous and occurs between the acquisition of consecutive volumes.

But the subject moves



This is the brain
we set out to
image



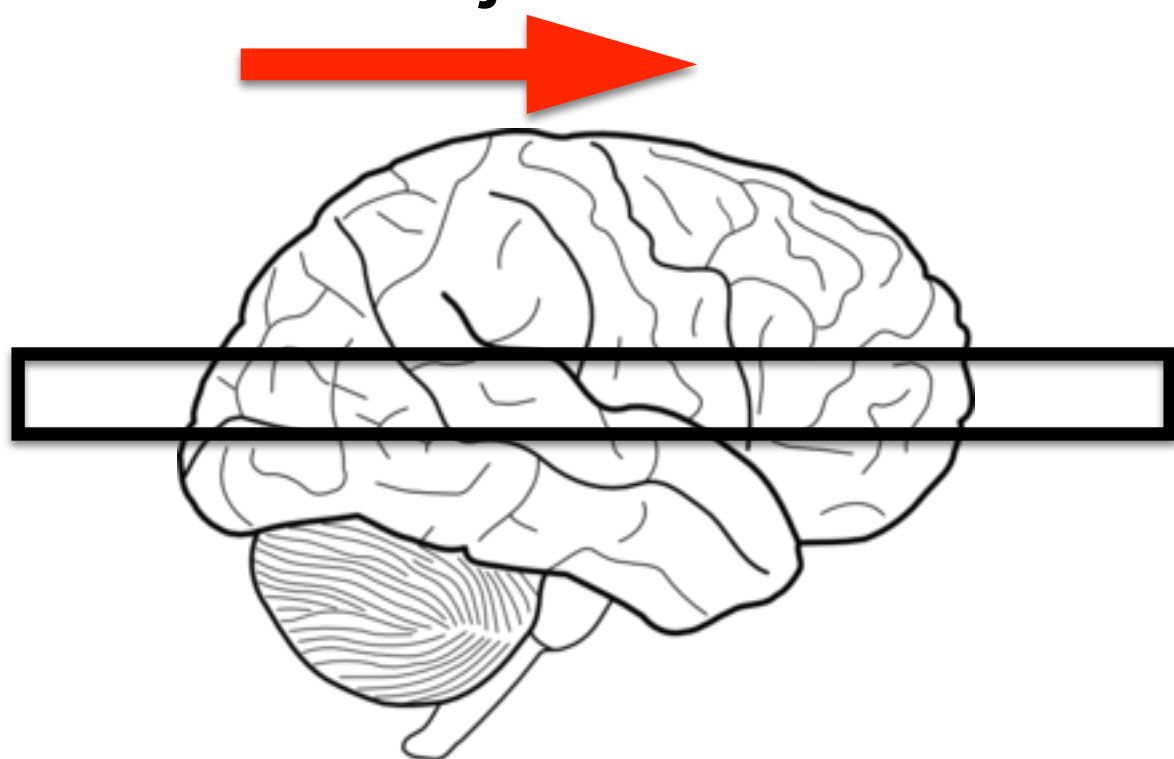
And more ...



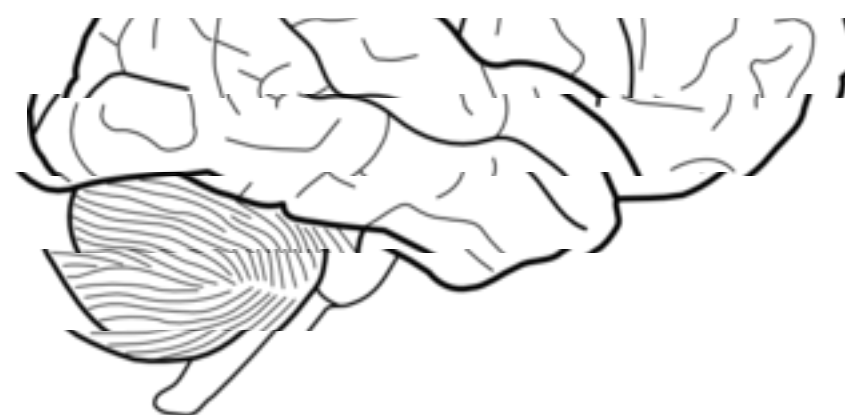
Intra-volume movement

One of the (possibly naive) assumptions of most movement correction is that any movement is instantaneous and occurs between the acquisition of consecutive volumes.

But the subject moves



This is the brain
we set out to
image

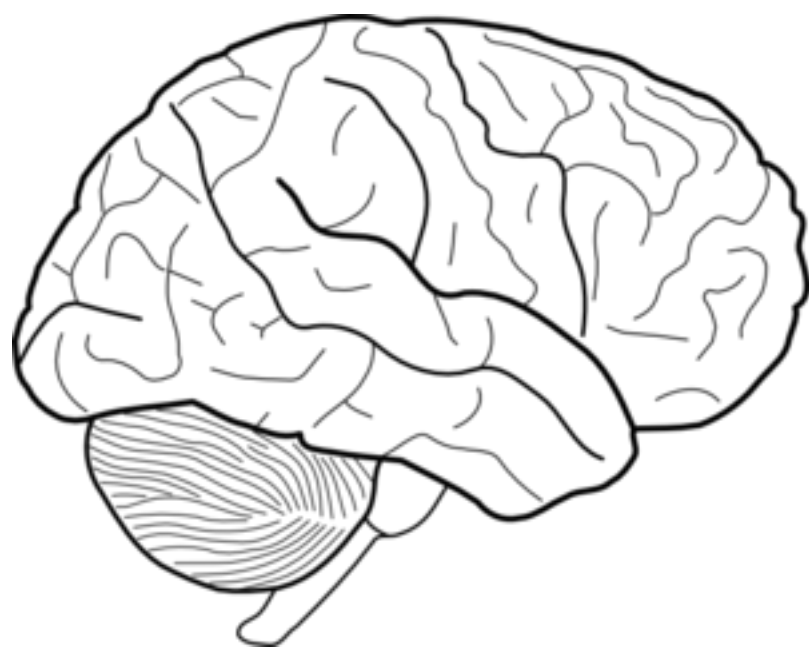


... and more ...

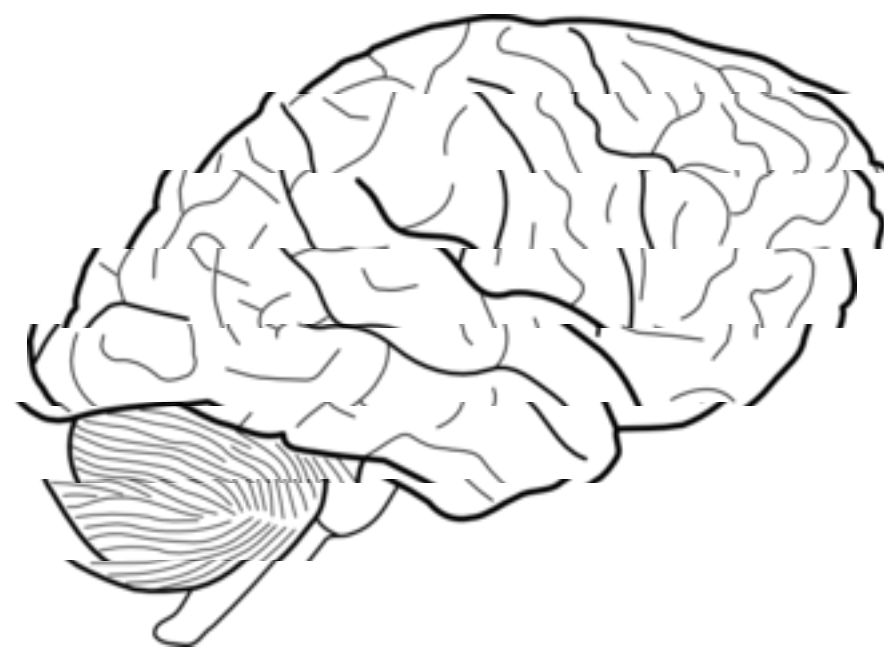


Intra-volume movement

One of the (possibly naive) assumptions of most movement correction is that any movement is instantaneous and occurs between the acquisition of consecutive volumes.



This is the brain
we set out to
image

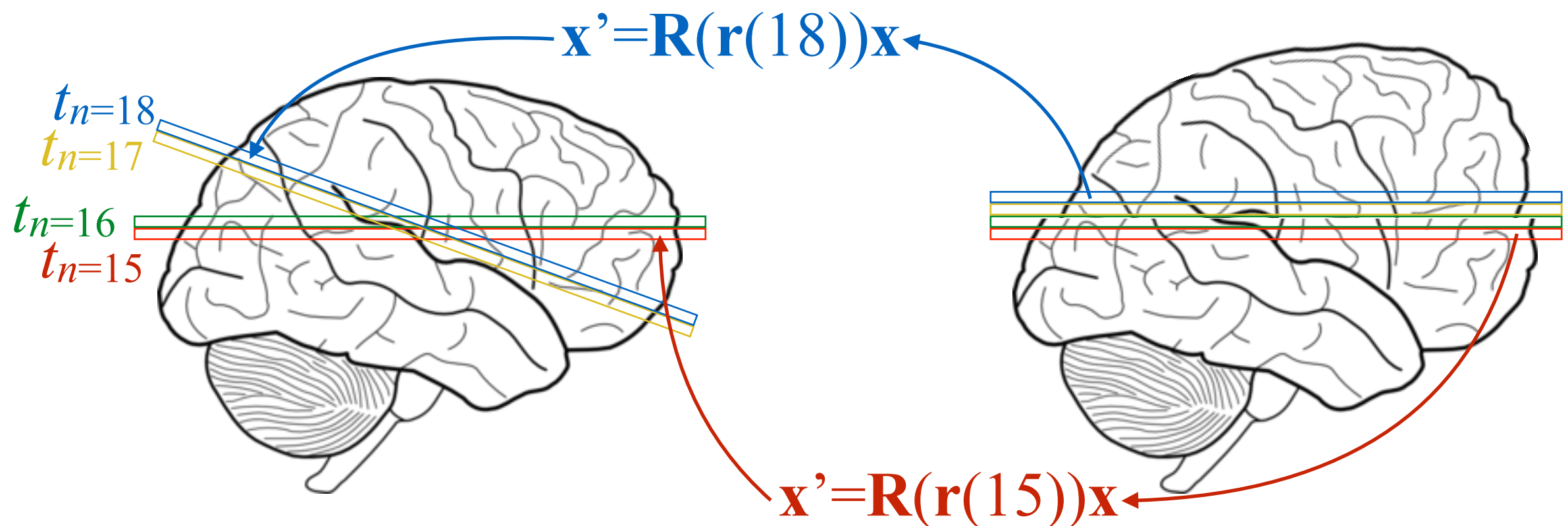


etc.



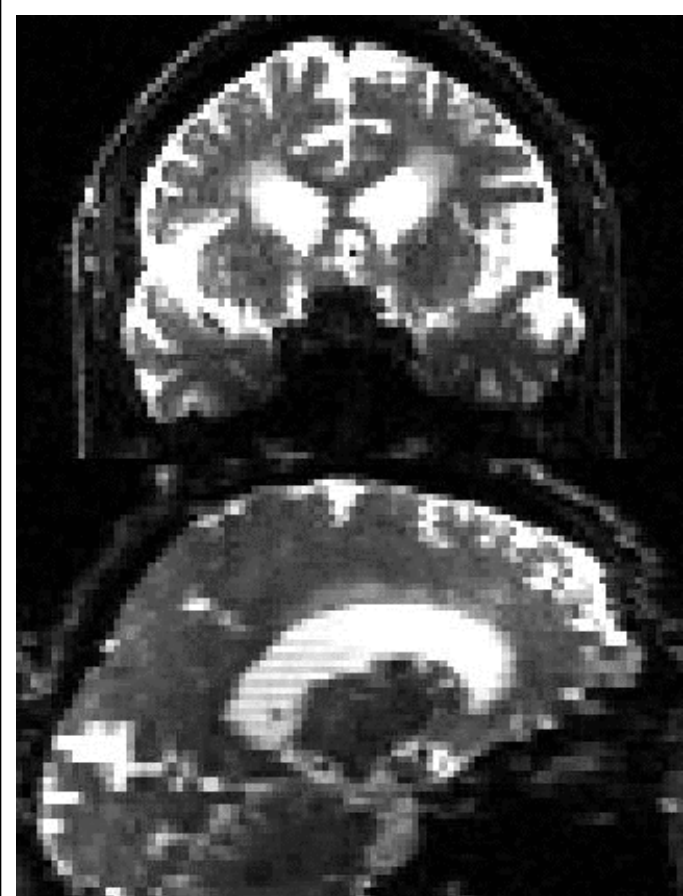
Intra-volume movement

- This is known as the “slice-to-vol” problem or the “intra-volume movement” problem.
- The new version of eddy addresses this problem.
- It estimates the slice wise movement through the same Gaussian Process based forward model.





Intra-volume movement

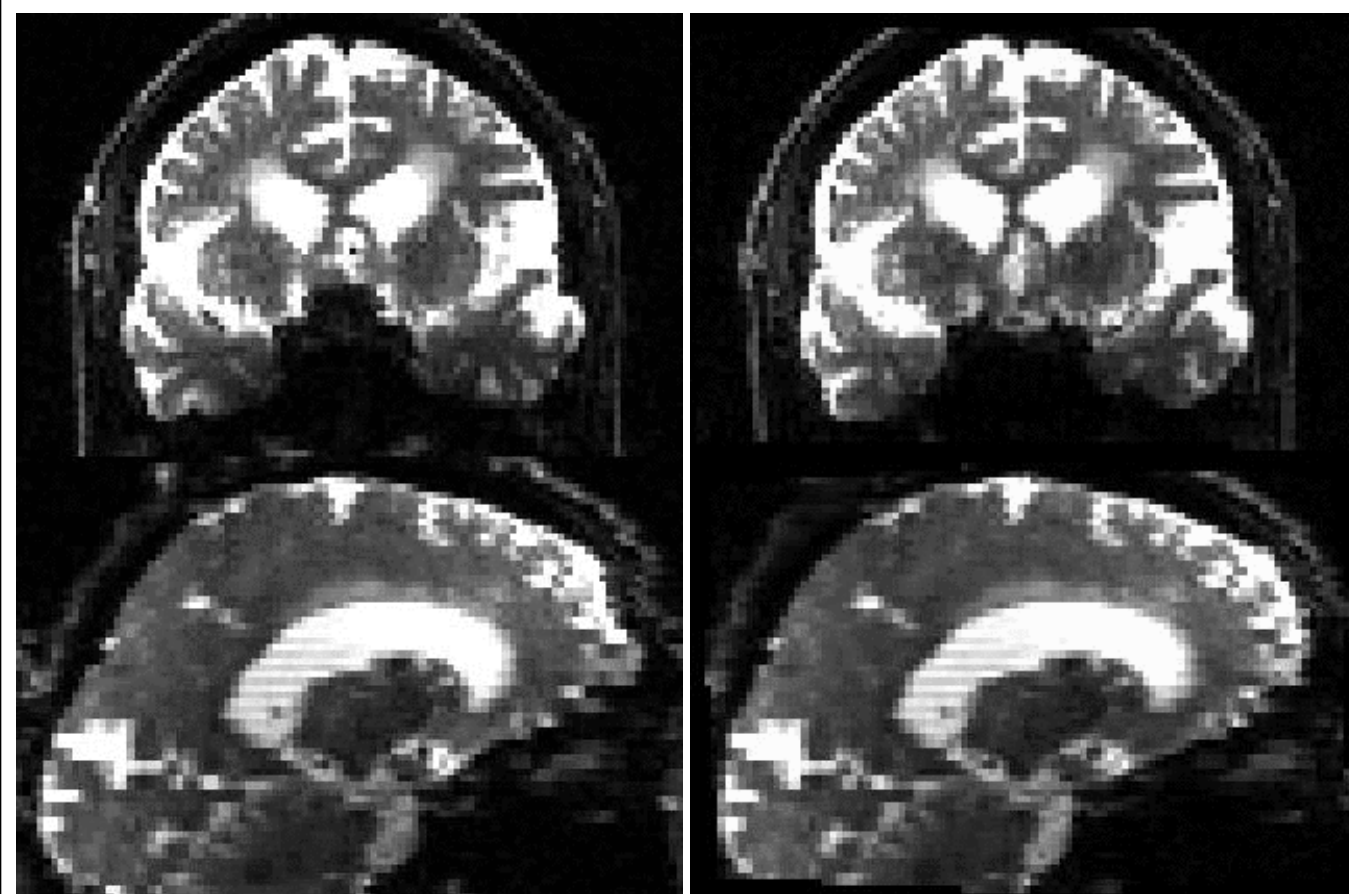


Original data

Problematic elderly subject. Lots of movement induced signal loss and intravolume movement



Intra-volume movement



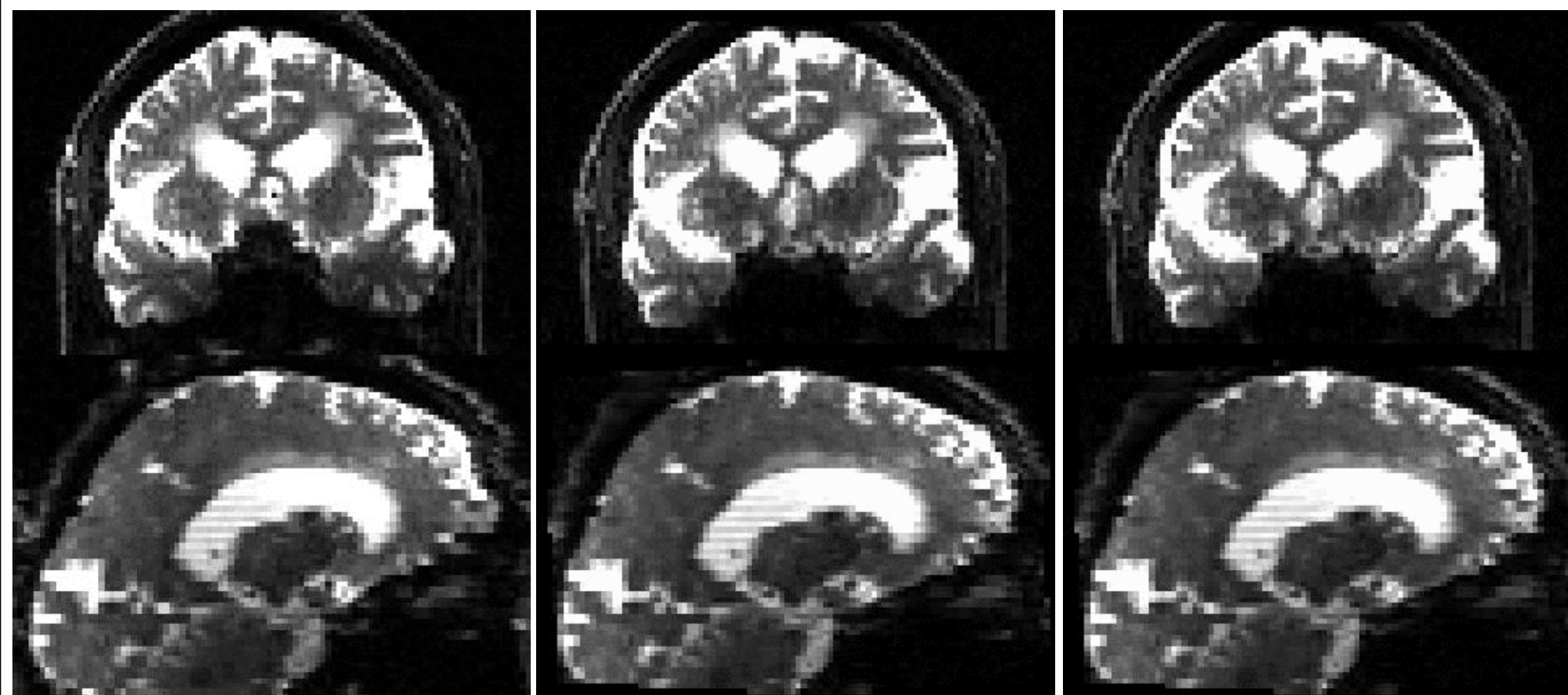
Original data

After correction
without outlier
correction

Problematic elderly subject. Lots of movement induced signal loss and intravolume movement



Intra-volume movement



Original data

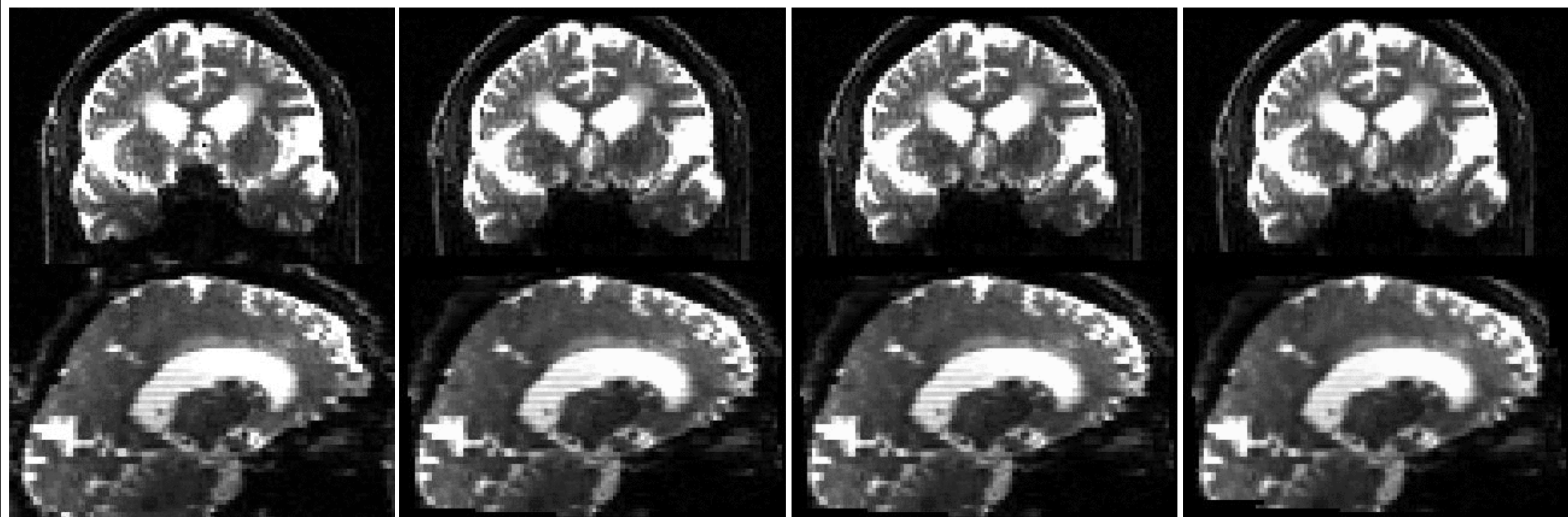
After correction
without outlier
correction

After correction
with outlier
replacement

Problematic elderly subject. Lots of movement induced signal loss and intravolume movement



Intra-volume movement



Original data

After correction
without outlier
correction

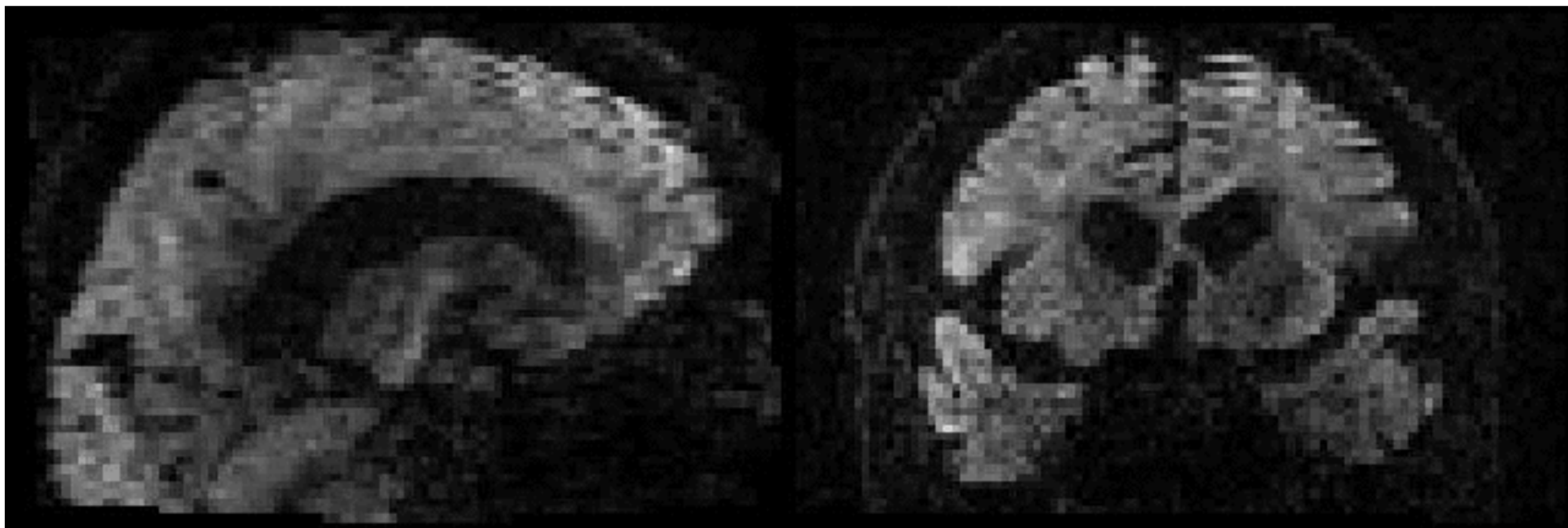
After correction
with outlier
replacement

After
intravolume
movement
correction.

Problematic elderly subject. Lots of movement induced signal loss and intravolume movement



Intra-volume movement



Highlighting the difference between just OLR
and OLR combined with S2V correction

Problematic elderly subject. Lots of movement
induced signal loss and intravolume movement