

# Sunnybrook Neuroimaging Summer School

Diffusion module – Tutorial 1 – Basic DWI data exploration

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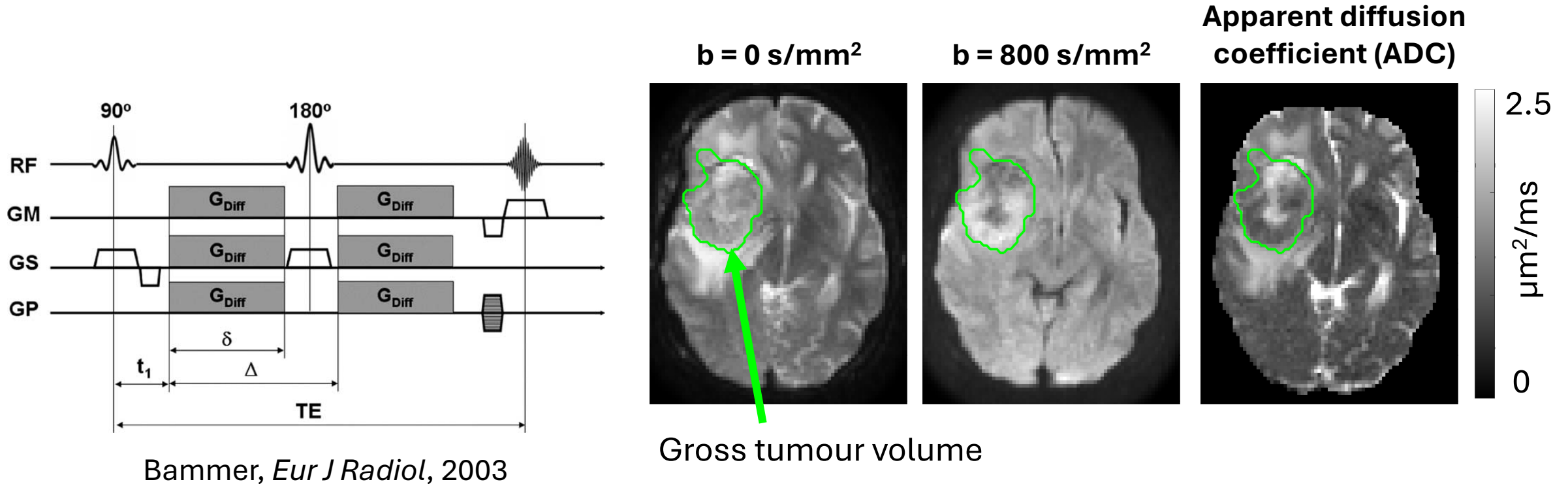
# Outline of topics

1. Inspecting DWI volumes
2. Creating ADC maps from DWI
3. Correcting geometric distortions
4. Quantifying ADC statistics

# Format

- Presentation of concepts
- Demonstration with me (you can follow along)
- Exercises on your own (with help available)

# Recap of diffusion-weighted imaging



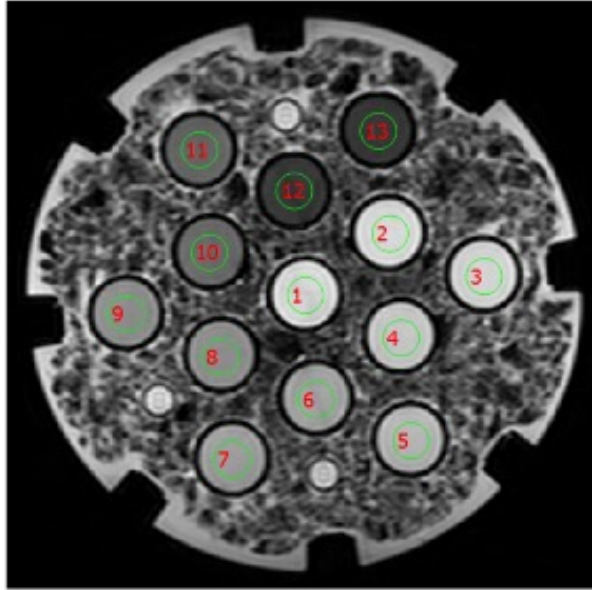
- Brownian motion of water attenuates signal
- Barriers restrict and hinder water diffusion (e.g., cell membranes)

# 1. Inspecting DWI volumes

# Demo 1.1

- Open a DWI volume with FSLeyes
- Page through the b-values
- View timeseries to inspect signal decay
- View the b-values

# NIST diffusion phantom



National Institute of Standards and Technology

- Thirteen vials sized 50 mL
  - Ten vials with polyvinylpyrrolidone (PVP) with concentrations from 10% to 50%
  - Three vials with water
- Three 5 mL water vials
- Reference diffusion coefficient measurements

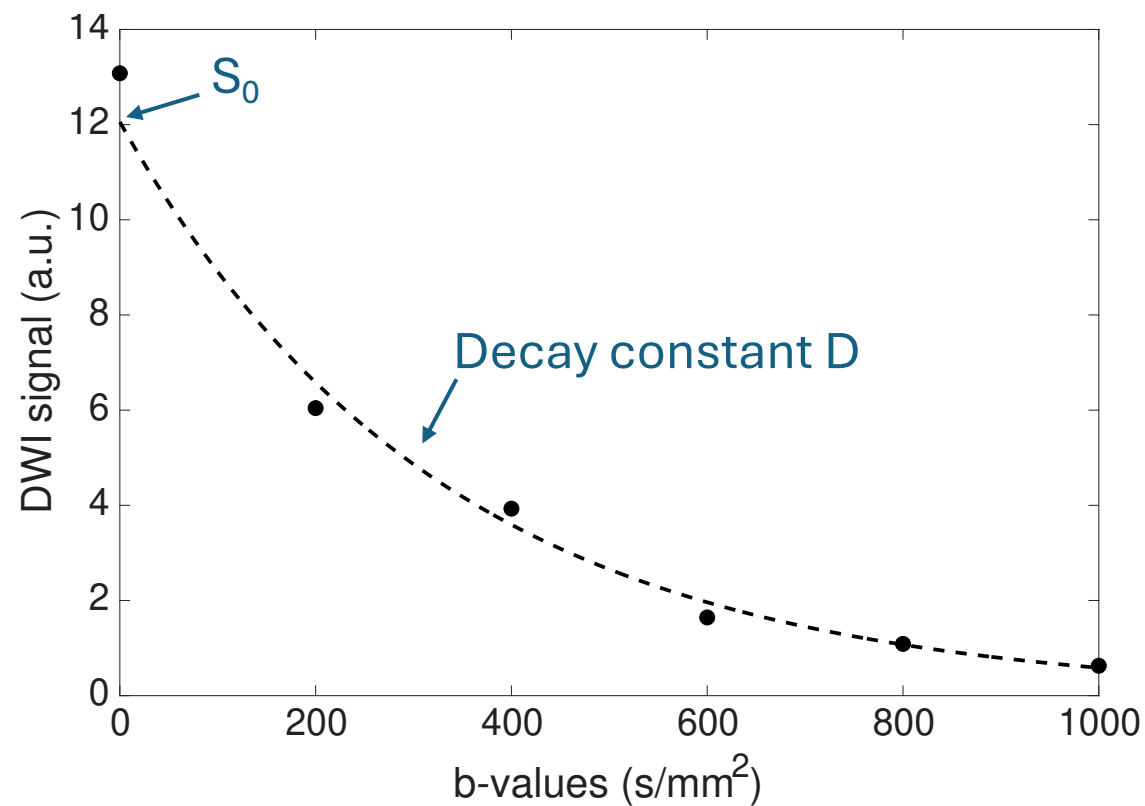
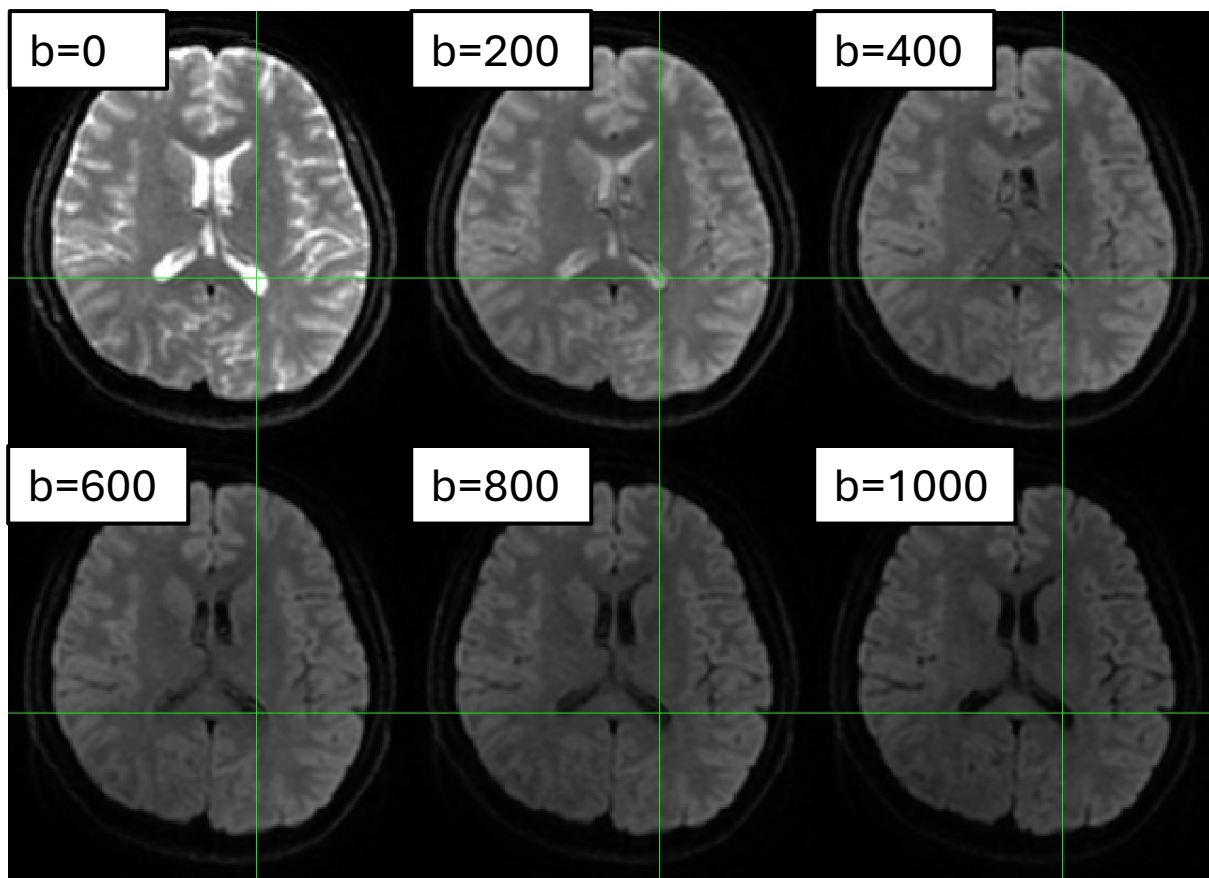
# Exercise 1.1

- a) Open “dwi\_phantom.nii.gz” and page through the b-values.  
This is the NIST DWI phantom cooled to 0 °C scanned at 1.5 T.
- b) Compare the T1-weighted imaging “t1w\_phantom.nii.gz” to the DWI
  - What geometric distortions can you identify in the DWI?
  - Do the distortions depend on the b-value?



## 2. Creating ADC maps from DWI

# ADC model



$$S(b) = S_0 \exp(-D \cdot b)$$

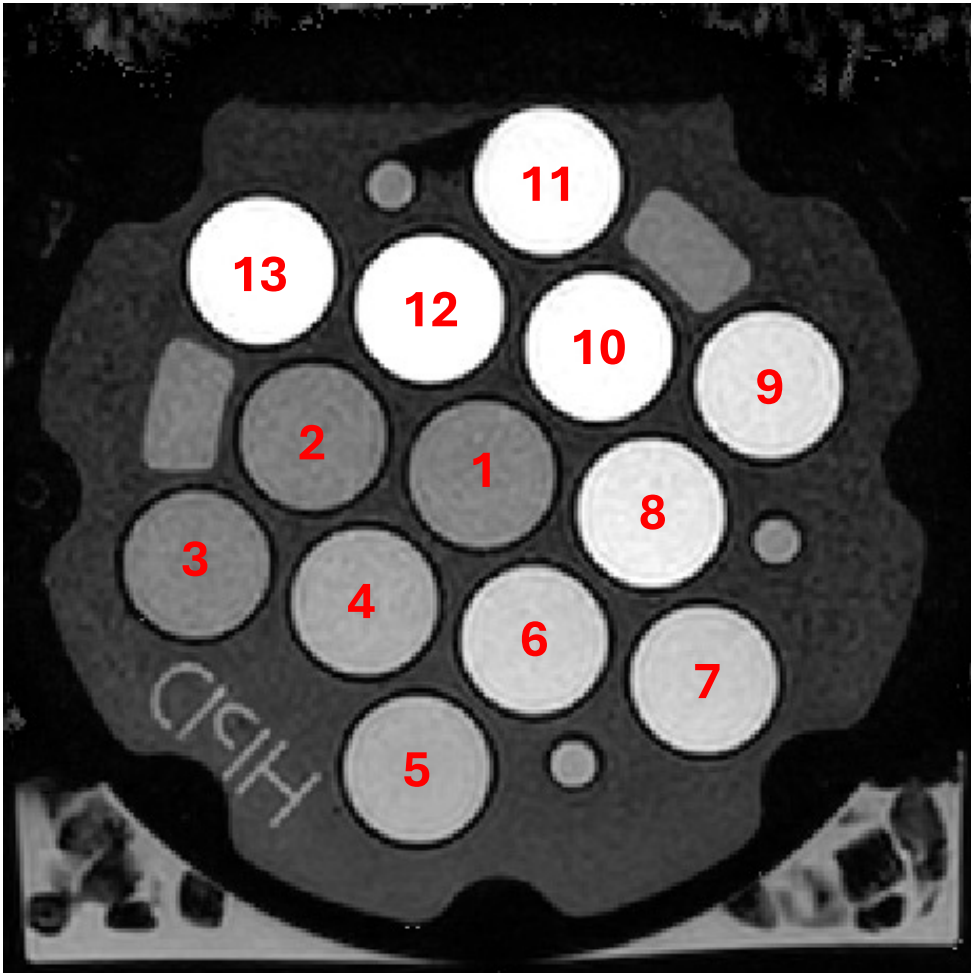
# Demo 2.1

- Create an ADC map with MRtrix3
- Inspect the fitting results with FSLeyes ( $S_0$  and ADC maps in the same volume)

Help: `dwi2adc -h`

```
dwi2adc -fslgrad dwi.bvec dwi.bval dwi.nii.gz adc.nii.gz
```

# Nominal ADC values for NIST phantom



Vial number	PVP conc. (%)	Nominal ADC ( $\times 10^{-3}$ mm <sup>2</sup> /s)
1	0	1.1
2	0	1.1
3	0	1.1
4	10	0.84
5	10	0.83
6	20	0.6
7	20	0.6
8	30	0.4
9	30	0.4
10	40	0.24
11	40	0.24
12	50	0.13
13	50	0.12

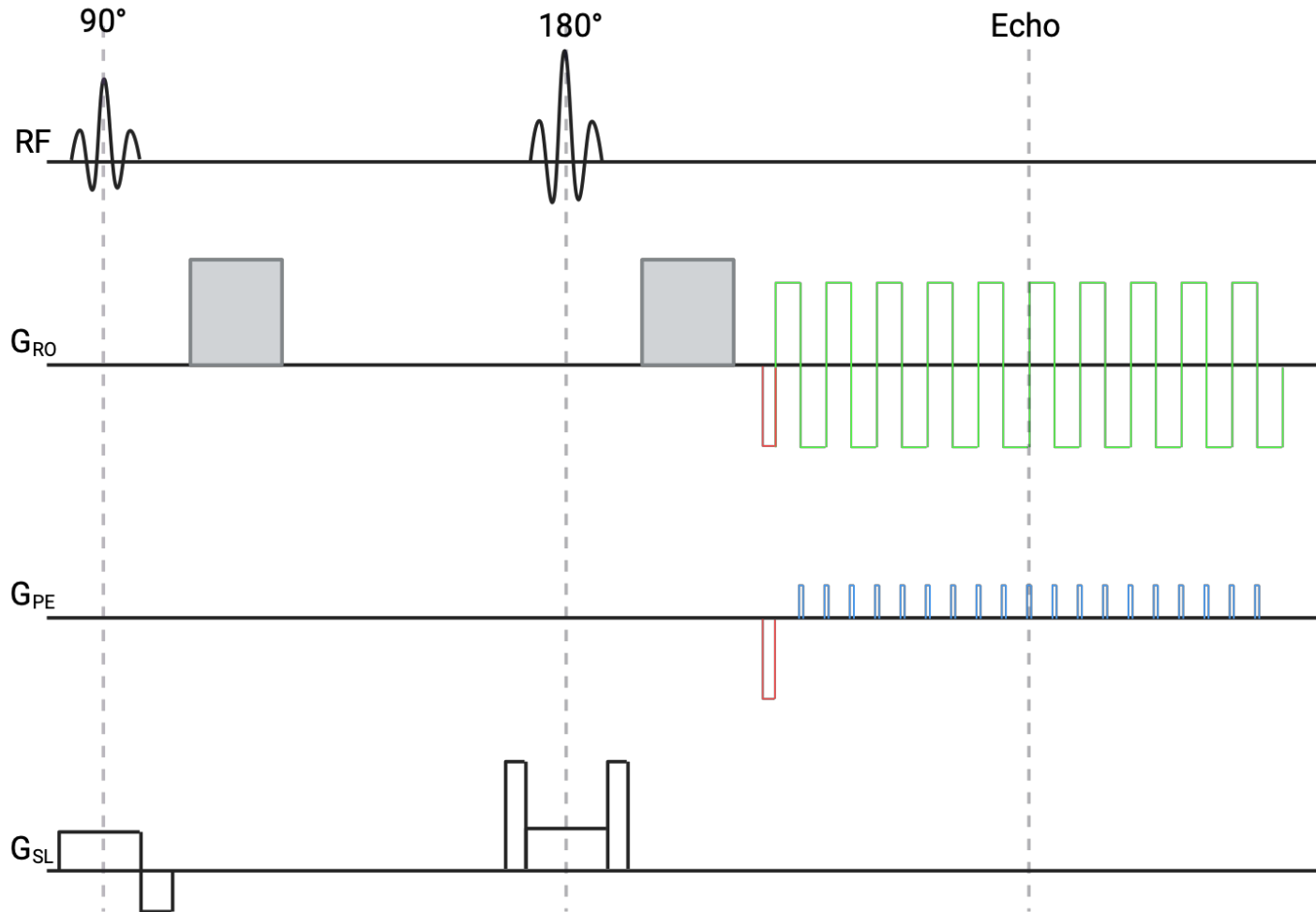
# Exercise 2.1

- a) Create an ADC map from “dwi\_phantom.nii.gz” using the `dwi2adc` function
- b) In an image viewer (e.g., FSLeyes), place the cursor over one voxel for each of the vials and record the ADC values
- c) Compare the recorded ADC values in (b) to the vendor-provided ADC values (“adc\_values\_vendor.xlsx”). Are they similar?

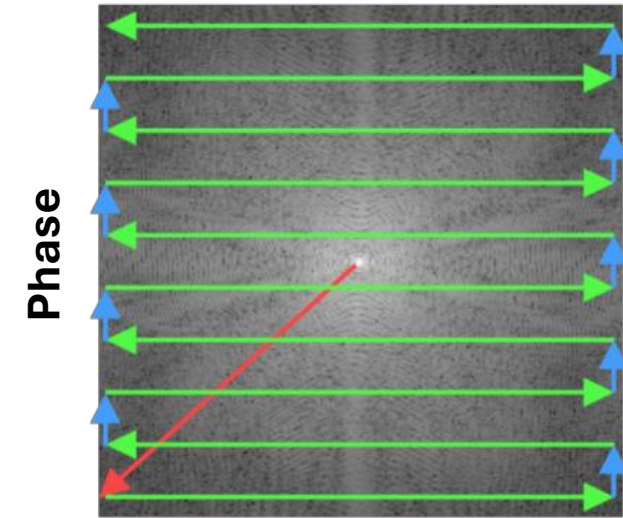
### 3. Correcting geometric distortions

Susceptibility distortions can be corrected with a reversed-blip (blip-down) acquisition

### DWI pulse sequence

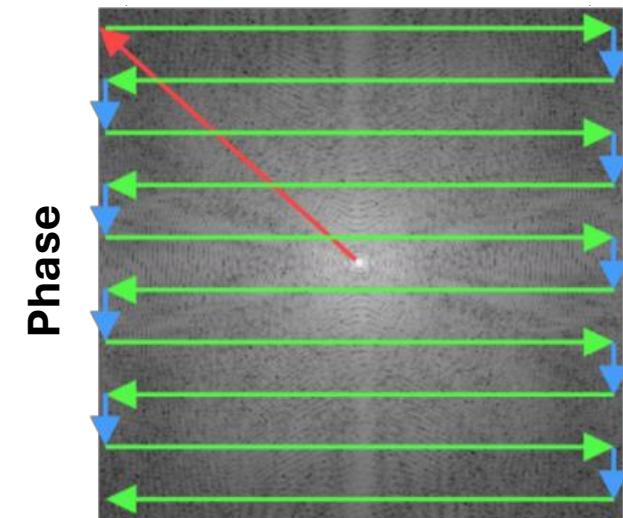


Blip-up



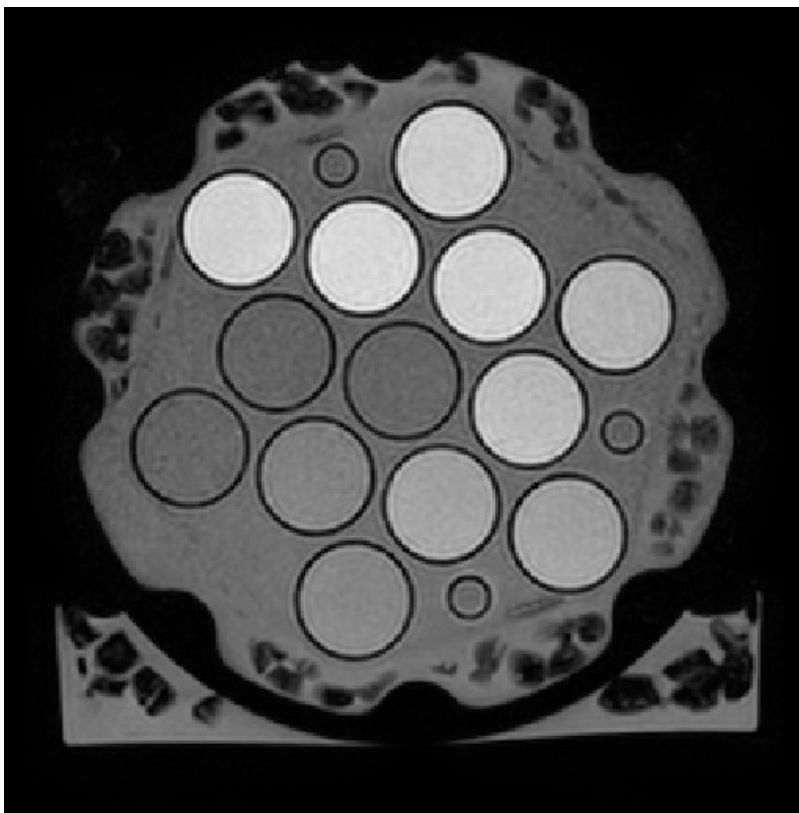
Readout

Blip-down

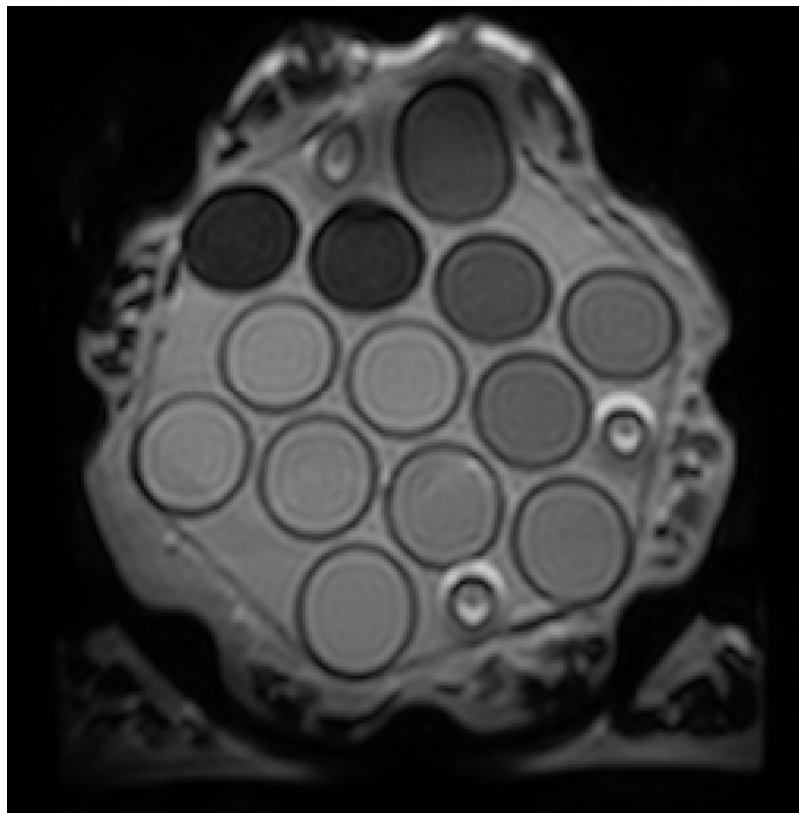


Readout

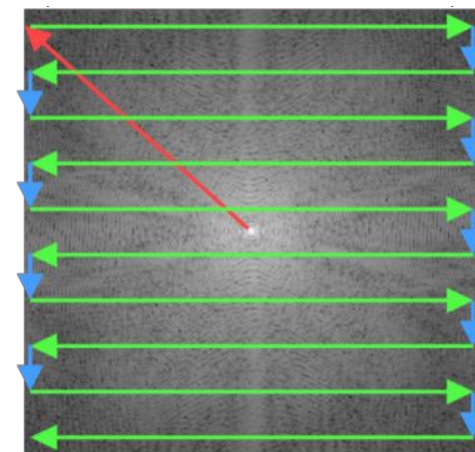
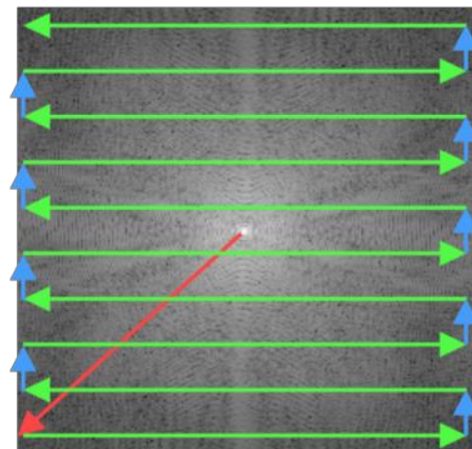
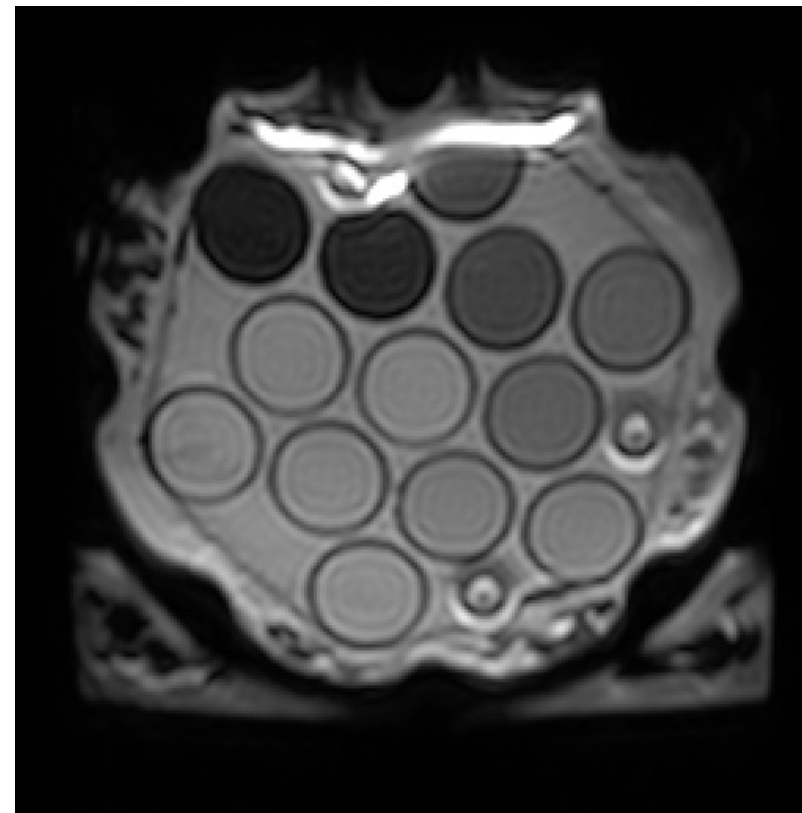
**T<sub>1</sub>-weighted imaging**



**DWI blip up**



**DWI blip down**





# Demo 3.1

- Correct for susceptibility-induced distortions using topup

Create file `acqparams.txt` with the following lines

```
0 1 0 0.056
```

```
0 -1 0 0.056
```

```
fslroi dwi_phantom_28sl.nii.gz b0.nii.gz 0 1
```

```
fslroi dwi_phantom_rev_28sl.nii.gz b0_rev.nii.gz 0 1
```

```
fslmerge -t b0_merged.nii.gz b0.nii.gz b0_rev.nii.gz
```

```
topup --imain=b0_merged --datain=acqparams.txt --config=b02b0.cnf  
--out=topup_results --fout=field --iout=b0_unwarped --verbose
```

# Demo 3.2

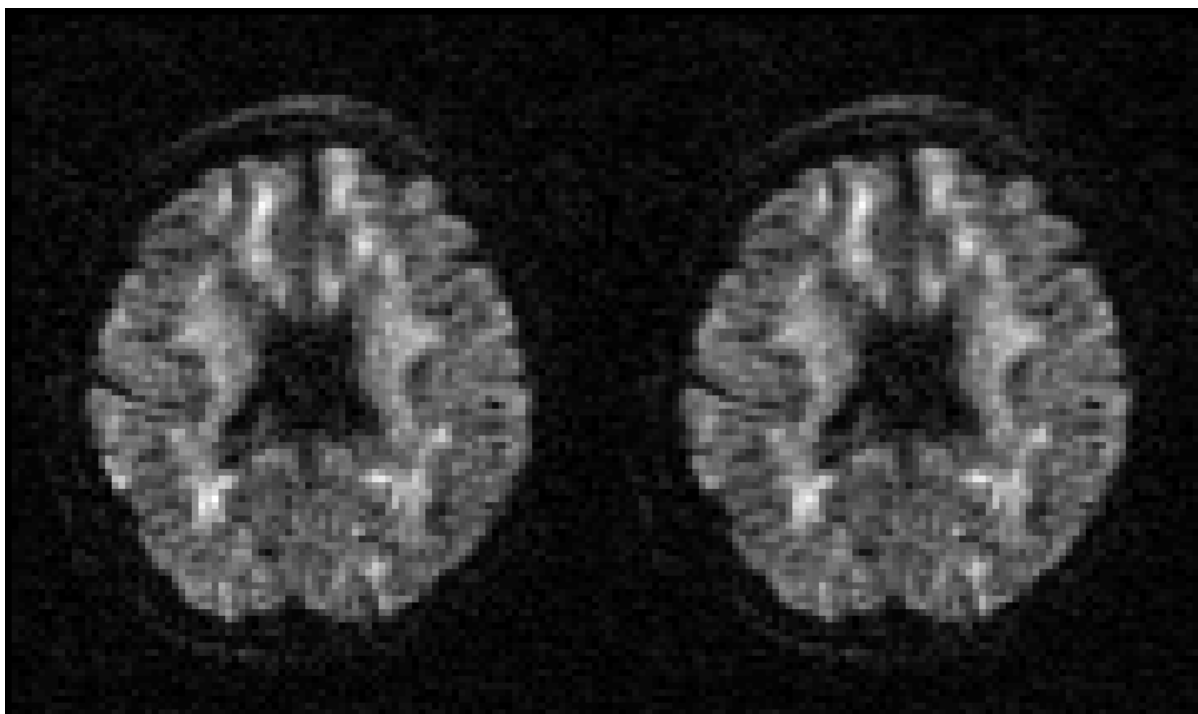
- Apply the results of topup to the full DWI scan

```
applytopup --imain=dwi_phantom_28sl --inindex=1  
--datain=acqparams.txt --topup=topup_results --out=dwi_corrected  
--method=jac --verbose
```

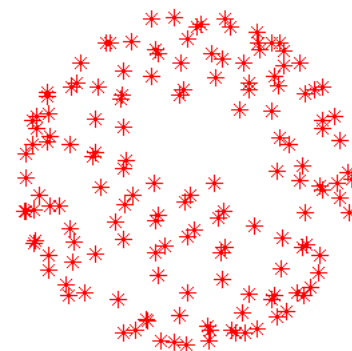
# Eddy current correction is also possible, but the data should be acquired in the right way

**Before correction**

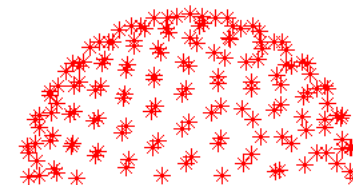
**After correction**



**Full-sphere  
sampling**



**Half-sphere  
sampling**



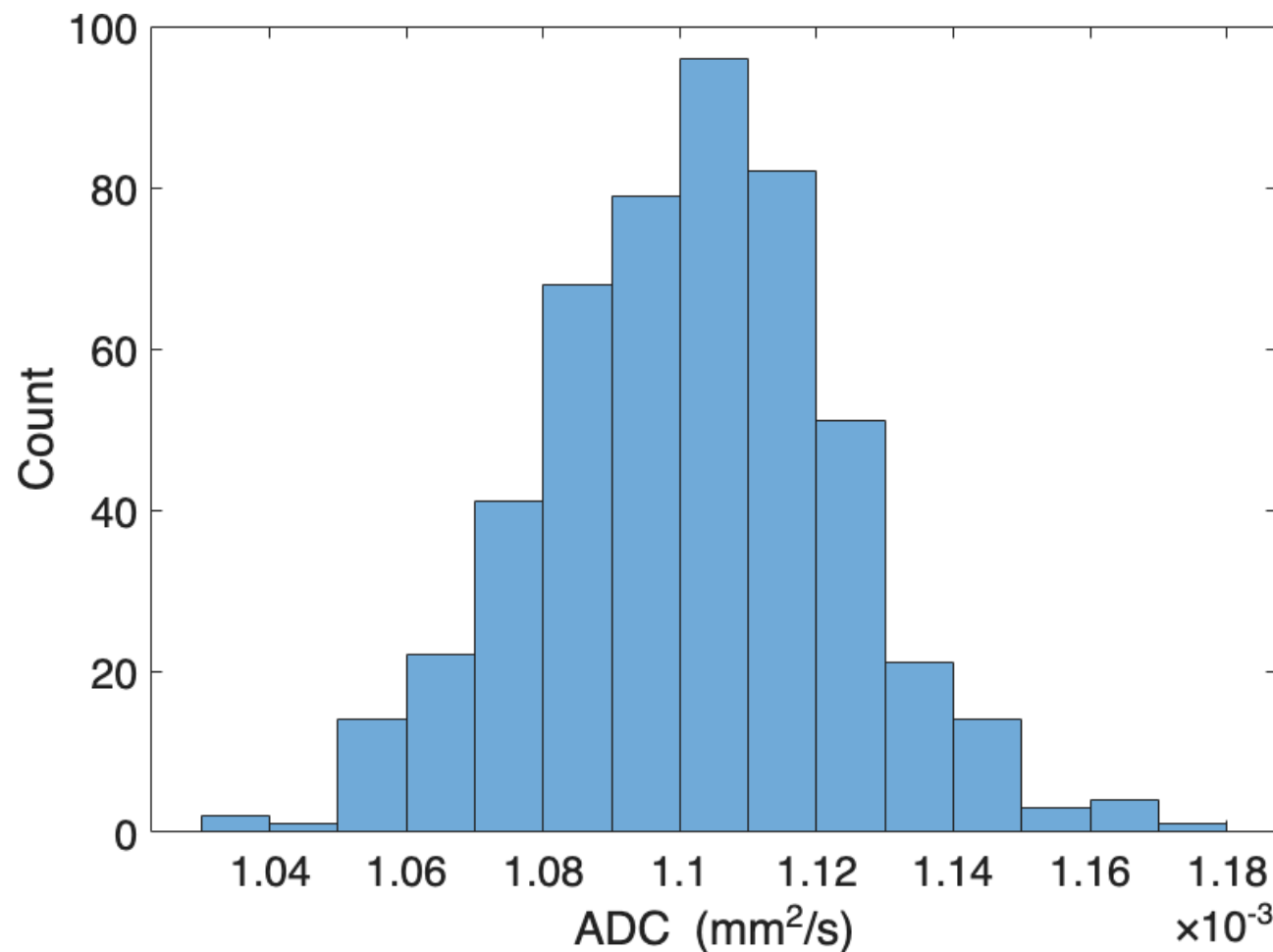
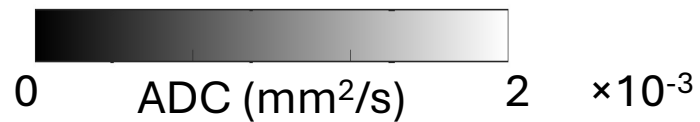
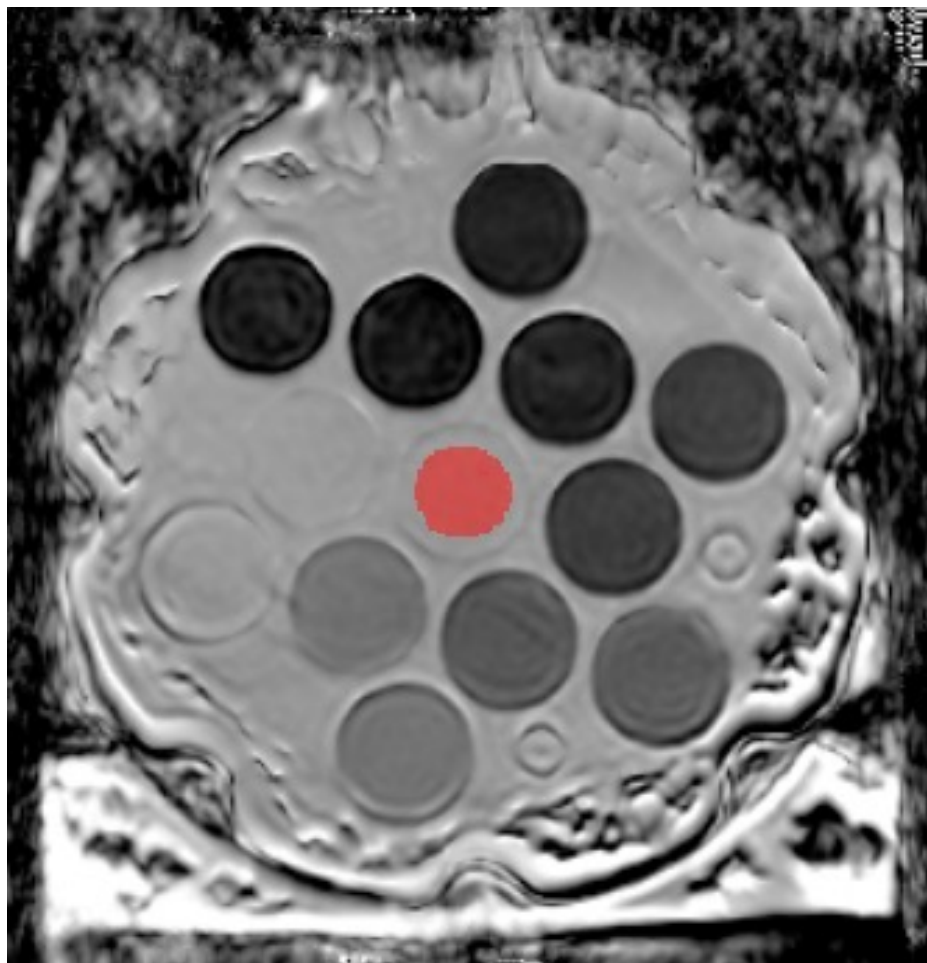
From: FSL eddy manual

# Main message about distortion correction: Think carefully when designing your acquisition protocol!

- Susceptibility correction: Needs a reverse-blip acquisition or a  $B_0$  field map
- Eddy current correction: Full-sphere sampling better than half-sphere
- Distortions can be reduced by changing acquisition parameters (with trade-offs, always with trade-offs...)

## 4. Quantifying ADC statistics

ADC statistics over regions often used for comparing between samples, subjects, etc.



# Demo 4.1

- Fit an ADC map to the distortion-corrected DWI
- Create a region-of-interest (ROI) over one of the vials
- Calculate the mean and standard deviation of ADC over the ROI

```
fslstats -t adc_corrected.nii.gz -k vial_1.nii.gz -m -s
```

# Exercise 4.1

- a) Create an ROI for each vial in the phantom in “adc\_corrected.nii.gz”
- b) Calculate the mean and standard deviation for each of the ROIs you created in (a) using the `fslstats` command
- c) Compare the ADC mean  $\pm$  SD to the vendor-provided ADC values

Hint: Calculate statistics for “vial\_1.nii.gz” through “vial\_13.nii.gz” and save to a text file using this command

```
for ((i=1; i<14; i++)); fslstats -t adc_corrected.nii.gz  
-k vial_${i}.nii.gz -m -s | sed -n 2p >> adc_measurements.txt
```



## Exercise 4.2

- a) Fit an ADC map to the human data “dwi.nii.gz”
- b) Create an ROI over white matter and an ROI over cerebrospinal fluid in the ventricles
- c) Calculate the mean and standard deviation of ADC over each of your ROIs using the `fslstats` command:  
`fslstats -t adc.nii.gz -k mask.nii.gz -m -s`
- d) Find a value online for the diffusion coefficient of water at 37 °C. How does the value compare to the ADC of cerebrospinal fluid? Why is the ADC value of white matter much lower?