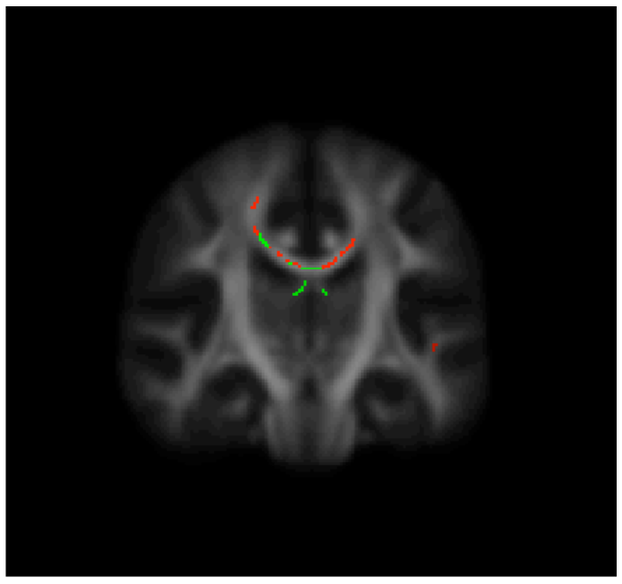
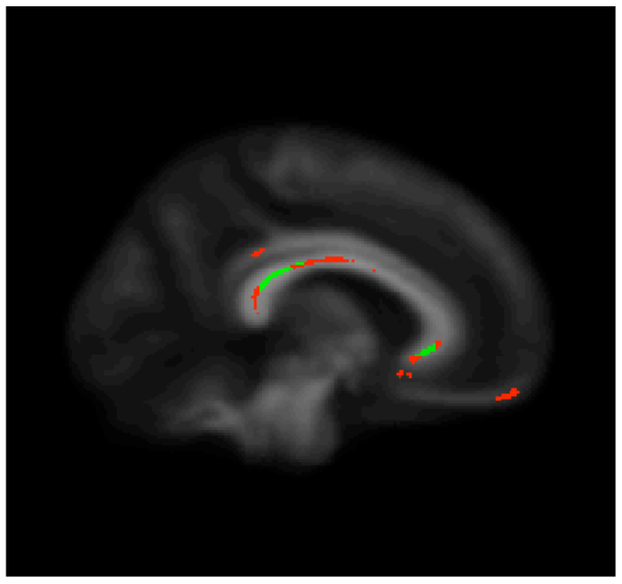
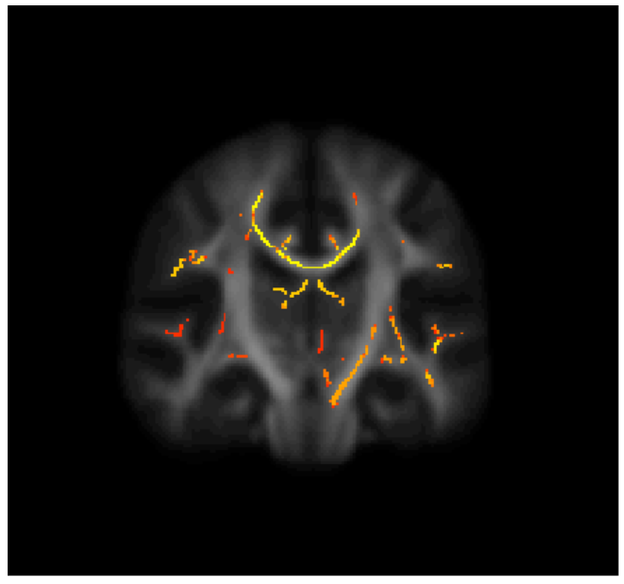
TFCE for TBSS

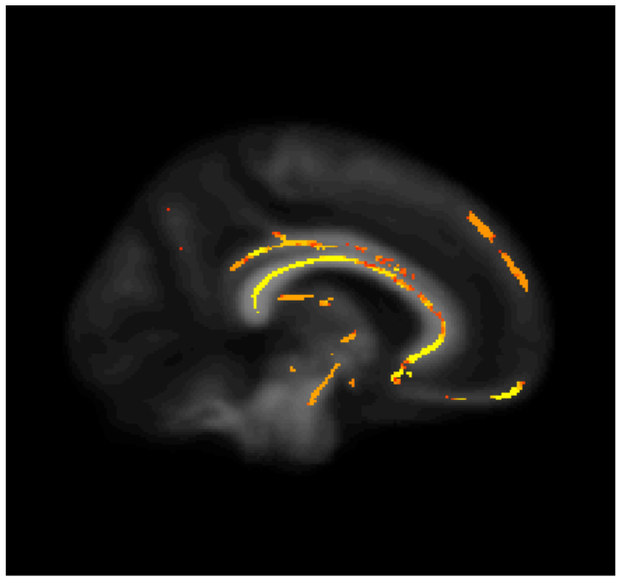
controls > schizophrenics

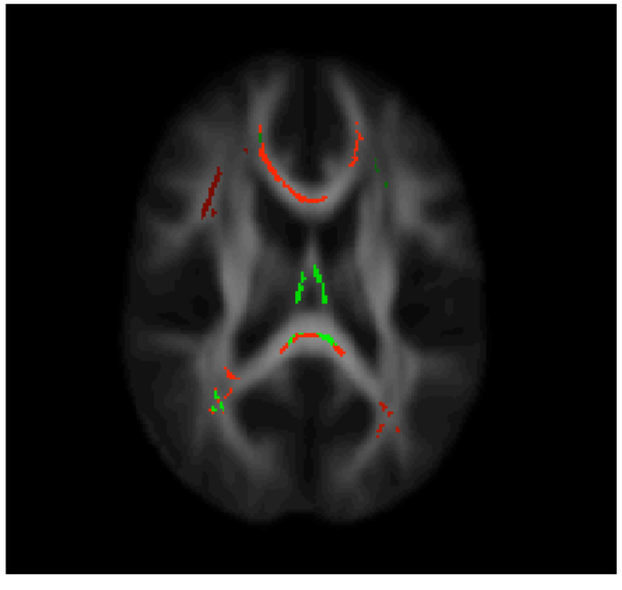
p<0.05 corrected for multiple comparisons across space, using randomise



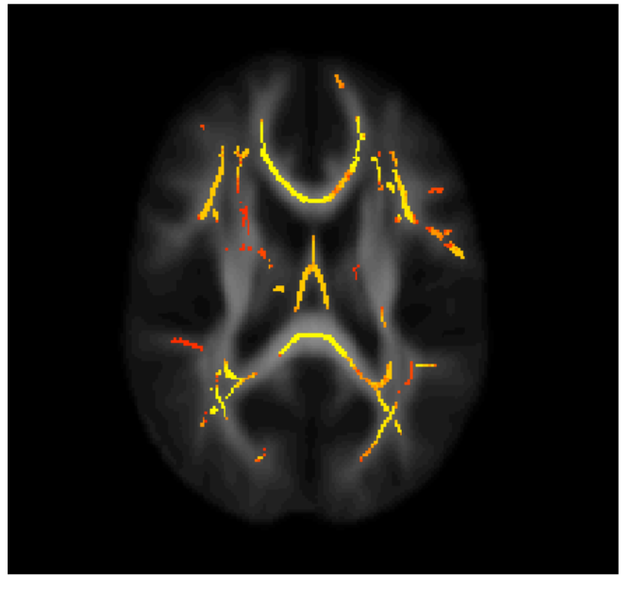






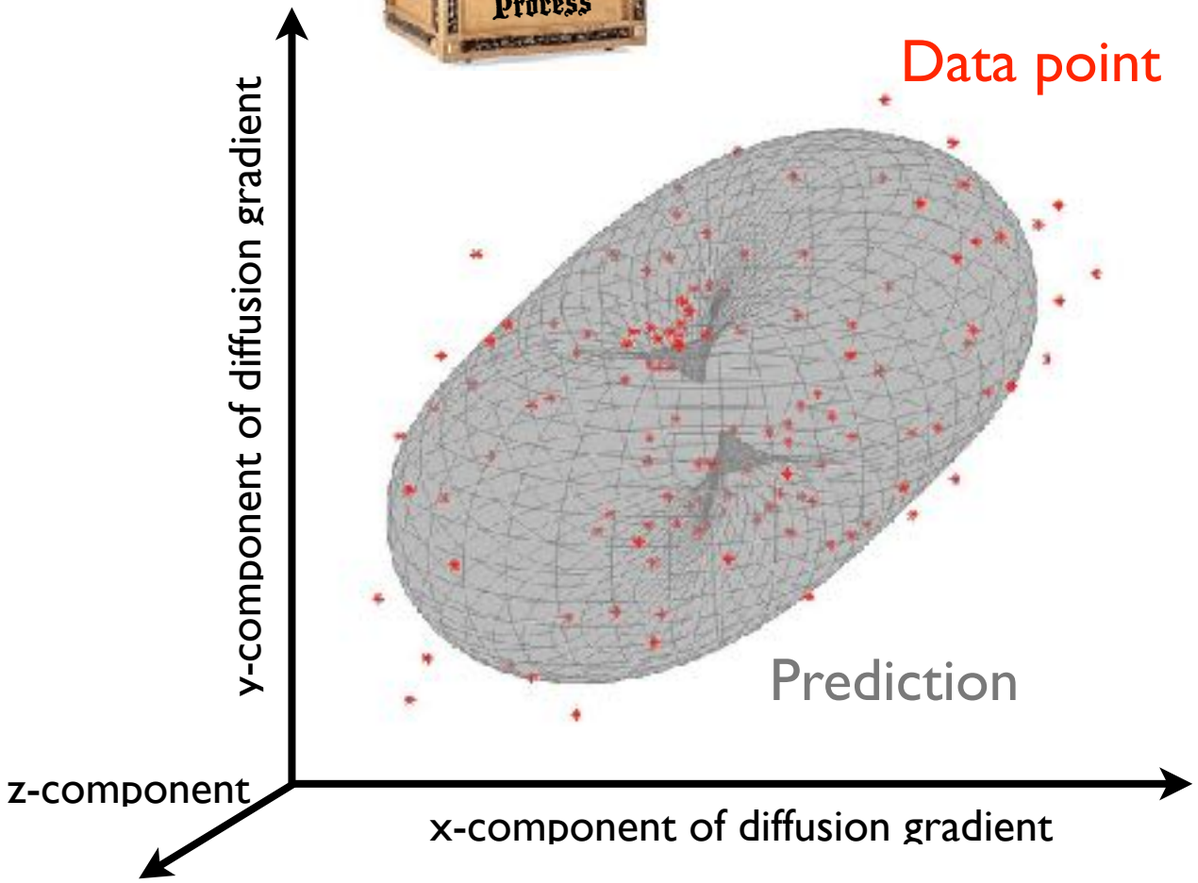


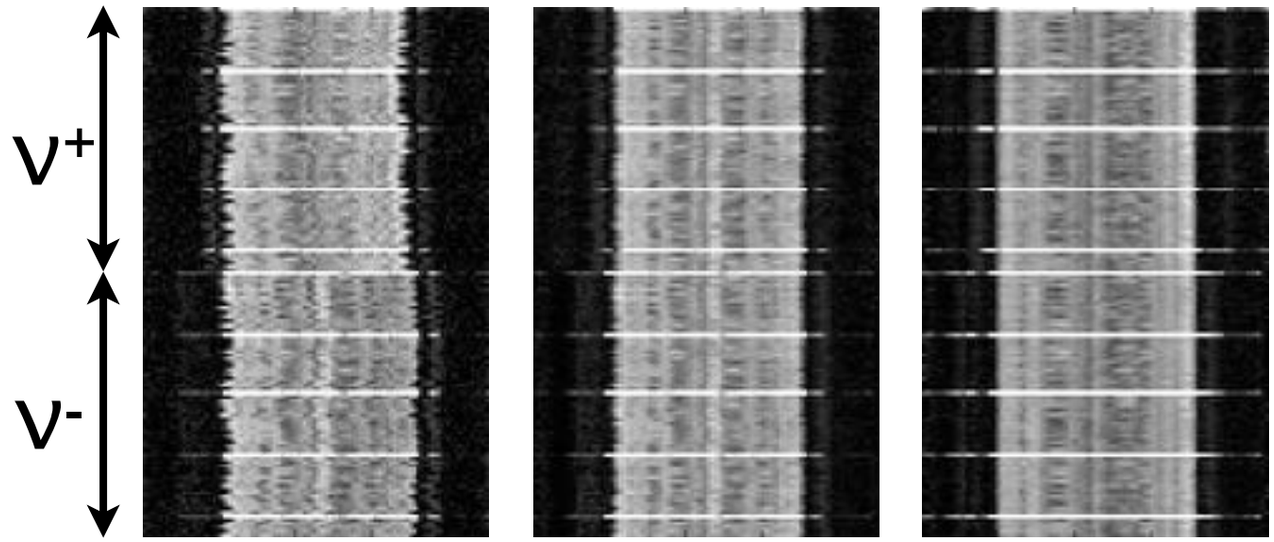
cluster-based:
cluster-forming
threshold =
2 or 3

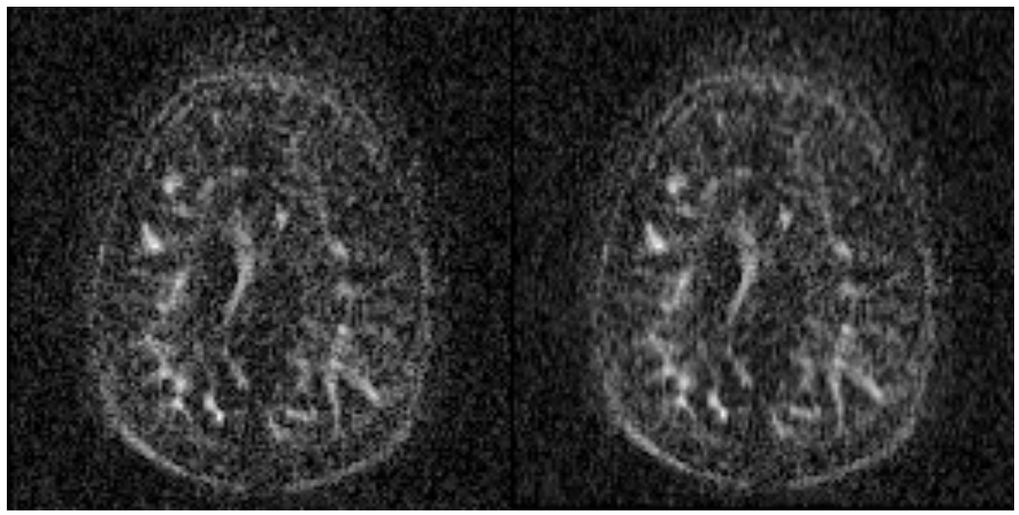


TFCE

eddy and topup - tools for processing of diffusion data



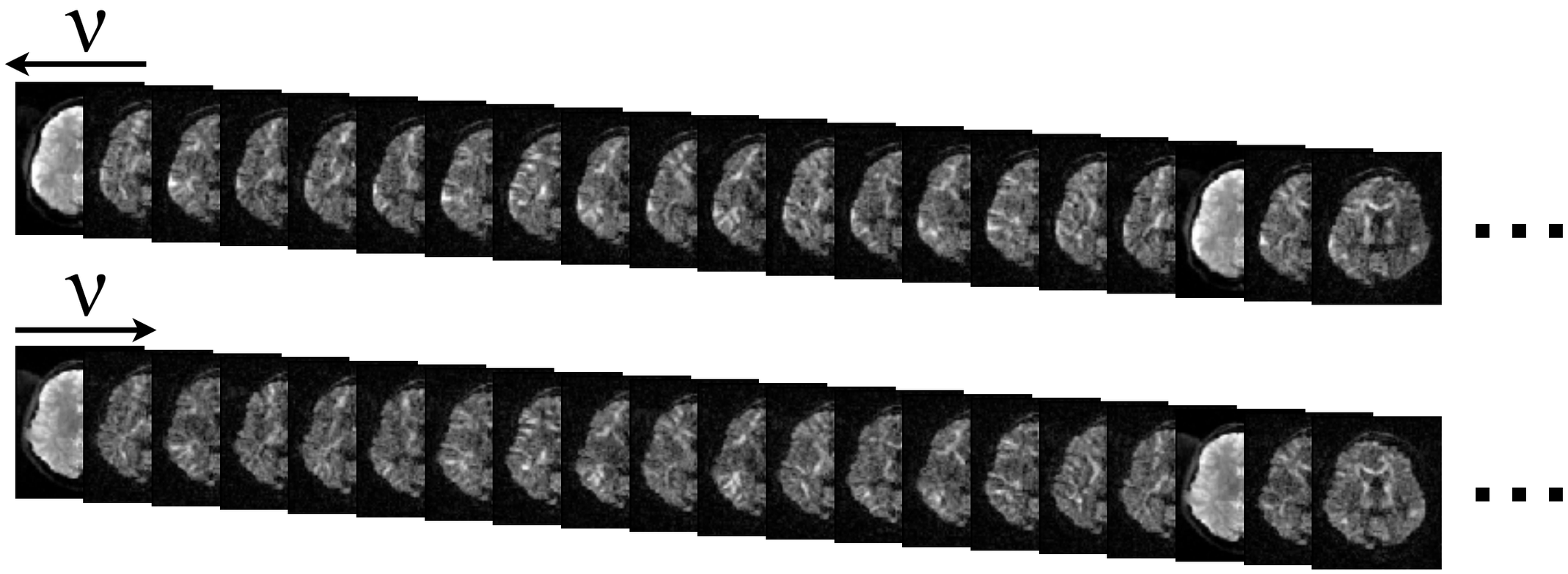




Outline of the talk

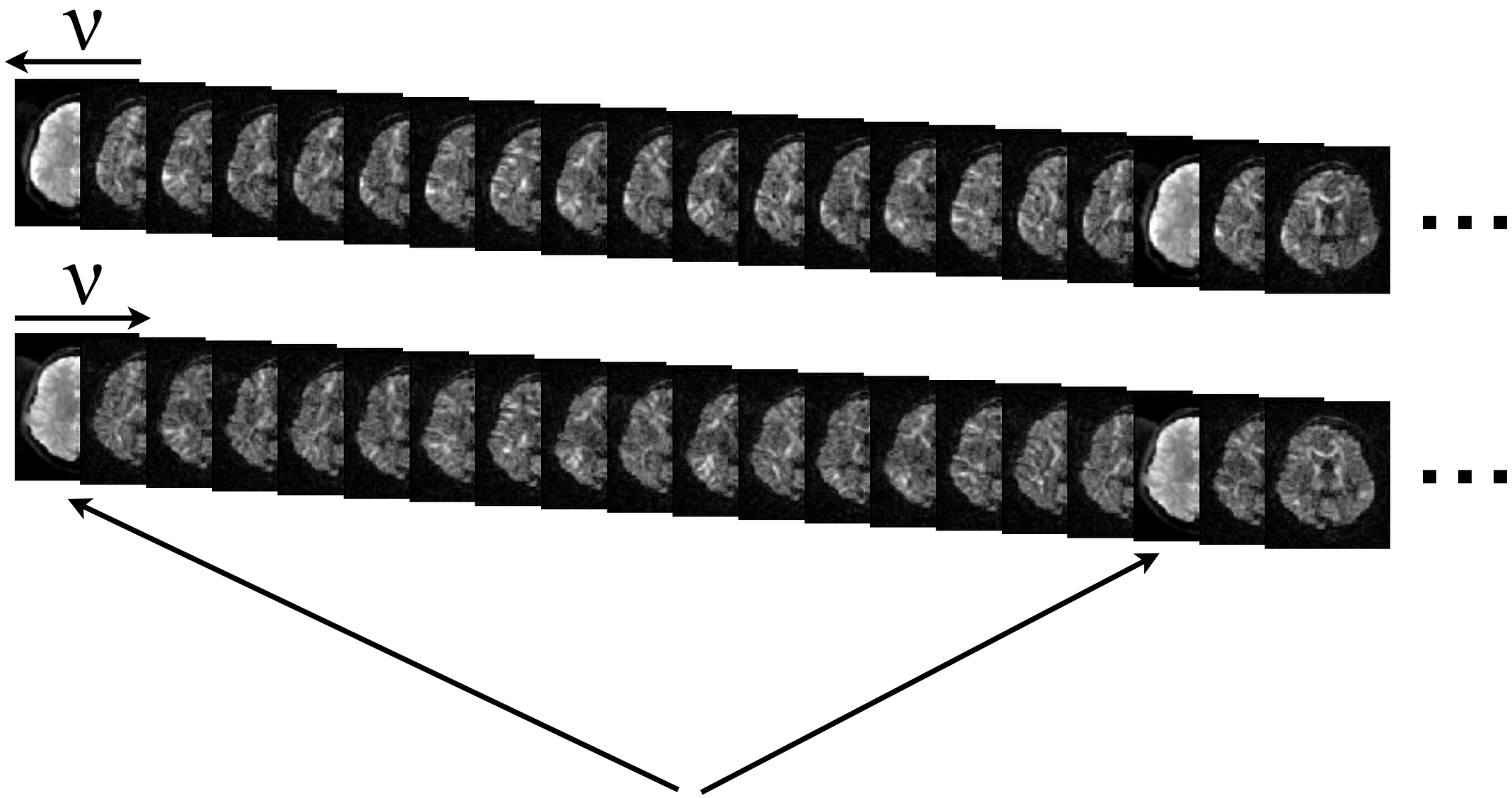
- What is the problem with diffusion data?
- Off-resonance field
  - How does it cause distortions?
  - Where does it come from?
- Registering diffusion data
  - How topup works
  - How eddy works
- Practicalities
- Some results
- Quality control
- "Advanced" eddy features

Practicalities



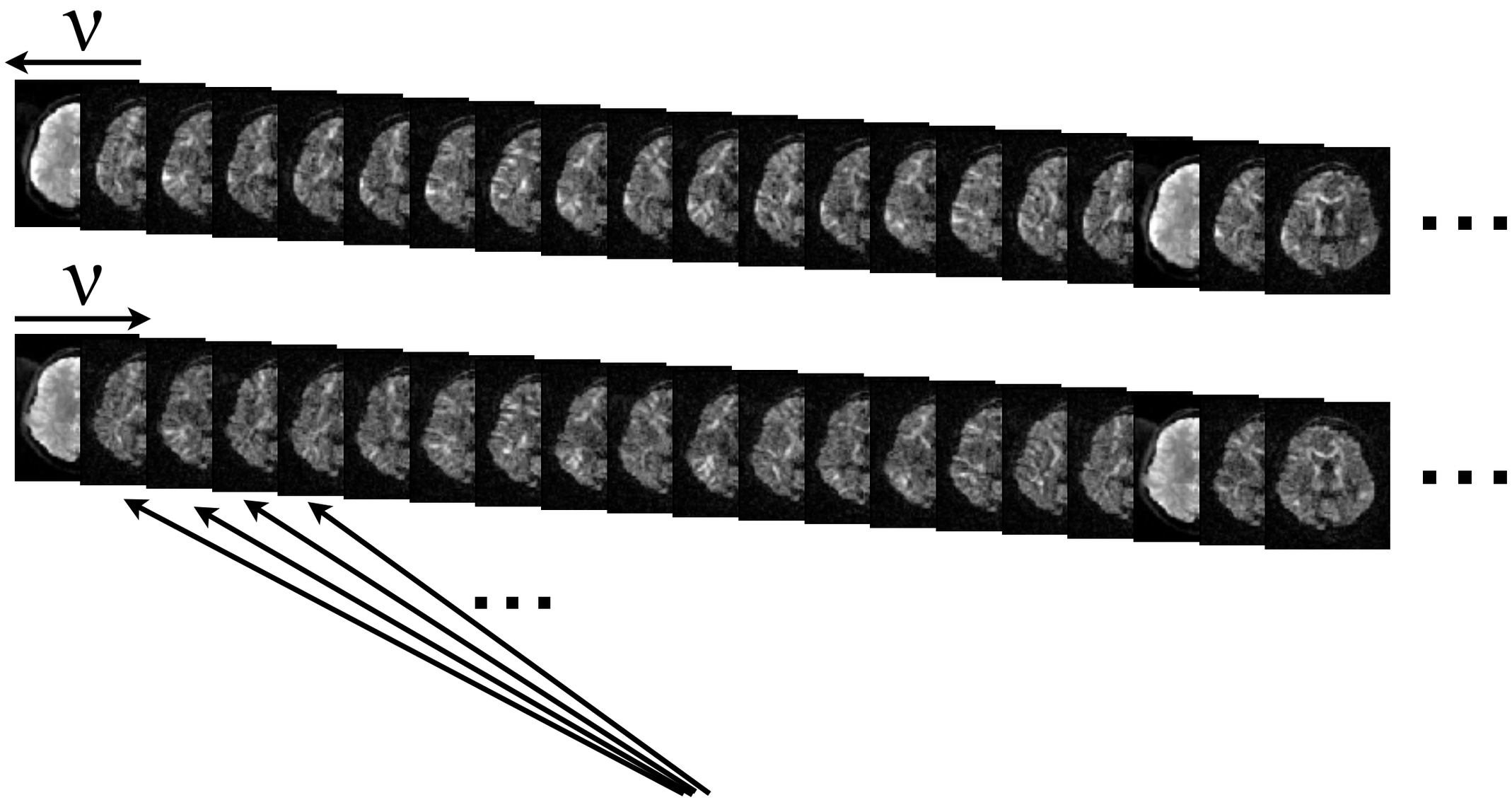
- Our example data consists of:
  - *N* diffusion weighted volumes and *n* *b*=0 volumes
  - *b*=0 volumes interspersed
  - Two repetitions, phase-encode L→R and R→L
  - Same diffusion table for both repetitions

Practicalities



Affected by susceptibility distortions

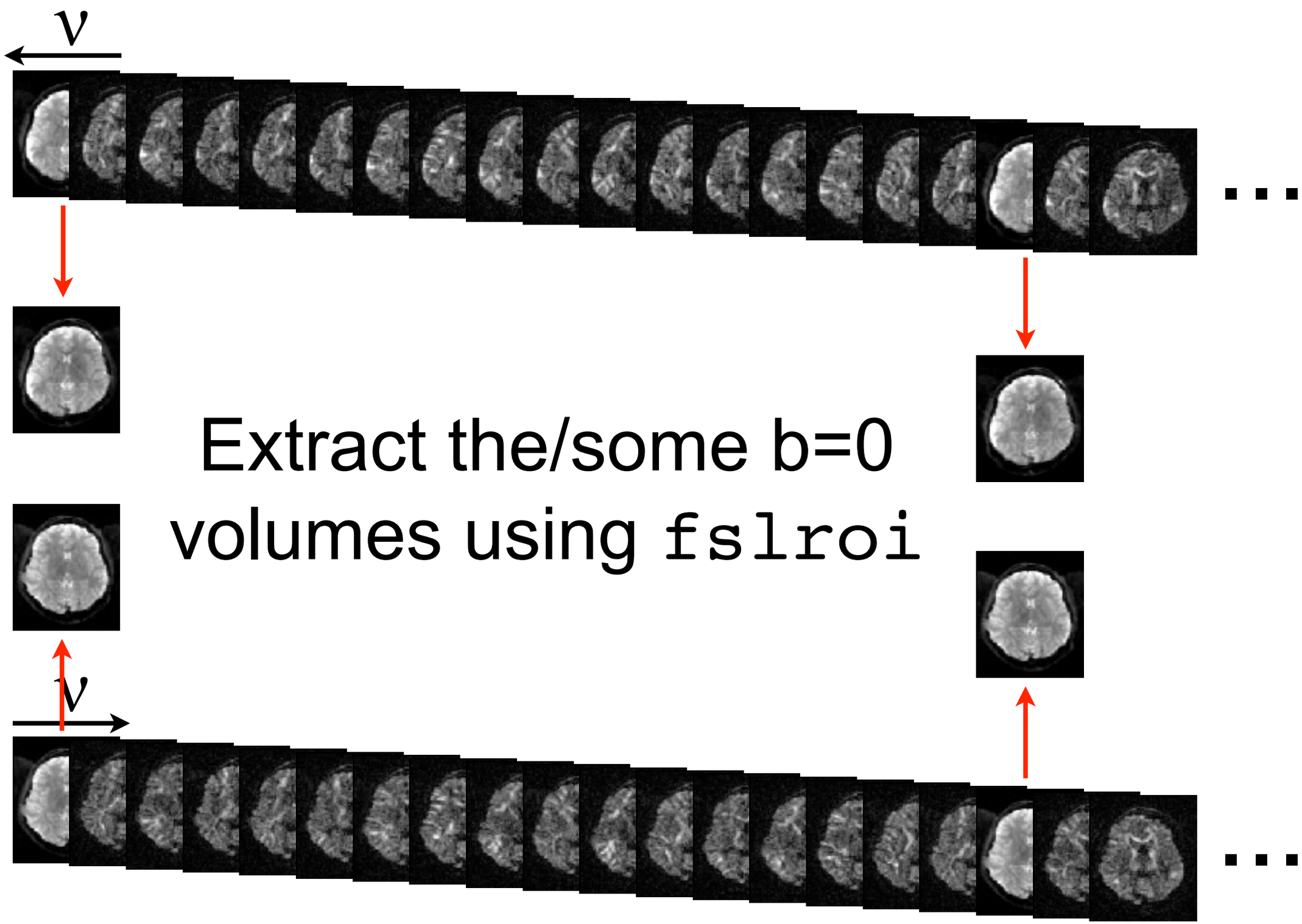
Practicalities



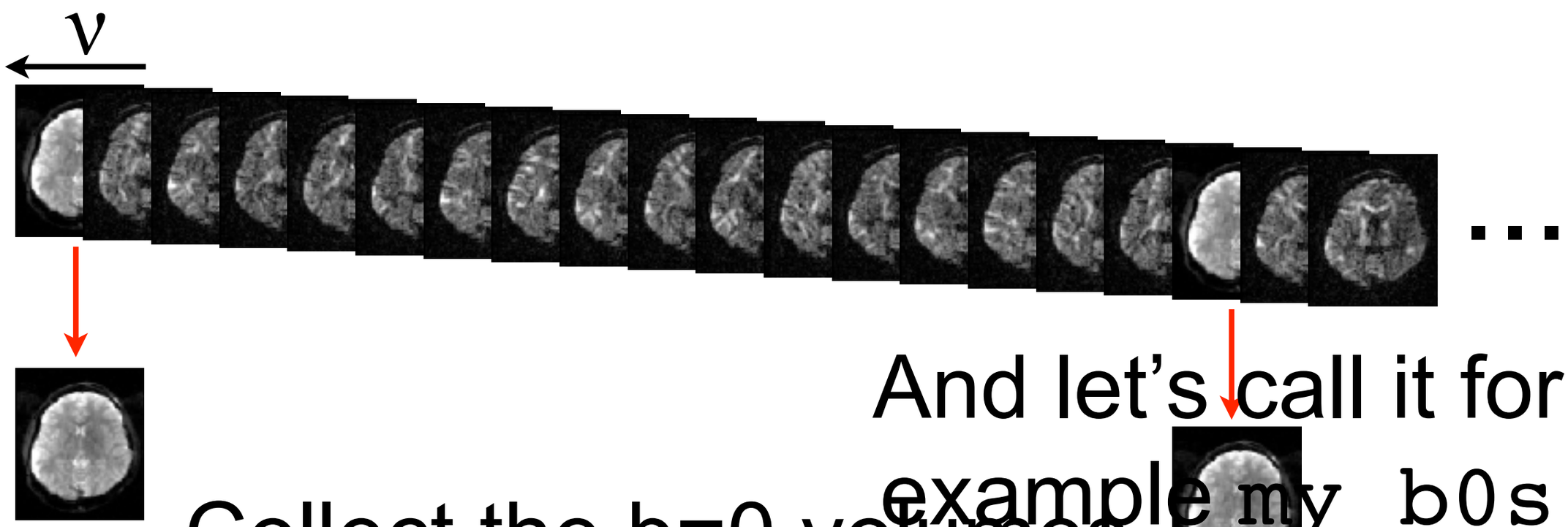
Affected by susceptibility distortions
AND eddy current distortions

And everything is of course affected by subject movement.

So, let's start with susceptibility

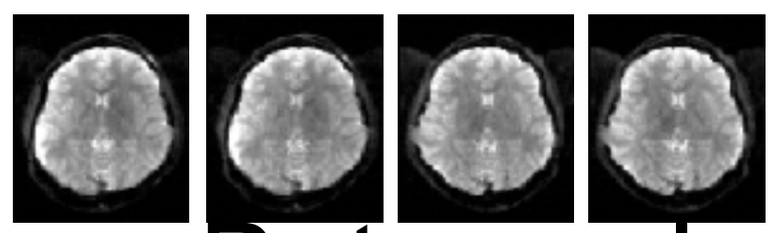


So, let's start with susceptibility



And the tool for that is `topup`

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



`my_b0s`

But we also need to inform topup about the acquisition parameters

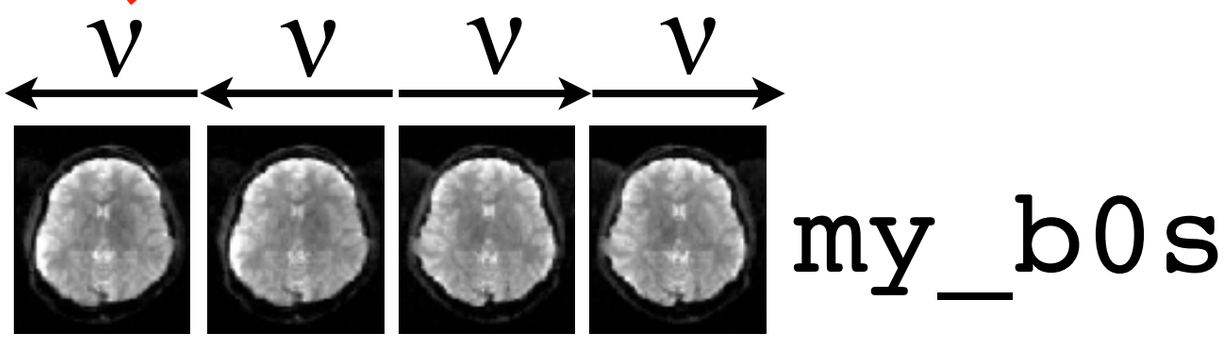
And the tool for that is `topup`

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

Means PE in x-direction, L→R

```
-1  0  0  0.051
```

Total readout time (in seconds)

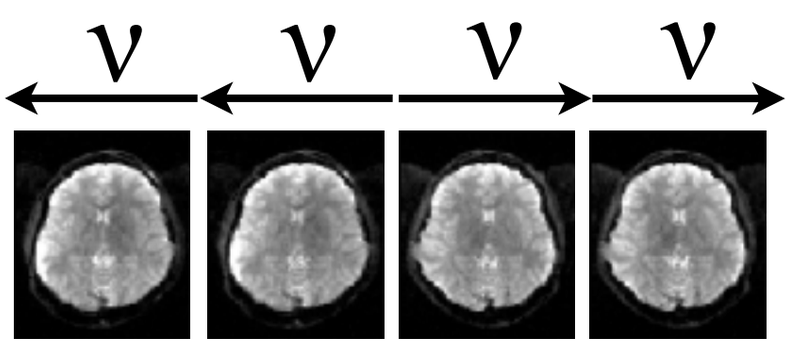


And the tool for that is `topup`

```
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`

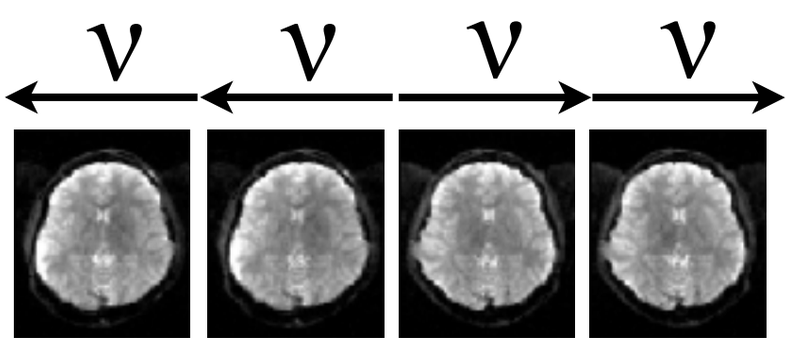


`my_b0s`

And the tool for that is `topup`

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

And then some technical details



`my_b0s`

```
-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`

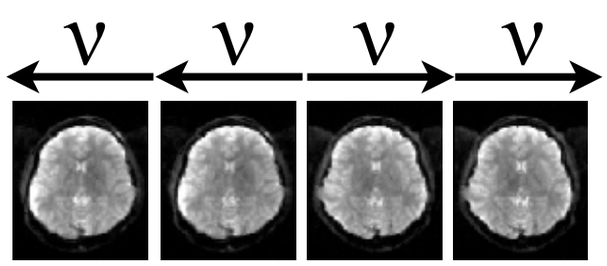
And finally we need to tell it where to put the results

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

`my_topup_movpar.txt`

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

```
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_b0s`

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

`acqparams.txt`

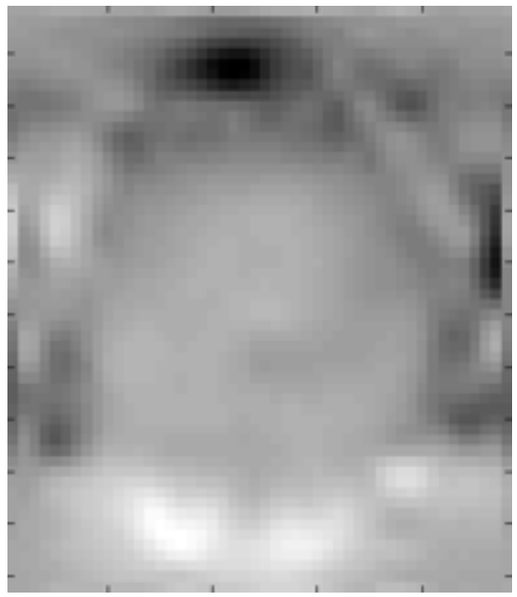
`b02b0.cnf`

And the tool for that is `topup`

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

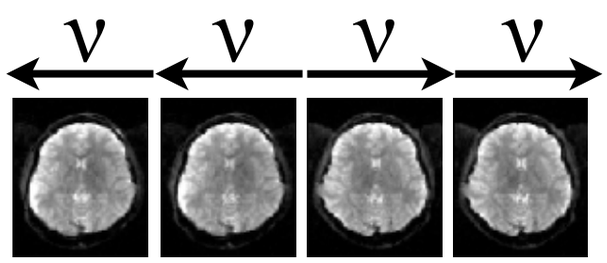
```
topup --imain=my_b0s --datain=acqparams.txt --config=b02b0.cnf --out=my_topup
```

`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
```



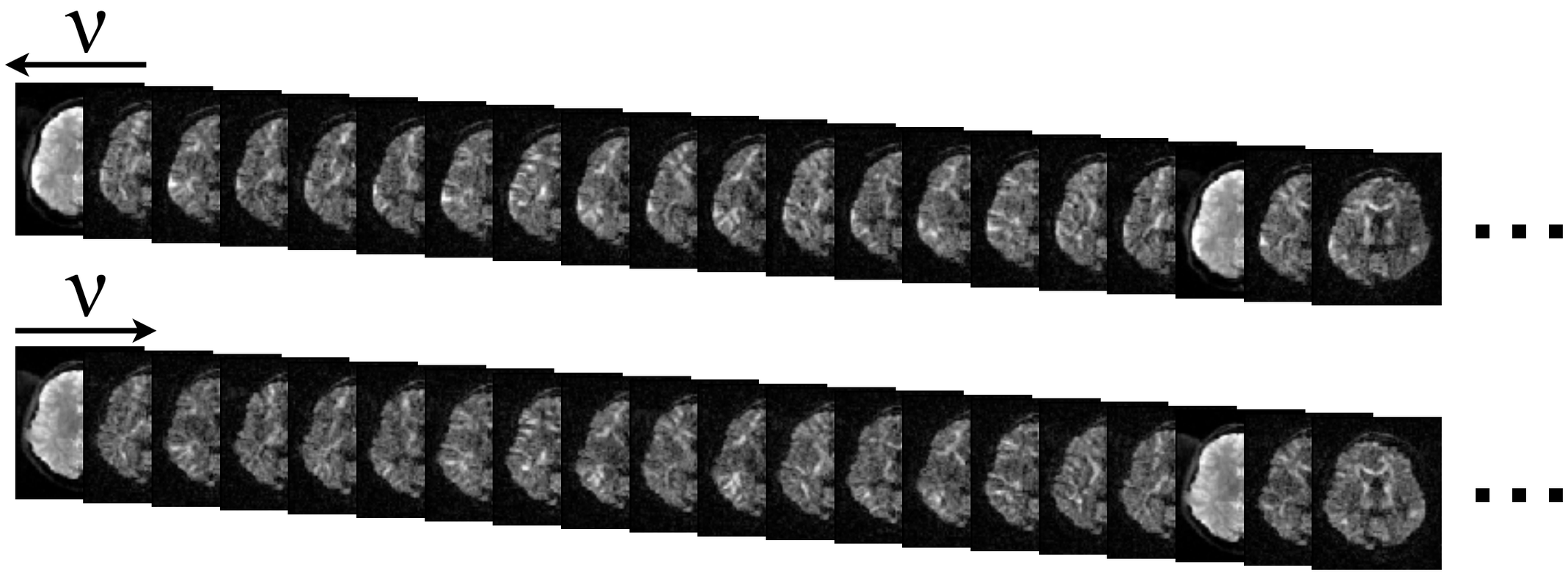
`my_b0s`

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

`acqparams.txt`

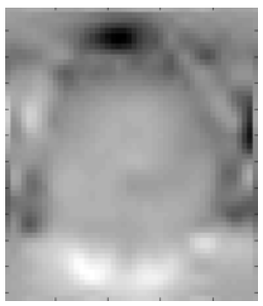
`b02b0.cnf`

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



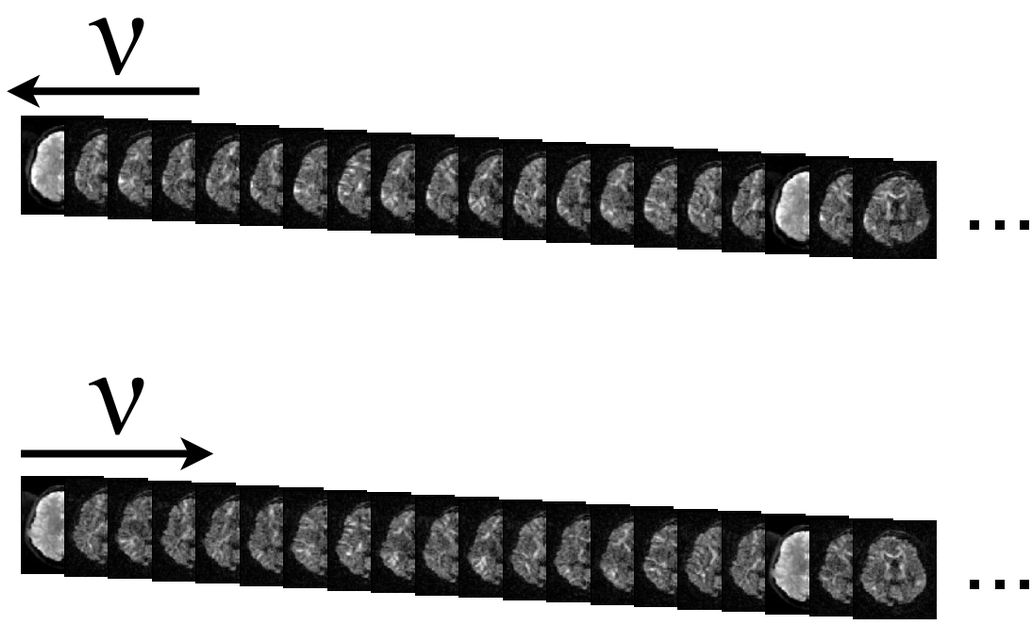
```
-1 0 0 0.051
-1 0 0 0.051
1 0 0 0.051
1 0 0 0.051
```

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
```

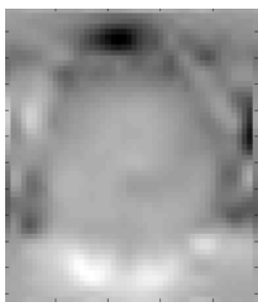
my_topup_movpar.txt

Collect all data in one file



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



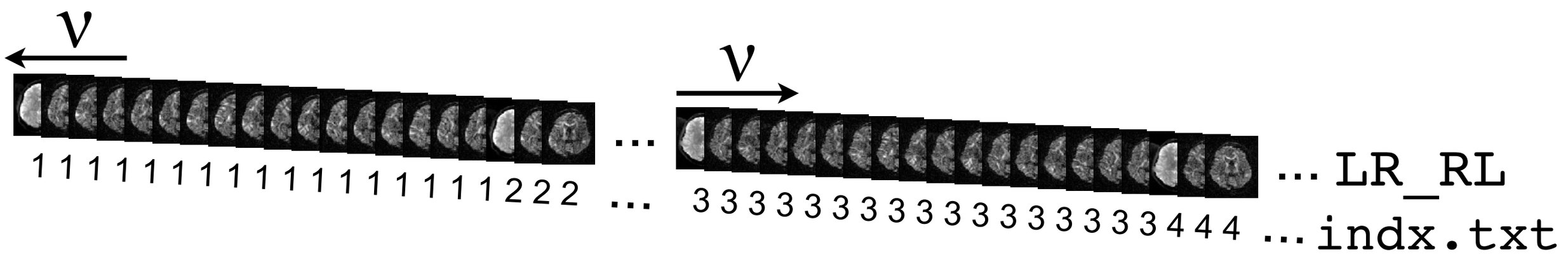
```
-1 0 0 0.051
-1 0 0 0.051
1 0 0 0.051
1 0 0 0.051
```

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
```

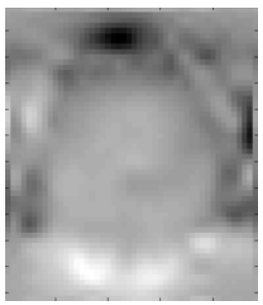
my_topup_movpar.txt

Inform eddy of acquisition parameters



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

my_topup_fieldcoef.nii



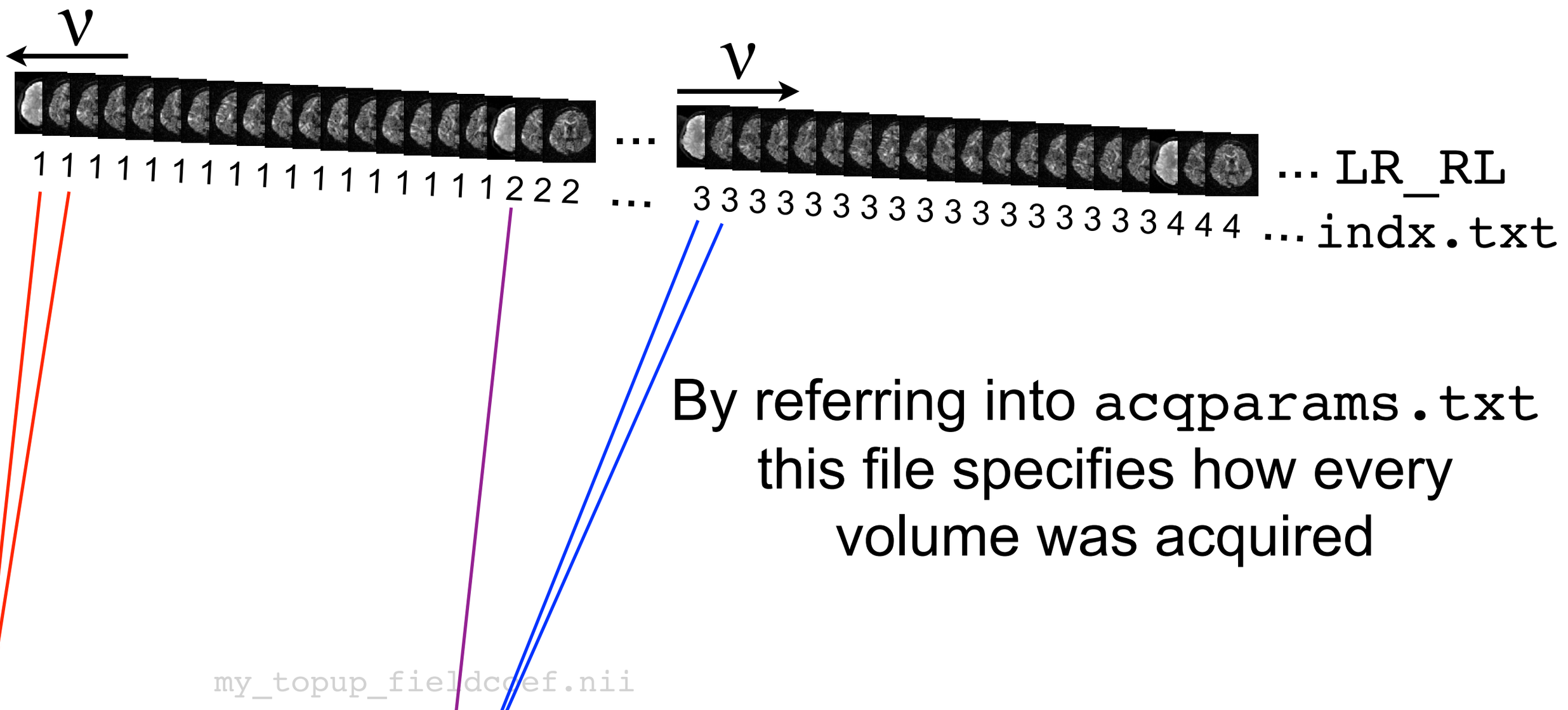
```
-1 0 0 0.051
-1 0 0 0.051
1 0 0 0.051
1 0 0 0.051
```

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

Inform eddy of acquisition parameters



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

my_topup_fieldcoef.nii

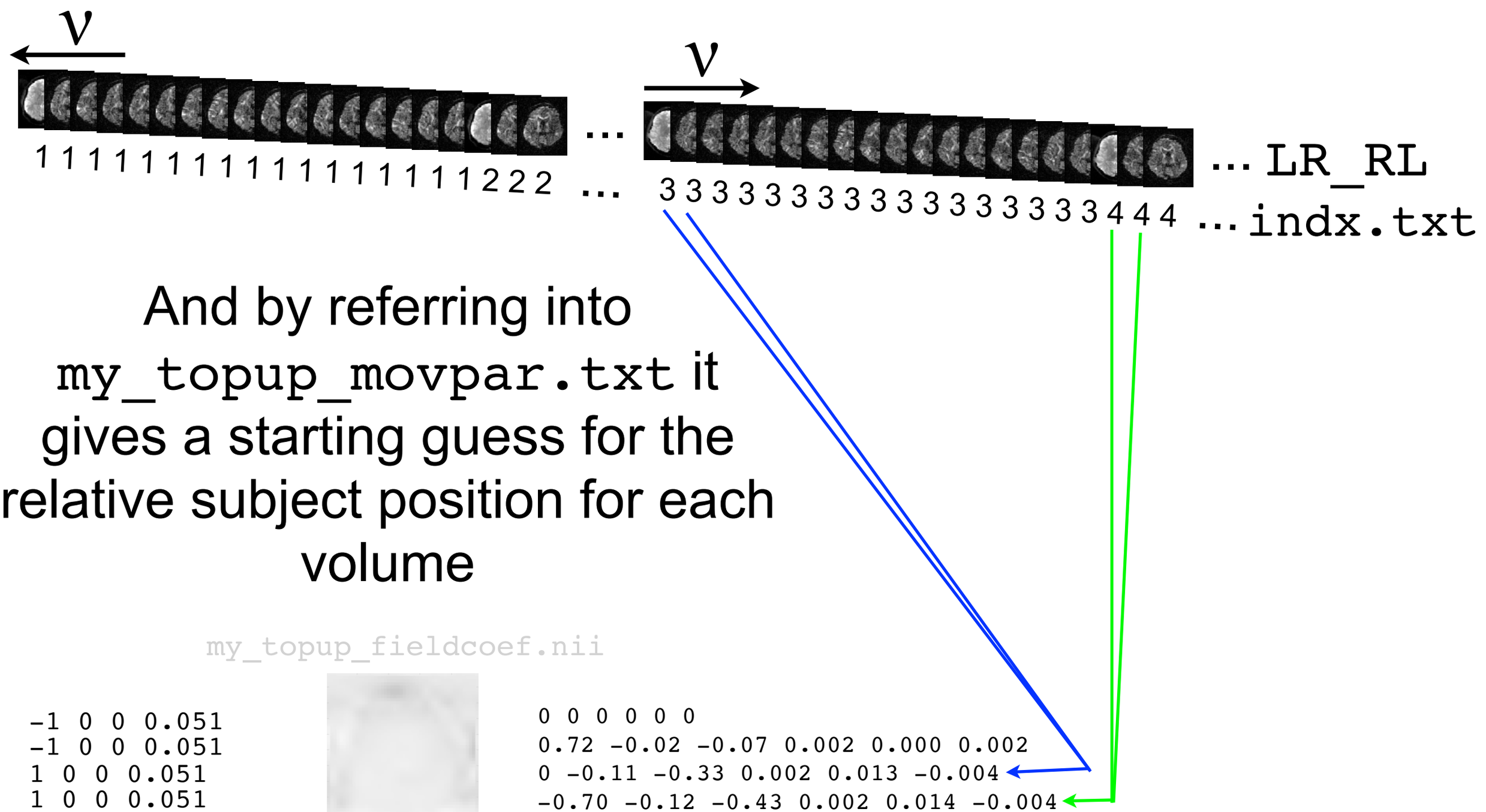
```
-1  0  0  0.051
-1  0  0  0.051
 1  0  0  0.051
 1  0  0  0.051
```

`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`

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

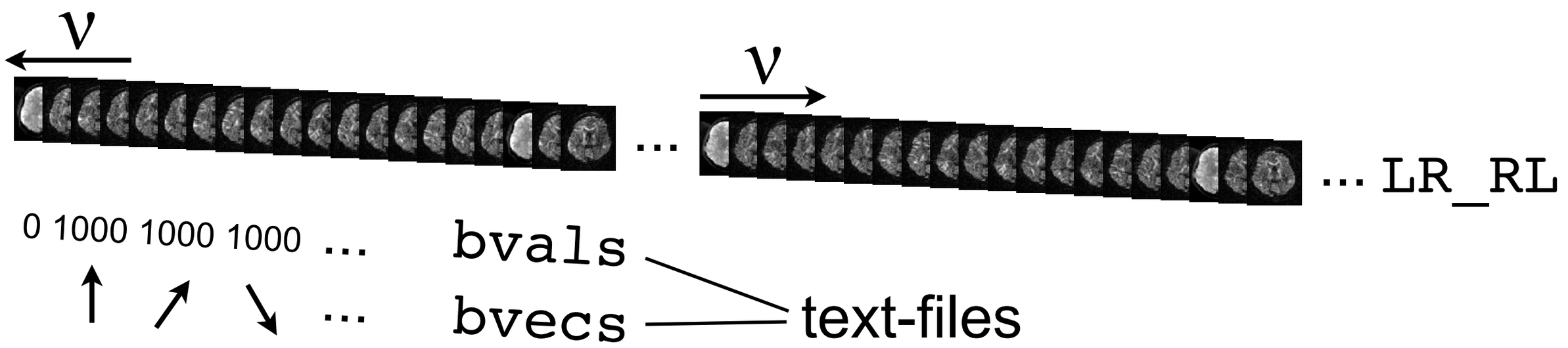
```
-1 0 0 0.051
-1 0 0 0.051
1 0 0 0.051
1 0 0 0.051
```

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
```

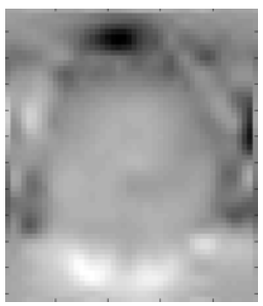
my_topup_movpar.txt

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

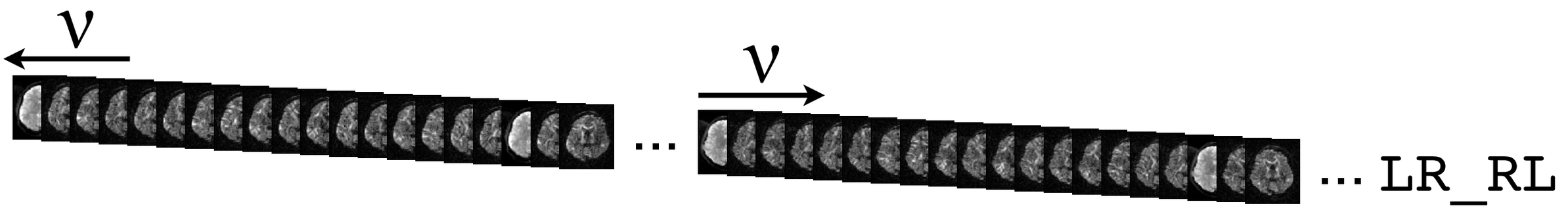


```
-1 0 0 0.051
-1 0 0 0.051
1 0 0 0.051
1 0 0 0.051
```
acqparams.txt

```
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

```
1111...
```
indx.txt

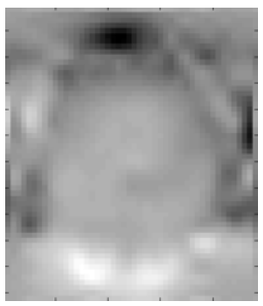
And where the brain is



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



```
-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

1111...

indx.txt

0 1000 1000 1000 ...

bvals

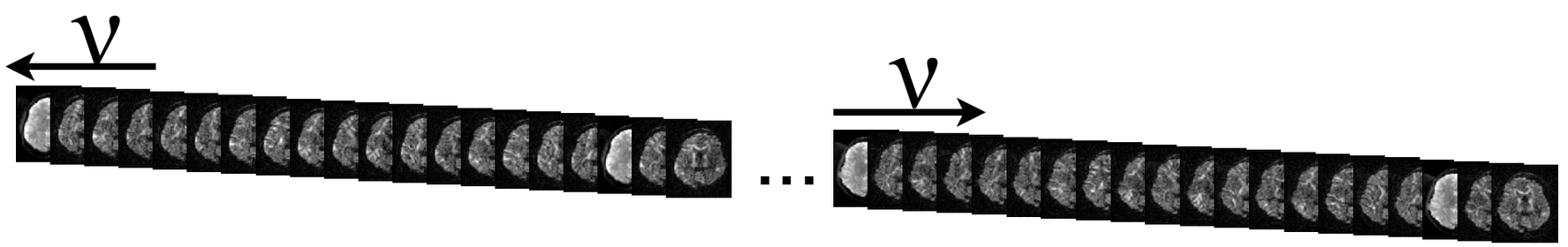
↑ ↗ ↘ ...

bvecs

And now we can run eddy

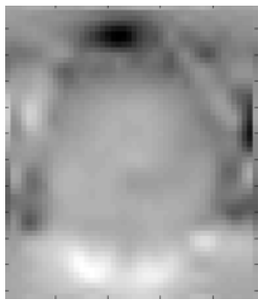
```
eddy --imain=LR_RL --acqp=acqparams.txt
--index=indx.txt --bvecs=bvecs
--bvals=bvals --mask=brain_mask
--topup=my_topup --out=my_eddy
```

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



brain_mask.nii

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

```
1111...
```

indx.txt

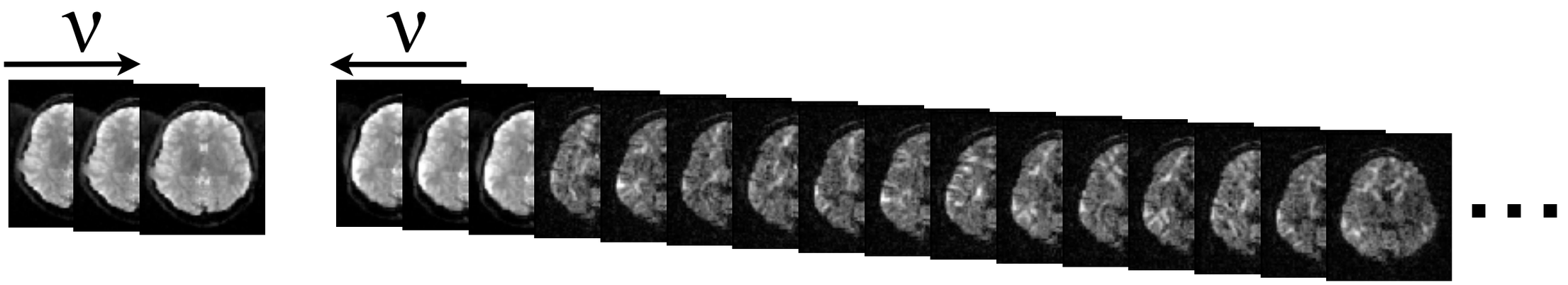
```
0 1000 1000 1000 ...
```

bvals

↑ ↗ ↘ ...

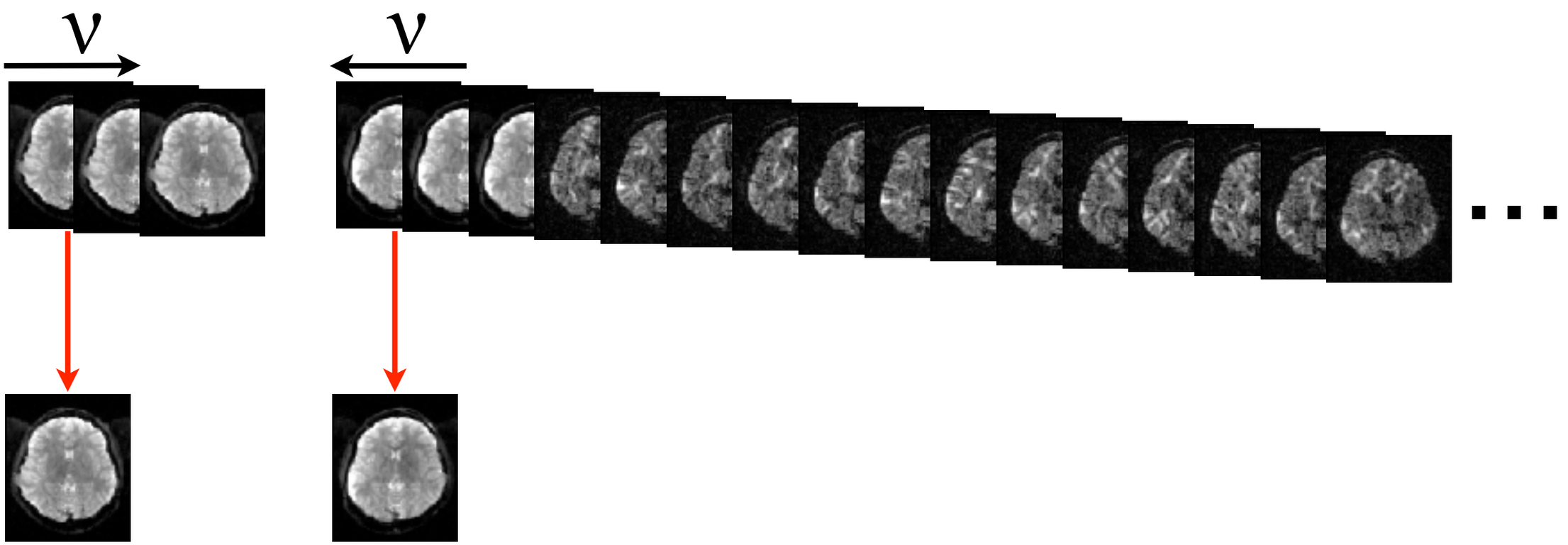
bvecs

A simpler (and perhaps more realistic) example



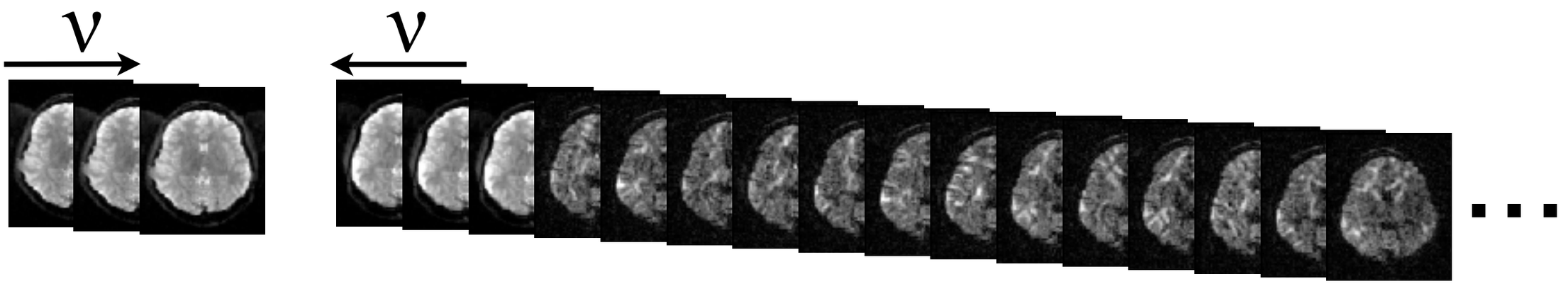
- Data consists of:
  - *N* diffusion weighted volumes and *n* *b*=0 volumes
  - *b*=0 volumes interspersed, but 2–3 are up front.
  - 2–3 b=0 volumes with opposing PE acquired just before the acquisition of the diffusion data set.

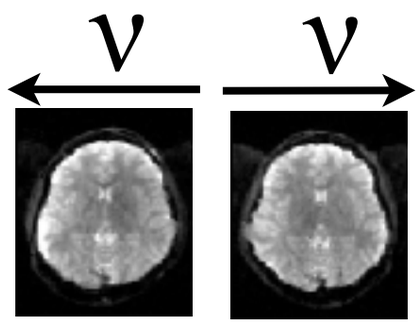
A simpler (and perhaps more realistic) example



Extract one “good” *b*=0 volume for each PE-direction using `fslroi`

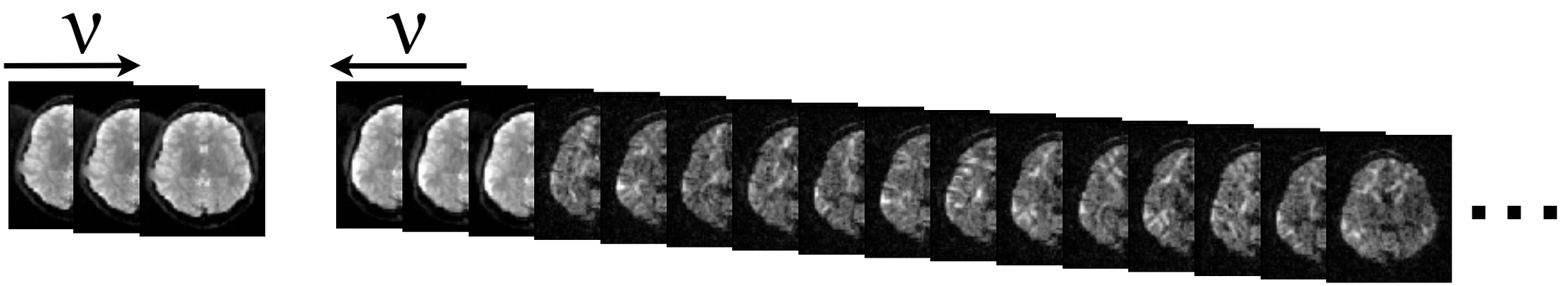
A simpler (and perhaps more realistic) example

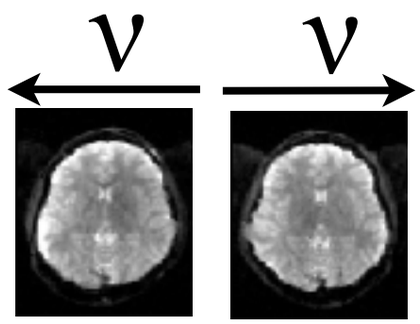




Collect them into one 4D file using `fslmerge`

A simpler (and perhaps more realistic) example

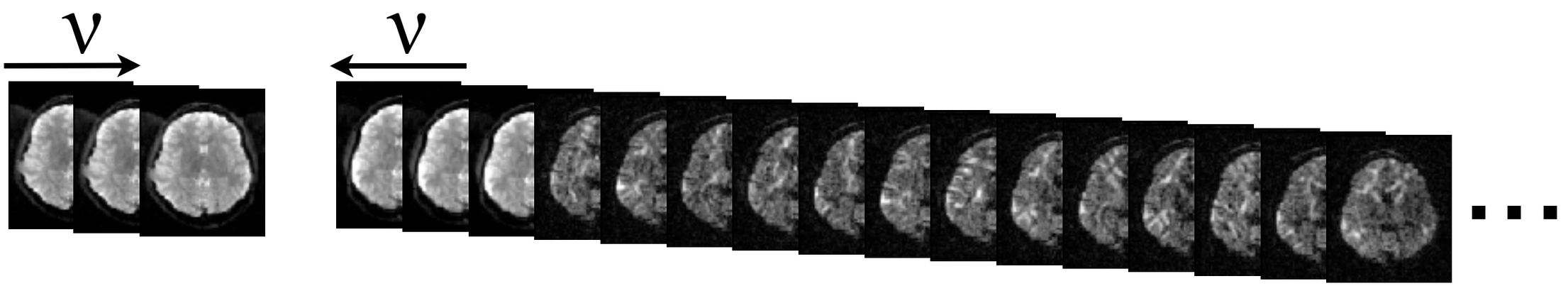


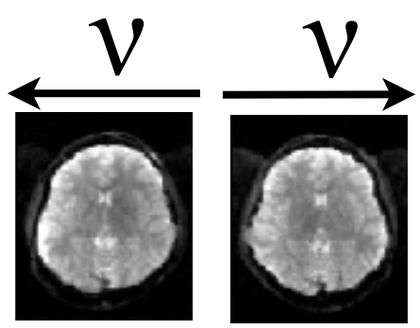



```
-1  0  0  0.051
1  0  0  0.051
```

Create text file `acqparams.txt`

A simpler (and perhaps more realistic) example



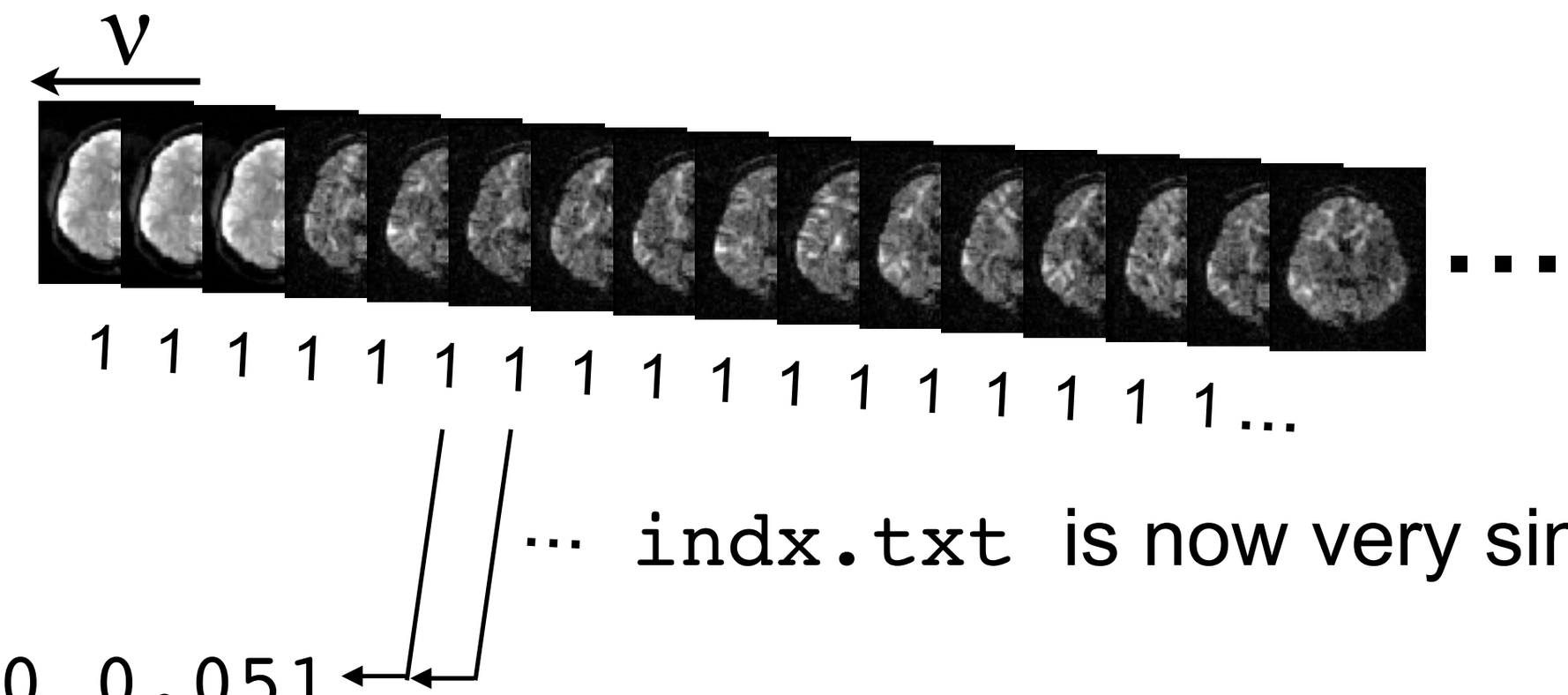



```
-1  0  0  0.051
1  0  0  0.051
```

And run `topup`

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

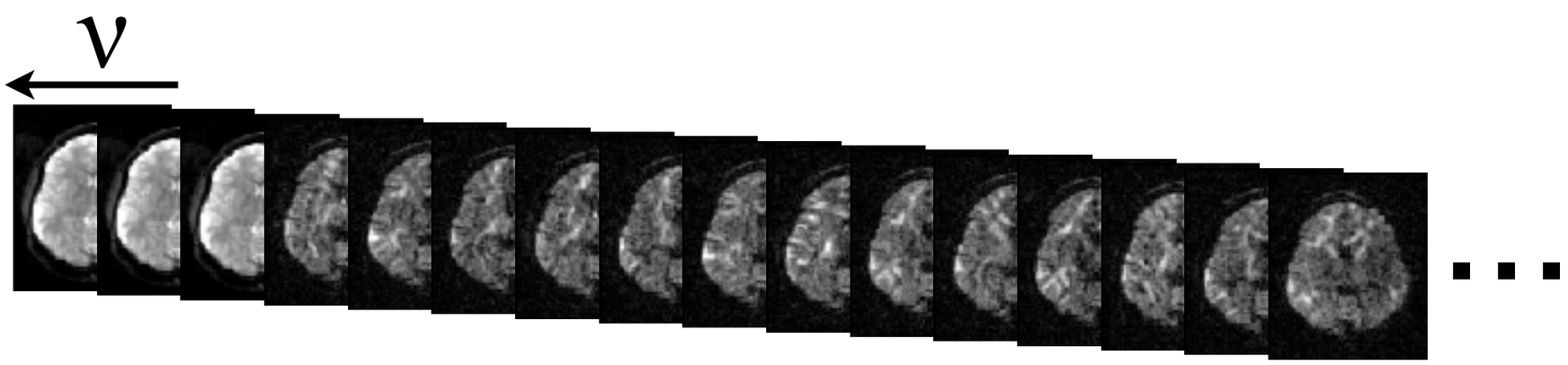
A simpler (and perhaps more realistic) example



... `indx.txt` is now very simple

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

A simpler (and perhaps more realistic) example




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

And the `eddy` command is the same as before (N.B. you need to create `brain_mask.nii.gz` in the same way as before)

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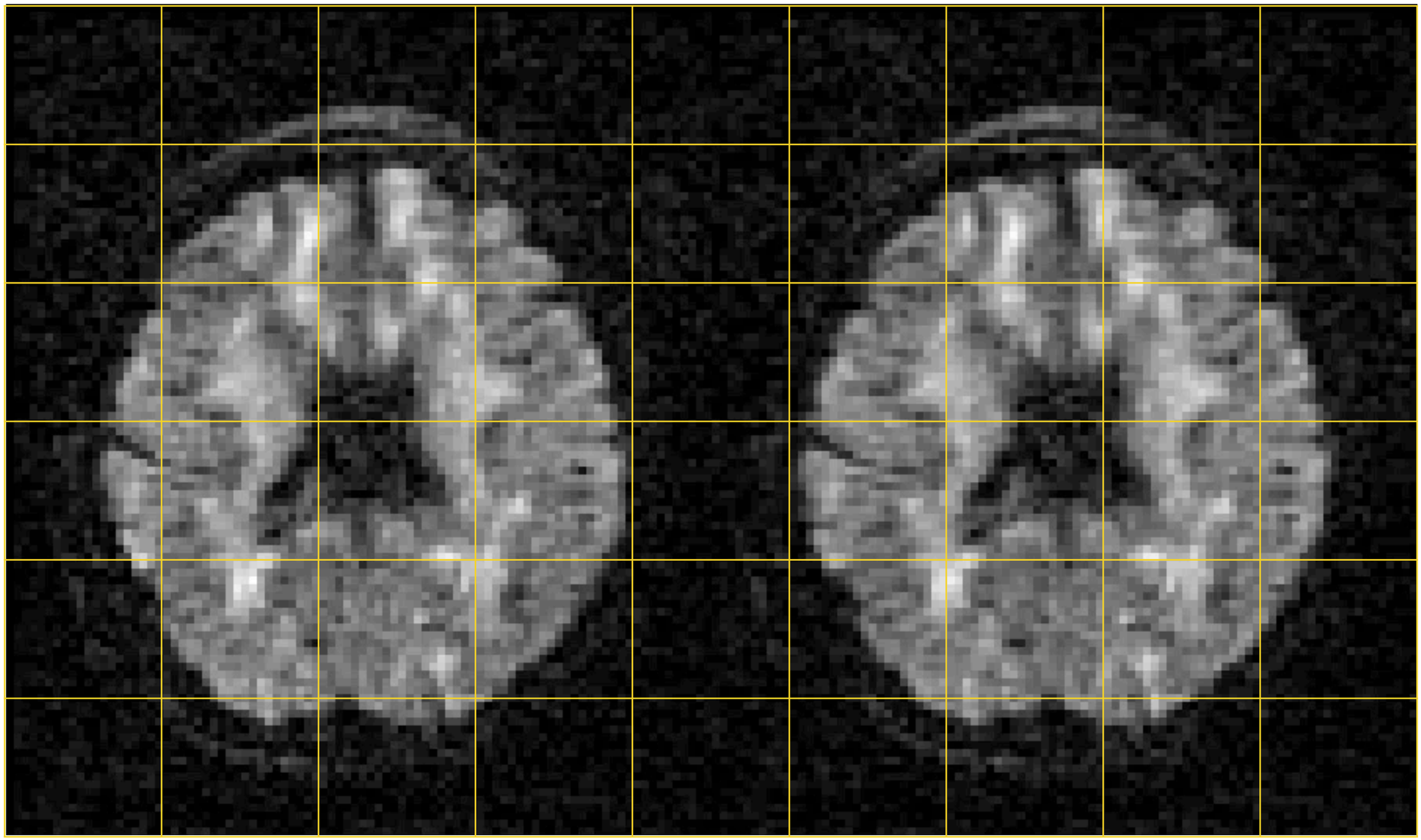
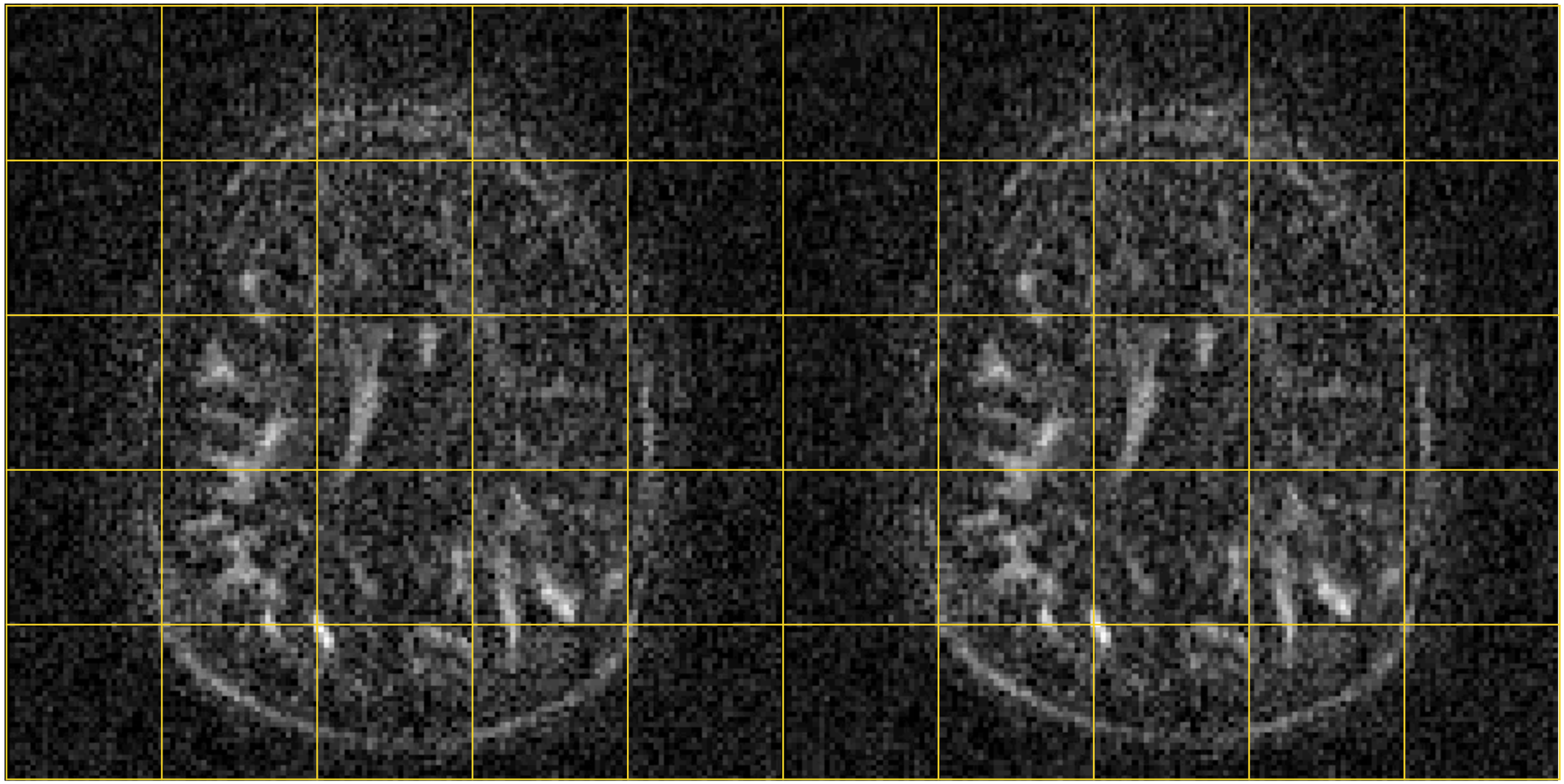
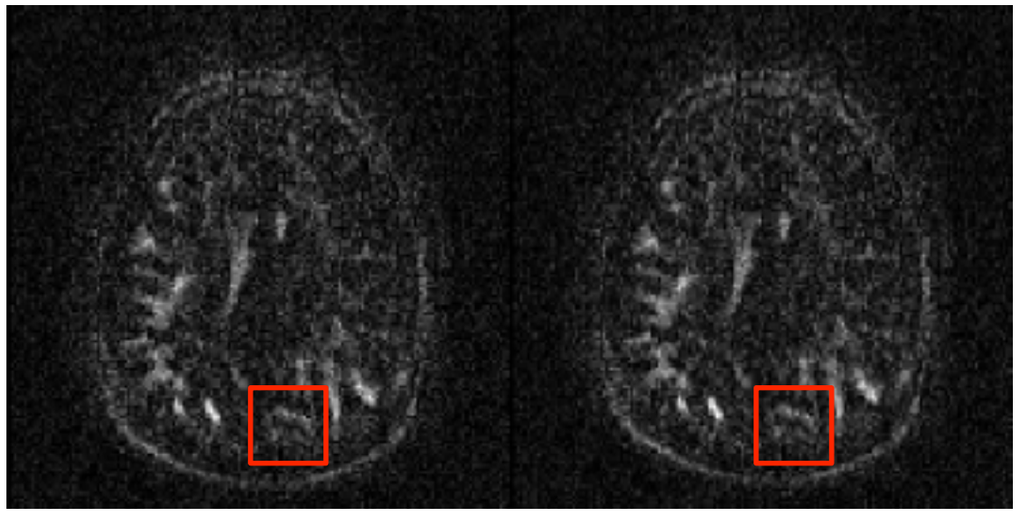
HCP-data, 150 directions, b=3000, blip-up-blip-down

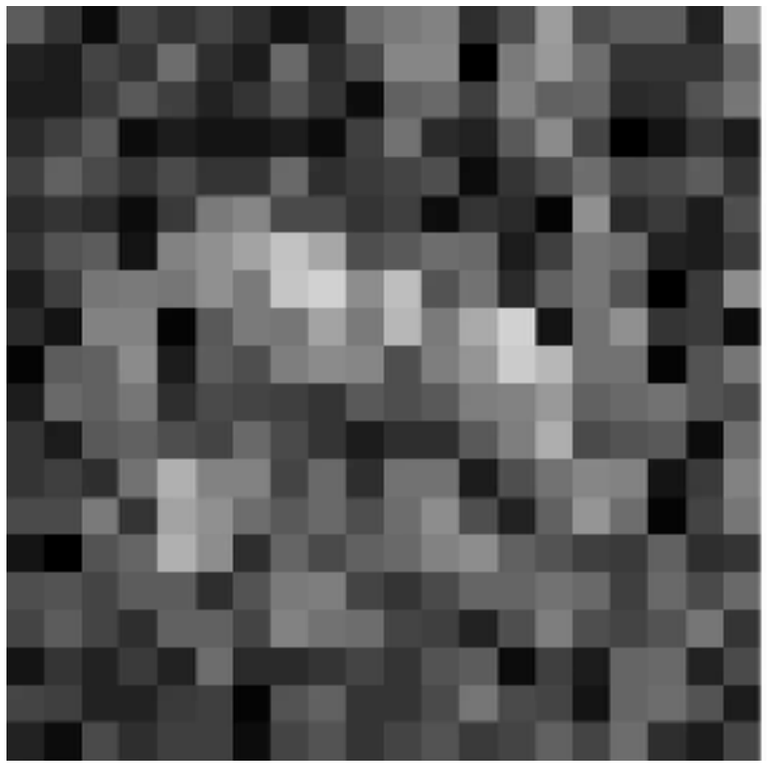


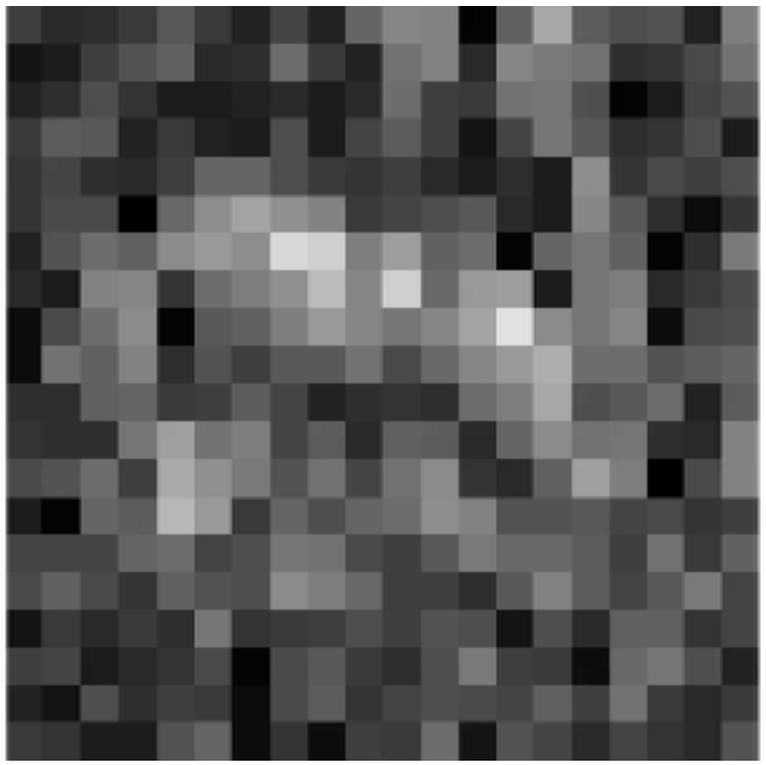
MGH-data, 198 directions, b=10000!



MGH-data, 198 directions, b=10000!







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EDDY QC: data quality summary

QUAD
(subject)

S1/qc.json
S2/qc.json
S3/qc.json
.
.
.
Sn/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

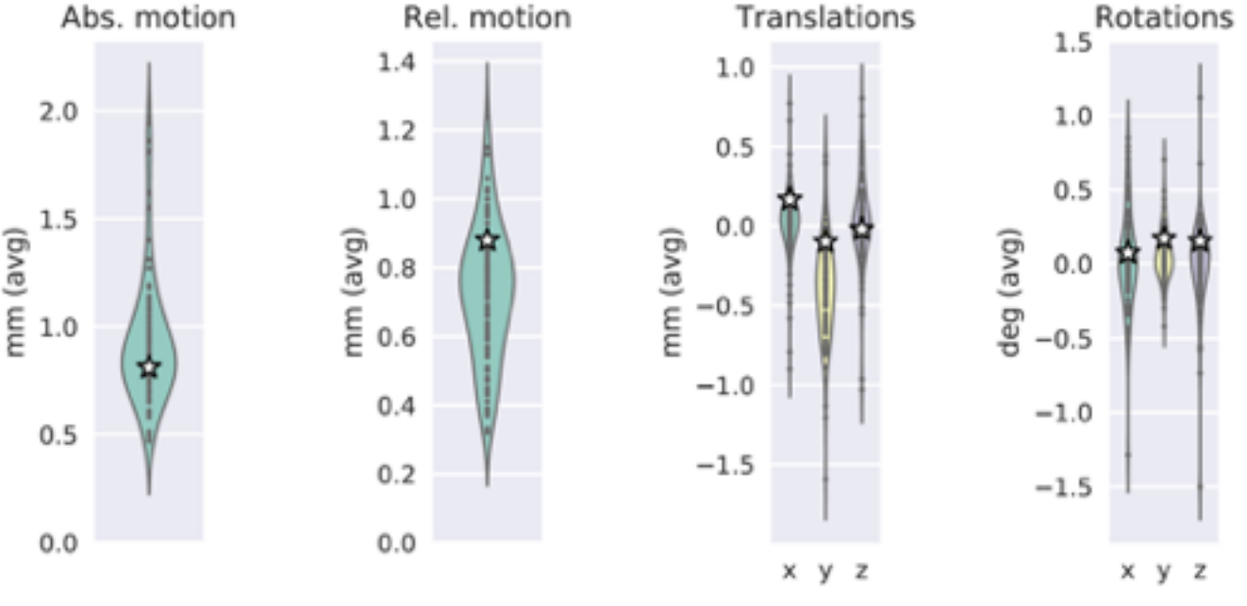
Average abs. motion (mm)	0.81
Average rel. motion (mm)	0.88
Average x translation (mm)	0.17
Average y translation (mm)	-0.10
Average z translation (mm)	-0.02
Average x rotation (deg)	0.07
Average y rotation (deg)	0.17
Average z rotation (deg)	0.15

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

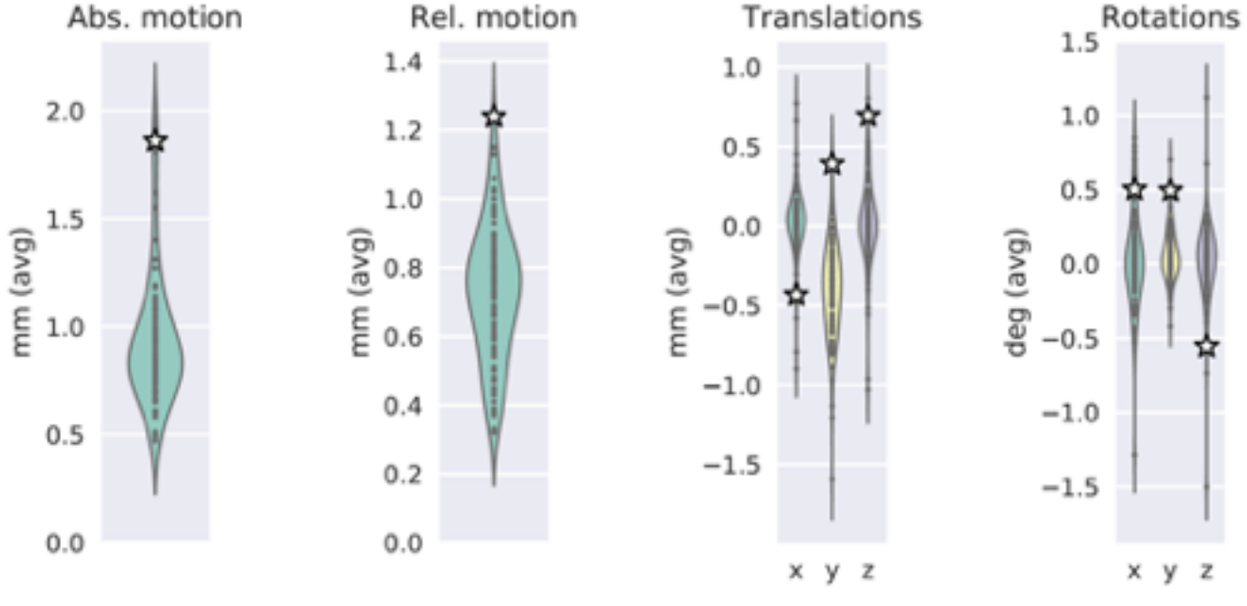
Average abs. motion (mm)	1.86
Average rel. motion (mm)	1.24
Average x translation (mm)	-0.43
Average y translation (mm)	0.39
Average z translation (mm)	0.69
Average x rotation (deg)	0.50
Average y rotation (deg)	0.49
Average z rotation (deg)	-0.55

Within-volume motion

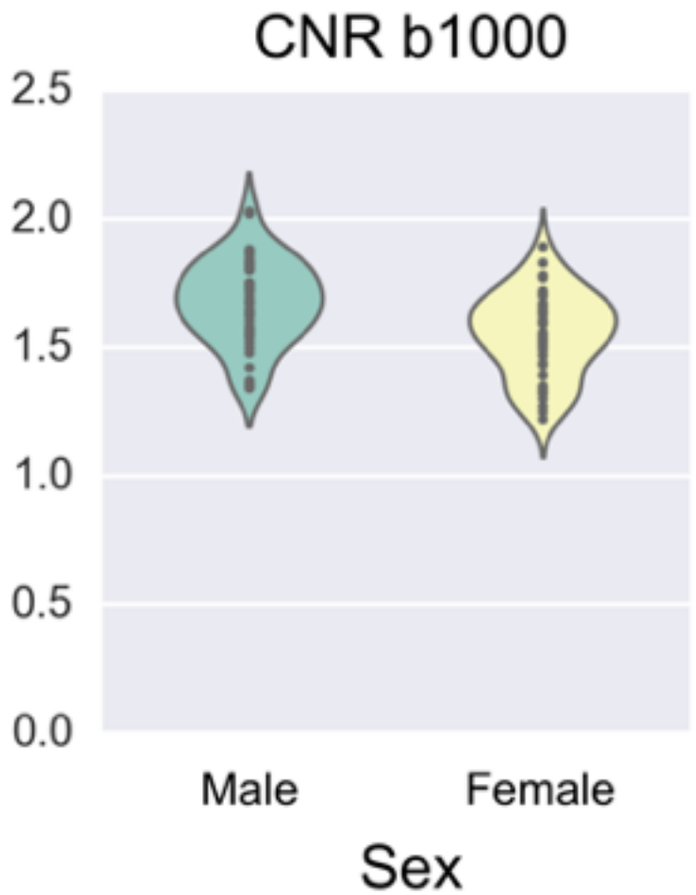
Avg std x translation (mm)	0.08
Avg std y translation (mm)	0.22
Avg std z translation (mm)	0.13
Avg std x rotation (deg)	0.15
Avg std y rotation (deg)	0.09
Avg std z rotation (deg)	0.11

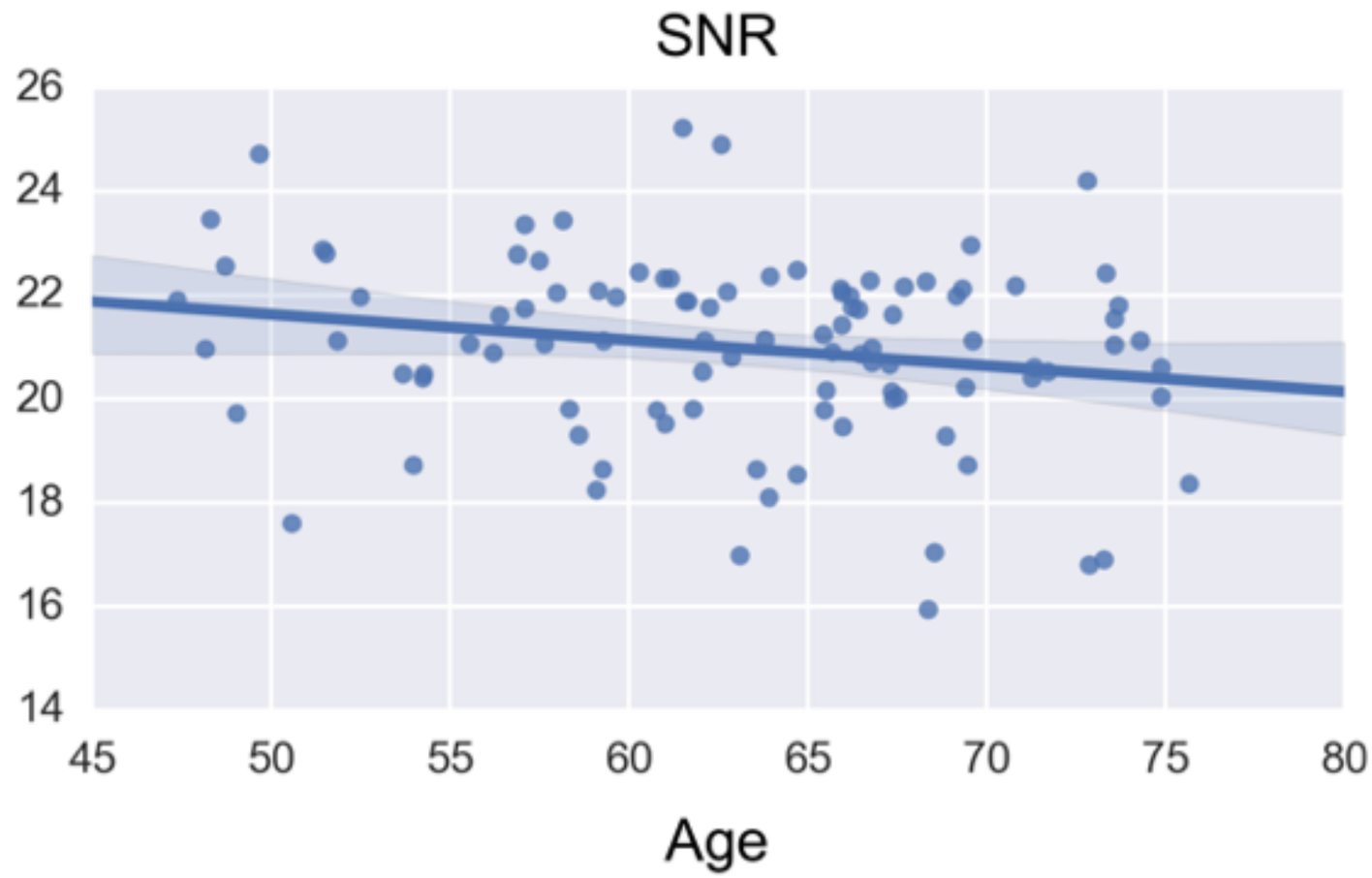
Outliers

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

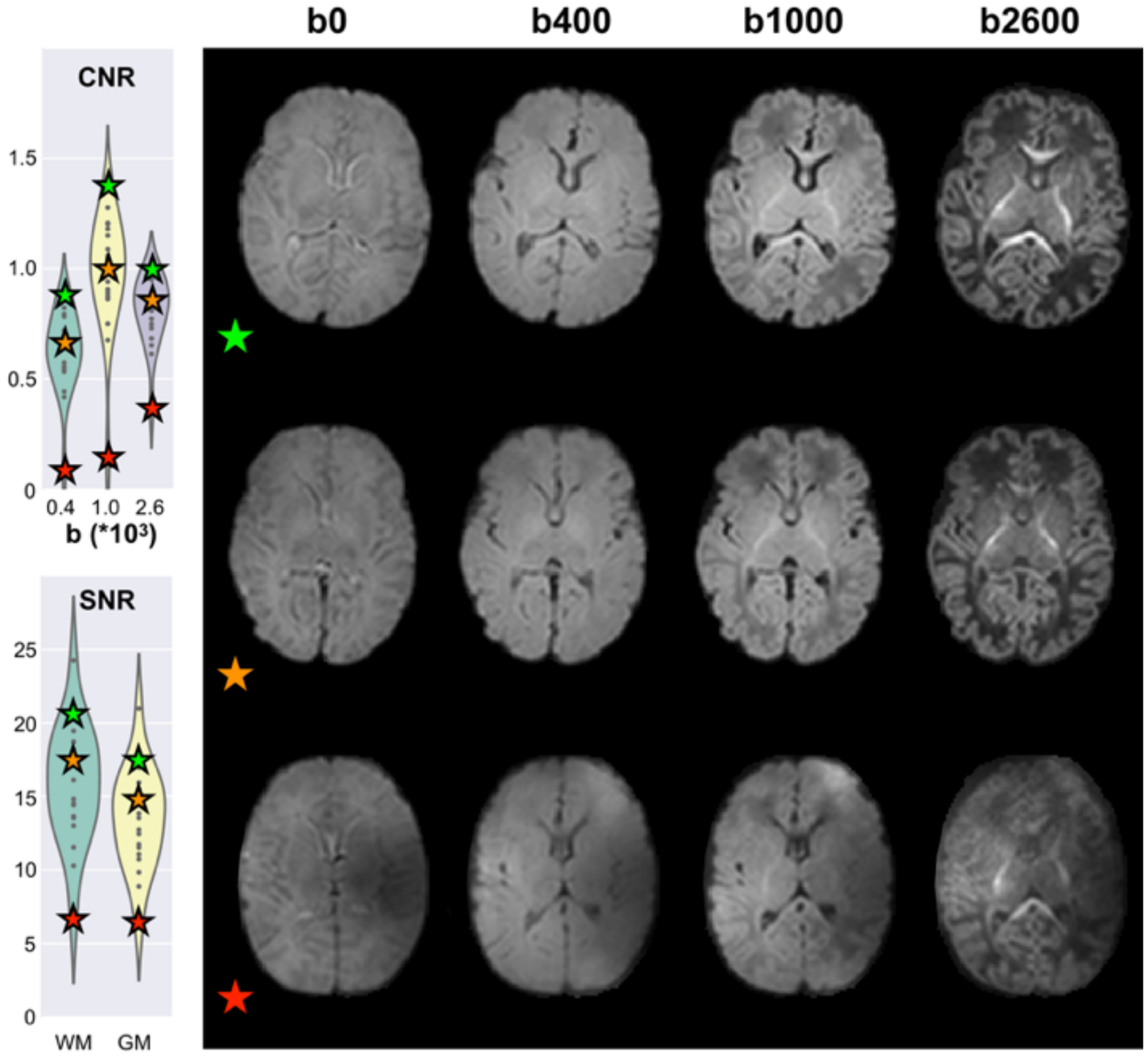


EDDY QC: group report





Data quality illustration



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