# Explore DWI data, with FSLview

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### 0. Objective

The goal of this tutorial is to explain how to conduct a careful examination of diffusion-weighted imaging (DWI) data, using FSLview.

In my experience of helping the users of the NODDI matlab toolbox, I have encountered many individuals who have never explored the raw DWI data in a way that, I think, is fundamental to understanding the information provided by the data. Many I have found to look at DWI data as a stack of 3-D volumes; they only examine each 3-D volume individually.

In this tutorial, I will show instead how to explore the data, one voxel at a time and along the stack. This strategy is key to appreciate the characteristics of DWI data and can help identify issues in data formatting and/or acquisition.

### 1. Prerequisite

You should have FSL installed and have downloaded the NODDI Example dataset. If not, FSL can be downloaded from here and NODDI Example dataset from here.

### 2. Basics of fslview

To launch **fslview**, you can use either Graphical User Interface (GUI) or Command Line Interface (CLI).

I will give the command for CLI below.

I have my data in the directory:

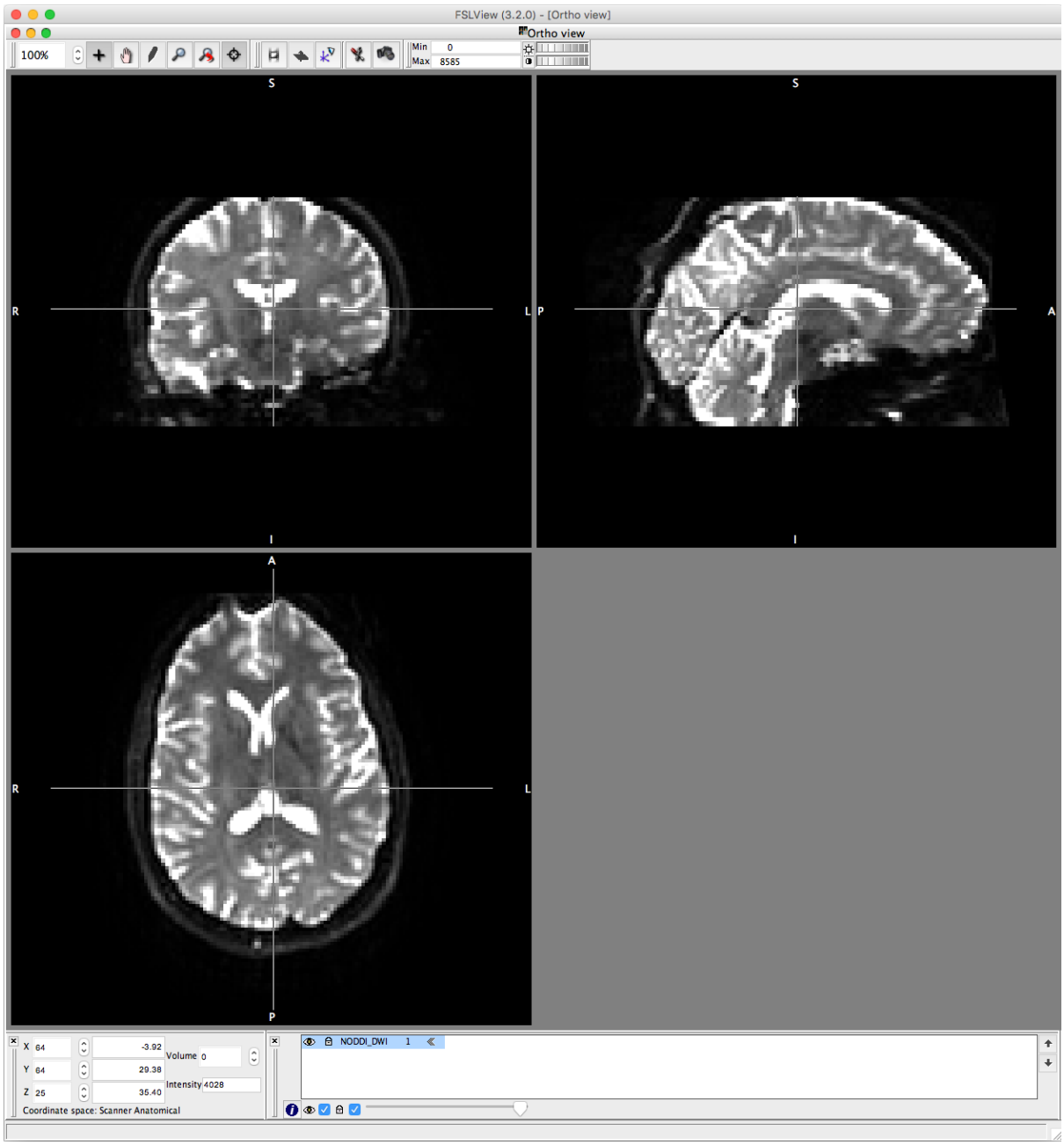
```
/Users/gzhang/unix/research/projects/NODDI/NODDI_example_dataset
```

So I need to do:

```
$cd /Users/gzhang/unix/research/projects/NODDI/NODDI_example_dataset
$fslview NODDI_DWI.hdr
```

Note that the `$` sign is the command line prompt, not part of the commands.

If you have done this successfully, you should see the following screenshot pop up:




## 2.1 Screenshot explained

Let me walk through what the screenshot shows in a bit detail:

A 3-D image (volume) is visualised by showing **three orthogonal slices** cutting through the volume, which are known as axial slice (bottom right), sagittal slice (top right), and coronal slice (top left).

These three slices **intersect at a voxel** the location of which is marked out by the intersecting lines in each slice view. This **intersection voxel** can be chosen by the mouse cursor.

The orthogonal slices relate to the coordinate of the intersection voxel in distinct ways. The axial slice includes every voxel sharing the same **z coordinate** as the intersection voxel; the sagittal slice the same **x coordinate**; and the coronal slice the same **y coordinate**.

The panel underneath these slice views provides important numerical information; zooming in on the screenshot to make the numbers more legible if necessary. They are explained below:

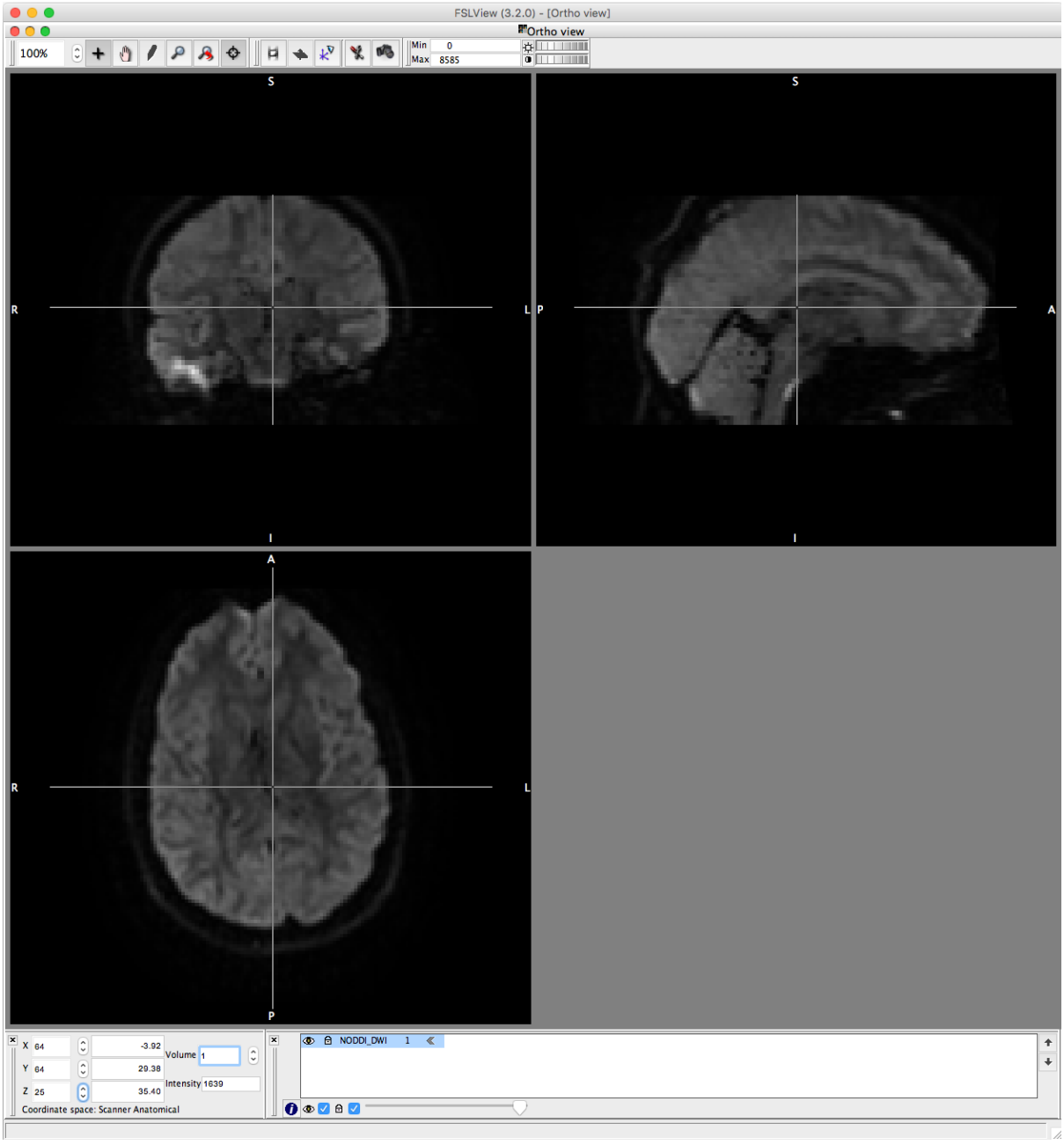
- The spatial **coordinate** of the intersection voxel, in terms of non-negative integers: x = 64, y = 64, z = 25, or [64, 64, 25]. The x axis runs from Right to Left; y from Posterior to Anterior; z from Inferior to Superior. fslview employs indexing that starts from 0. As such, [0, 0, 0] corresponds to the right most, most posterior and inferior voxel.

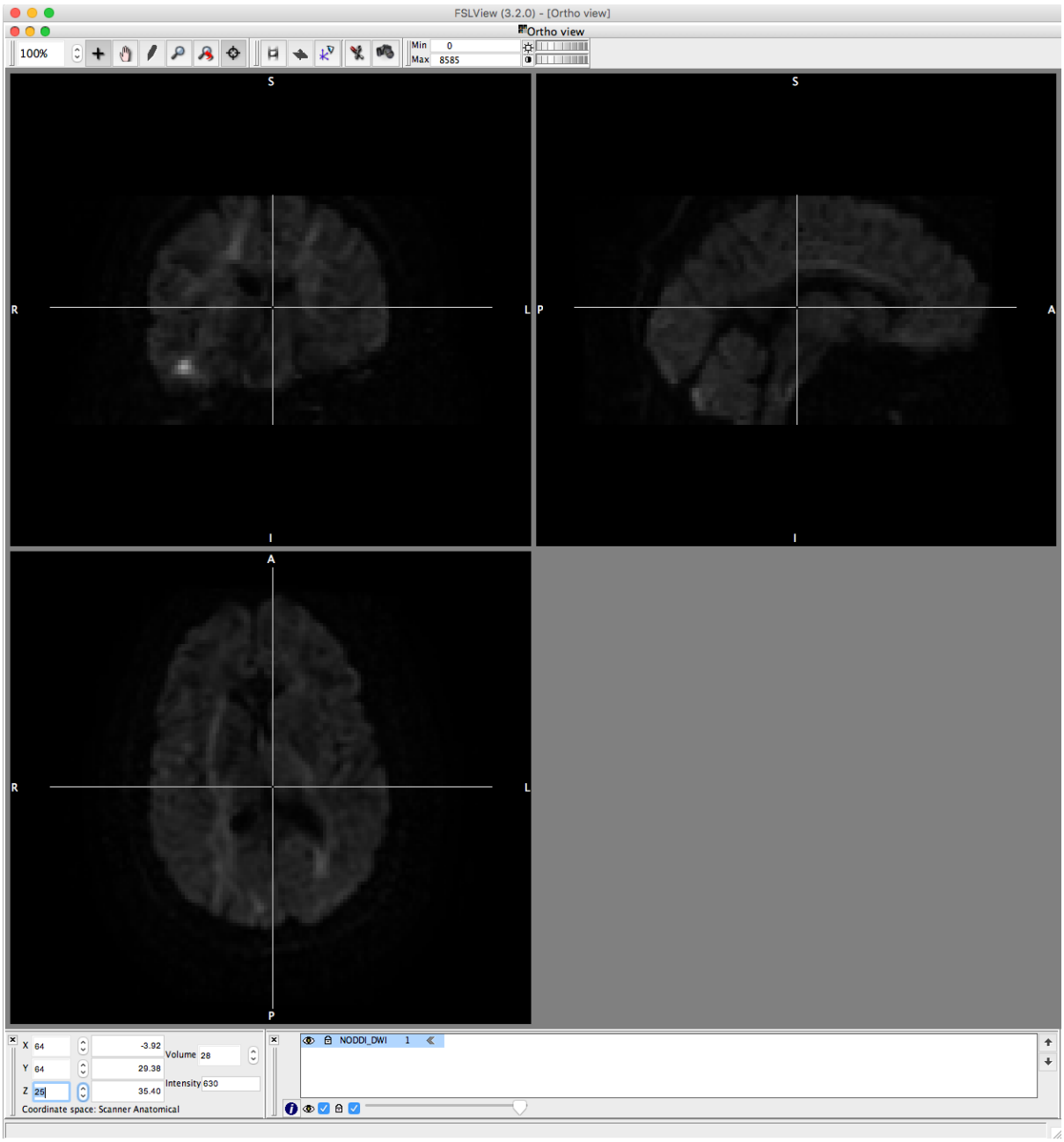
- The grayscale **intensity** of the intersection voxel: 4028.

- The **Volume index**, the "coordinate" of the shown 3-D volume within the 1-D stack of 3-D volumes (i.e., a 4-D volume): 0. NODDI_DWI.hdr is a 4-D volume that consists a stack of 3-D volumes. The Volume index also starts from 0, representing the first 3-D volume within the volume stack, which is a b=0 image.

### 2.2 Navigating through the 3-D volume stack

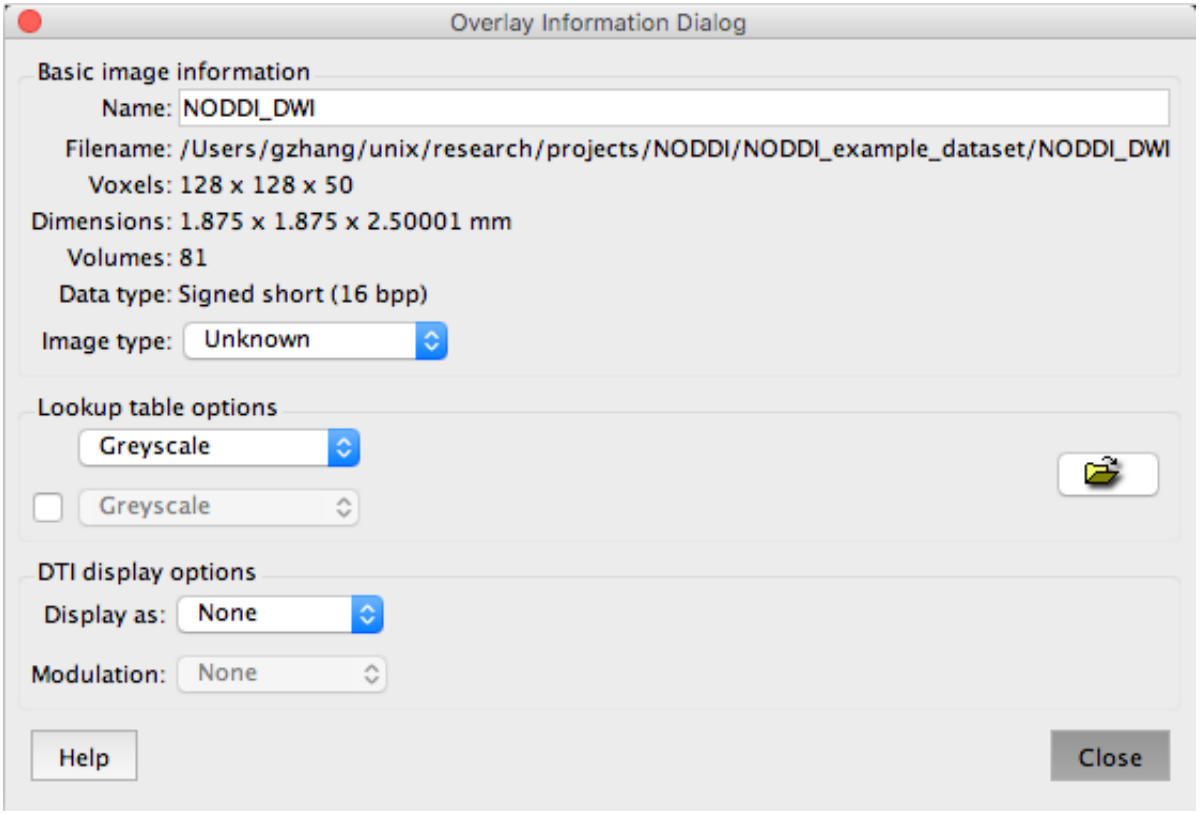
By manually altering the Volume index, one can display each 3-D volume within the stack. The screenshots below give two examples showing the first b=700 volume of b=700 (Volume index = 1) and the first b=2000 volume (Volume index = 28). The intensity of the intersection voxel is equal to 1639 and 630 respectively for the two volumes, showing rapid signal decay from increasing b-values.


FSLView (3.2.0) - [Ortho view]
Ortho view
100%
Min 0
Max 8585
S
R
L
I
P
A
X 64 -3.92
Y 64 29.38
Z 25 35.40
Volume 1
Intensity 1639
Coordinate space: Scanner Anatomical
NODDI_DWI 1




## 2.3 Accessing additional image information

Click the little icon with an “i” in the centre presents further information about the volume that looks like the screenshot below.

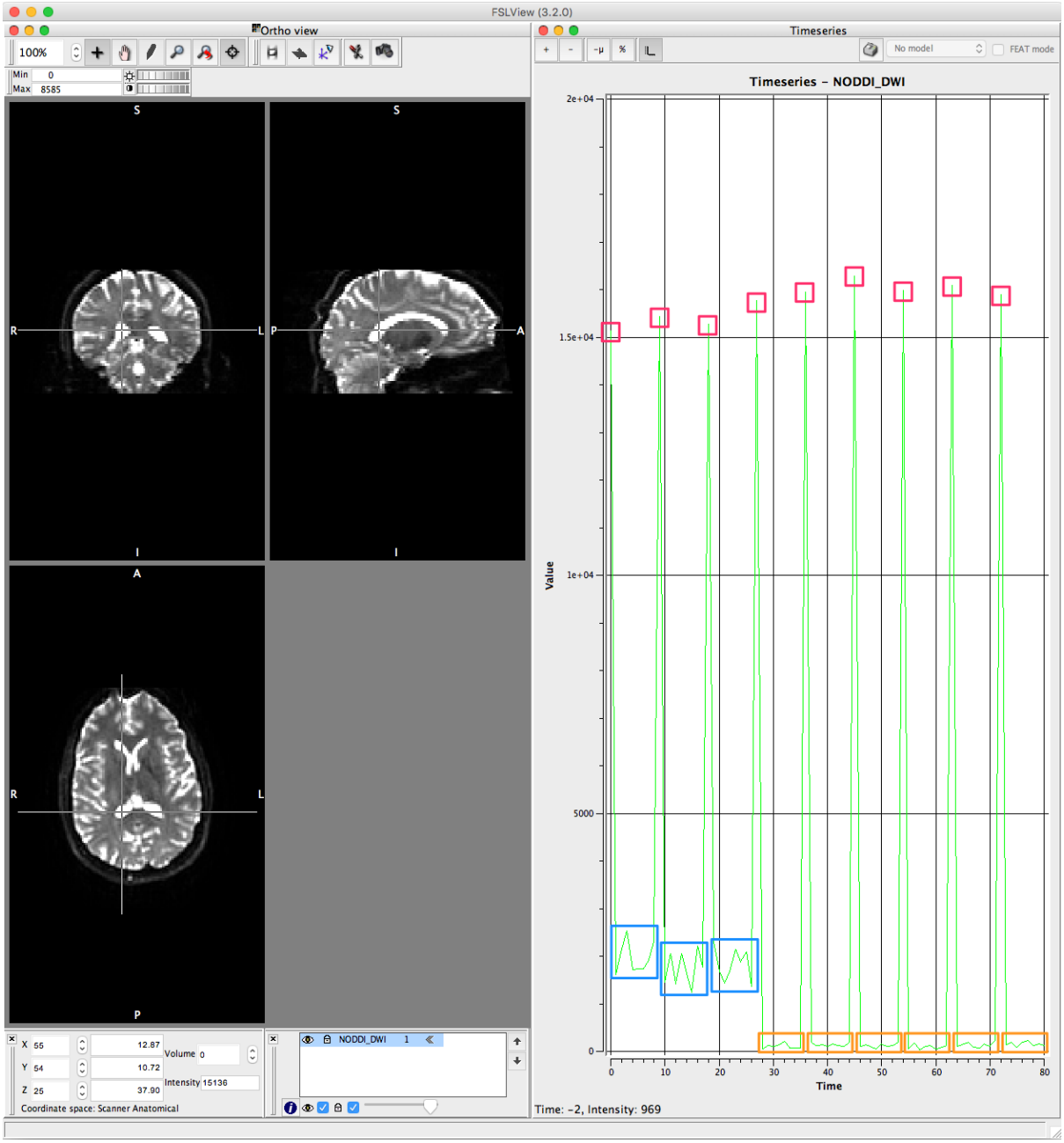



It shows the number of voxels along each spatial dimension (128 along the x axis, 128 along y, and 50 along z). It gives the dimension of each voxel (1.875 mm along x, 1.875 mm along y, and 2.5 mm along z). Finally, it gives the number of 3-D volumes in this 4-D volume (81).

These 81 volumes represent 81 settings under which a DWI measurement has been made. With the present view, we can examine the measurement made under one of these settings for each voxel within the 3-D volume. What we can not do is to examine all 81 measurements made for a given voxel; but we can with the "**Time Series**" view discussed next, which is the focus of this tutorial.

### 3. Time Series view

The Time Series view can be activated by choosing the menu option "**Tools**", then "**Timeseries**". This will show all the measurements along the Volume index dimension for the intersection voxel, as illustrated with the screenshot below:




This example has chosen a voxel in **the ventricle** as the intersection point ([55, 54, 25]). The signal intensity variation reveals how the measurements have been acquired. There are 9 high peaks (~16,000; marked out in small red squares) corresponding to the b=0 measurements. The 72 non b=0 measurements are evenly split up between the b=0's, i.e., 8 measurements per split. The first three sets have intermediate intensity values (~2,000), corresponding to the 24 b=700 measurements (marked out in blue rectangles). The last six sets have the lowest intensity values (~100), corresponding to the 48 b=2000 measurements (marked out in orange rectangles).

### 3.1 Check consistency with bval

This example shows that, for most common single- or multi-shell DWI acquisitions, one

can easily identify, from the time series, which measurements are acquired with which b-values. This information **must** be **consistent** with the **ordering** encoded in the **bval** file.

A common issue with data organisation is the **inconsistency** between how the measurements are ordered in the 3-D volume stack and how the b-values are ordered in the bval file. This is a simple but important thing to check when working with DWI data.

## 4. Exploration of DWI

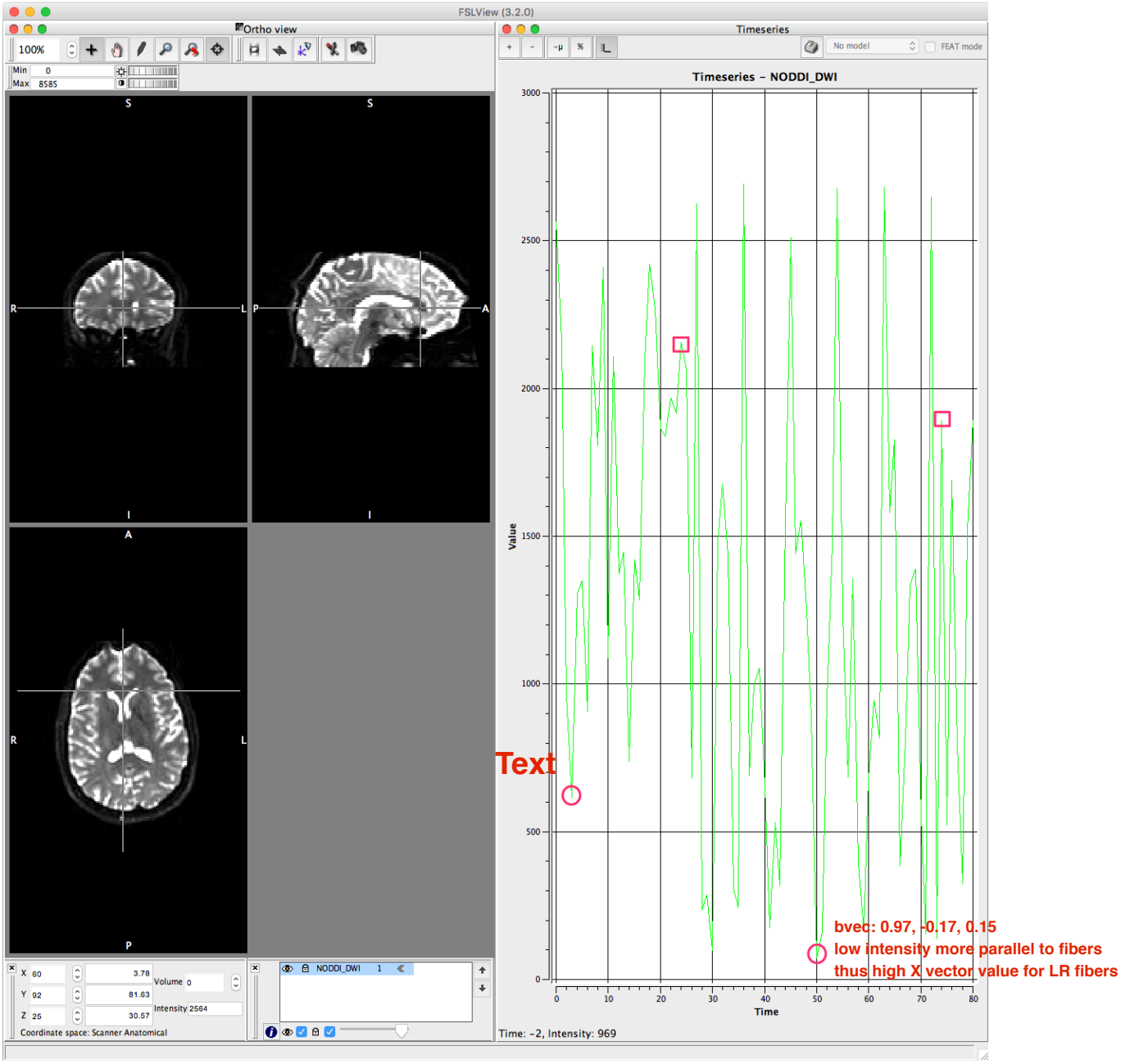
Now that we have all the tools to explore the raw DWI data, I will now examine several representative examples of typical gray matter (GM) and white matter (WM) regions.

### 4.1 DWI signals of White Matter

We will look at three examples, including two regions with coherently aligned axons and one region with crossing axons.

#### 4.1.1 Genu of the Corpus Callosum

The first example is a voxel in the **genu of the corpus callosum** ([60, 92, 25]), a region of WM known to exhibit the highest diffusion anisotropy. Compared to the ventricle voxel, the b=0 signals are significantly lower (~2500), with lower signal-to-noise ratio (SNR).




The b=700 measurements vary dramatically for different gradient directions, ranging from ~600 to ~2100. This **strong signal dependence on gradient direction** is the hallmark of diffusion anisotropy. Higher the signal is, more perpendicular is the corresponding gradient direction to the underlying (axon) fibres. Subject to the effect of noise, the highest signal (marked out with squares for b=700 and b=2000 respectively) correspond to the gradient direction that is the most perpendicular to the underlying fibres; the lowest signal (marked out with circles) to the gradient direction that is the most parallel to the underlying fibres.

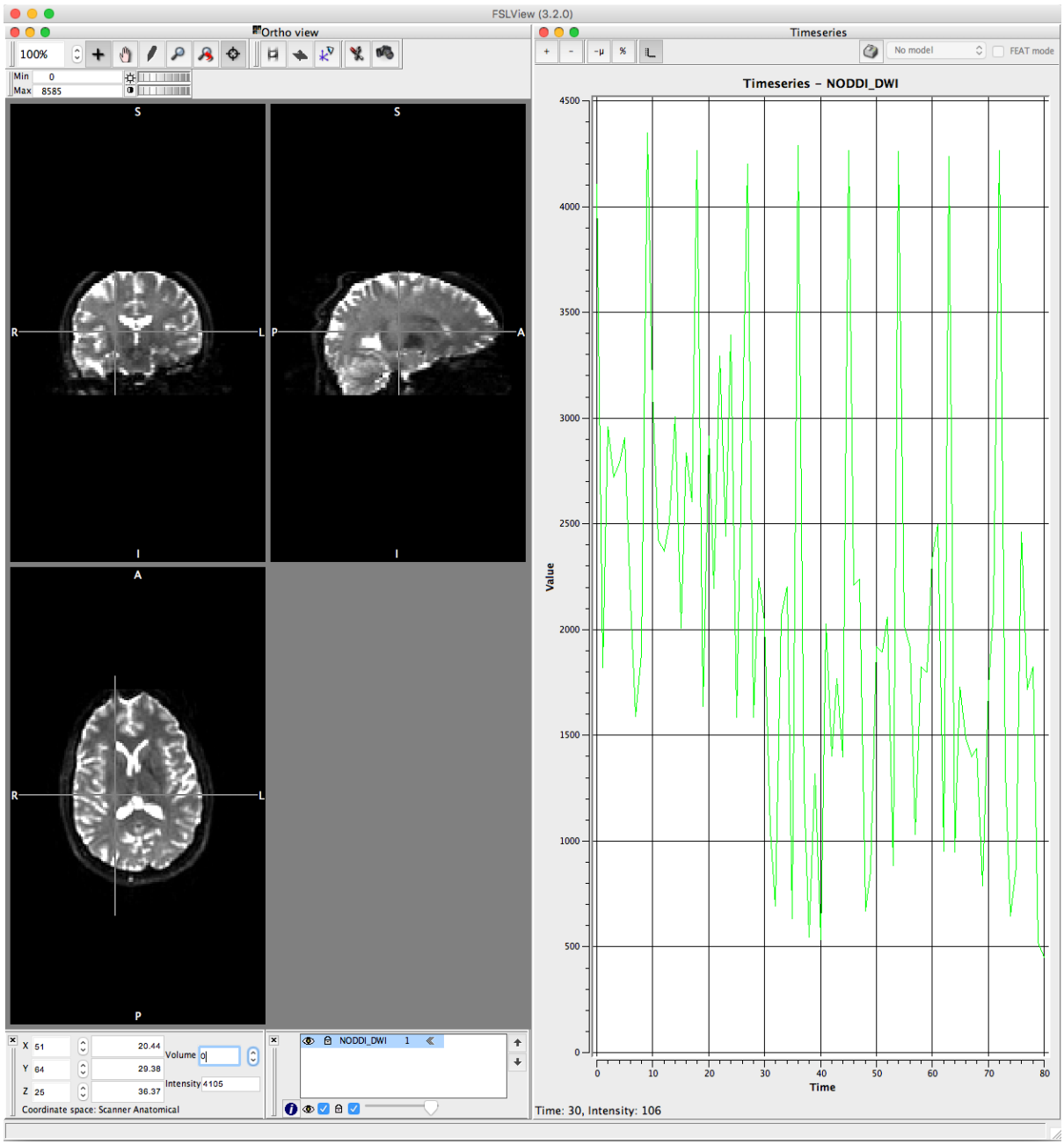
The same observation applies to b=2000 measurements but with even **more** significant dependence on gradient direction; the intensities range from ~100 to ~1900. This is the hallmark for the presence of significant restricted diffusion.

#### 4.1.1.1 Trick for Checking Diffusion Gradient Table bvec/bval table

As the underlying fibre orientation of this structure is known, we can use this information to **check** if we have the correct gradient directions. In the imaging reference frame, the fibres should run from left to right. The measurement with the least intensity should have a gradient direction that is along the same direction. In other words, the gradient vector should have a very large X component in absolute value and very small Y and Z components. Similarly, the measurement with the highest intensity should have a gradient direction with a very small X component.

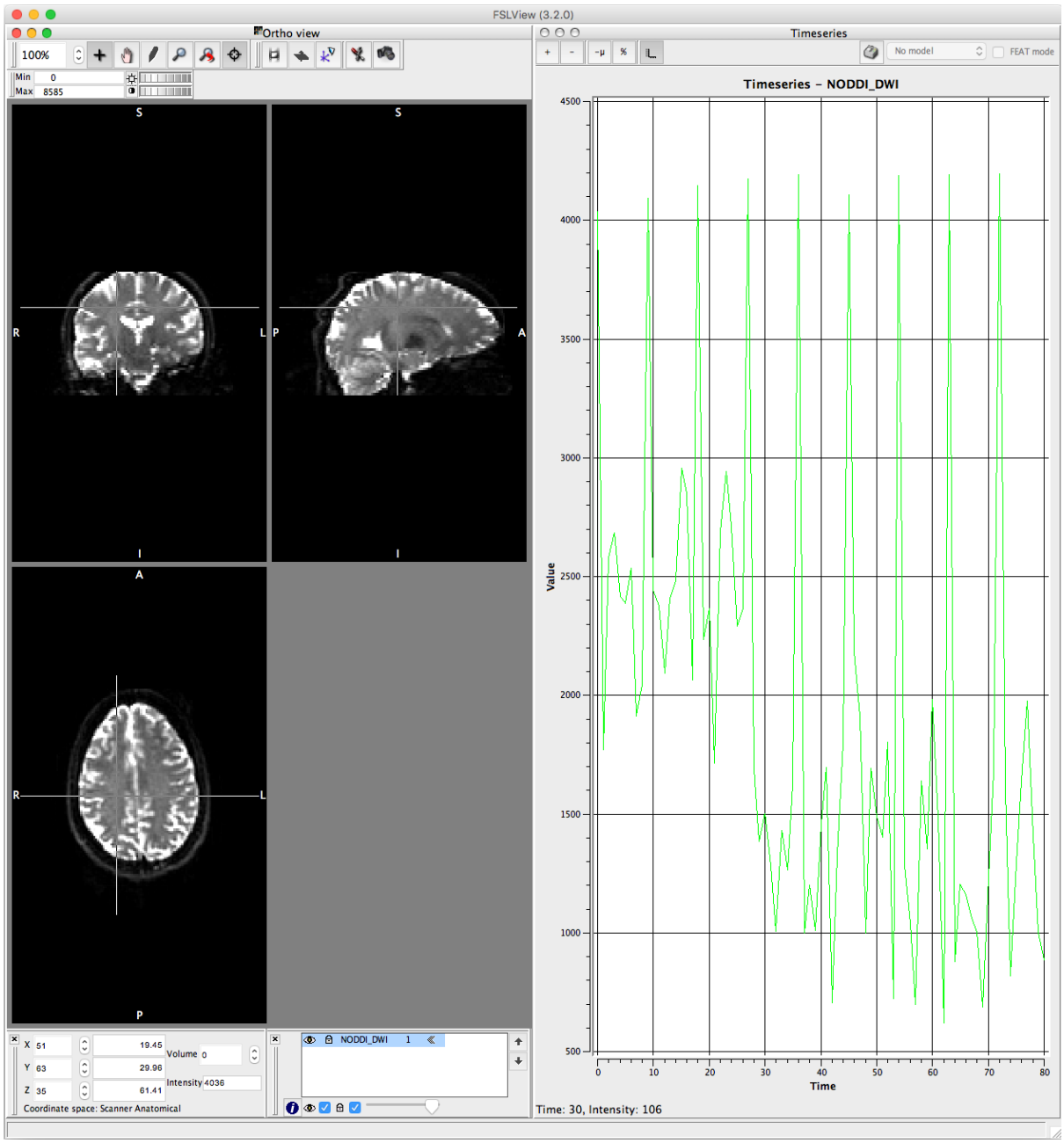
### 4.1.2 Posterior Limb of the Internal Capsule

The second example looks at a voxel in the **posterior limb of the internal capsule** ([51, 64, 25]). Here, the b=0 intensities (~4250) are higher than the genu of the corpus callosum, with improved SNR. The diffusion anisotropy is still very pronounced, although not as much as the genu of the corpus callosum.




### 4.1.3 Centrum Semiovalue

The final example is a voxel in **Centrum Semiovale**, a region known for the presence of crossing fibres between CC and the cortical spinal tract (CST). Here, the diffusion anisotropy is reduced further.

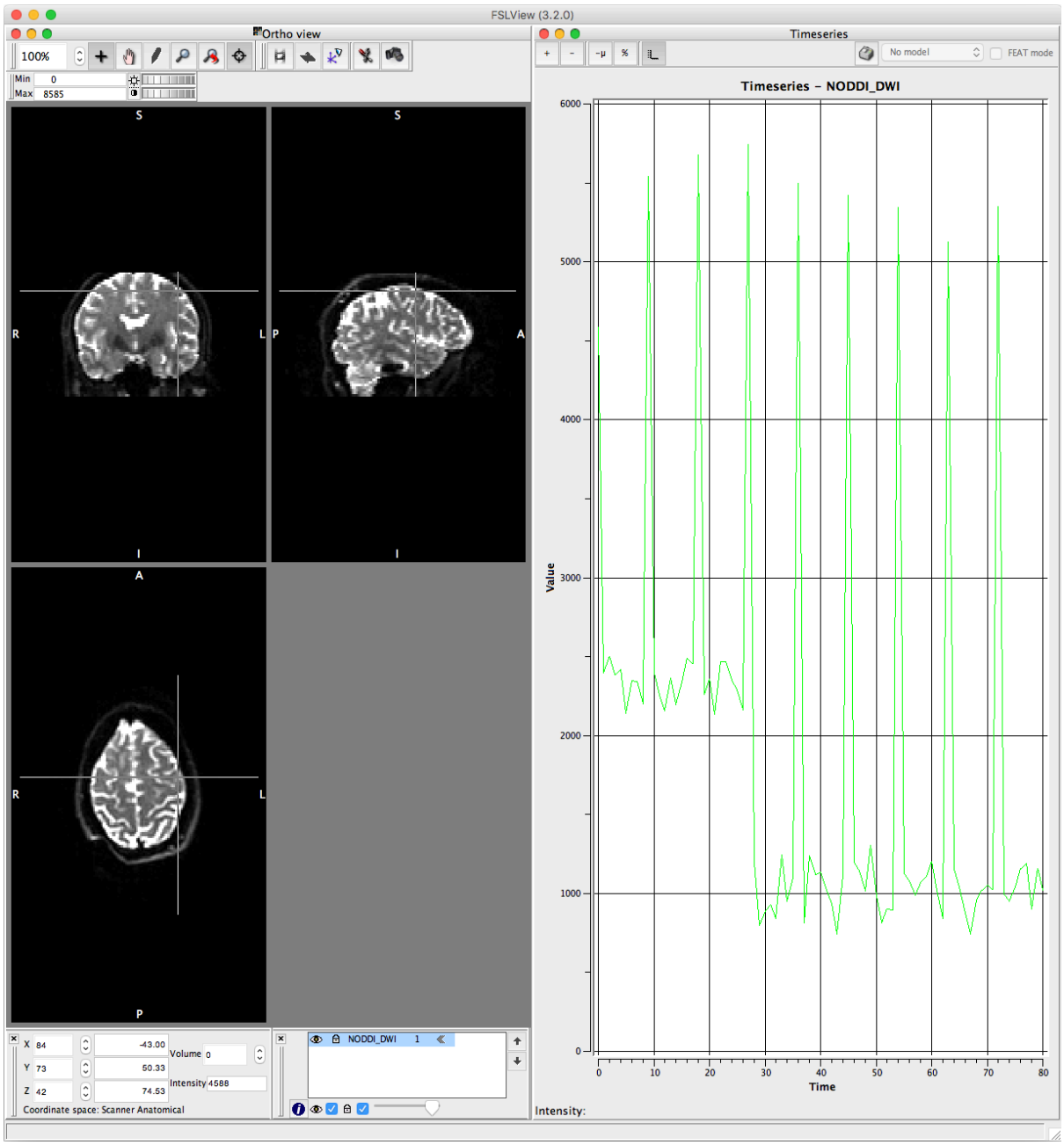



### 4.2 DWI signals of Gray Matter

We will look at three examples as well, including the cortex, the caudate and the thalamus.

#### 4.2.1 Cortex

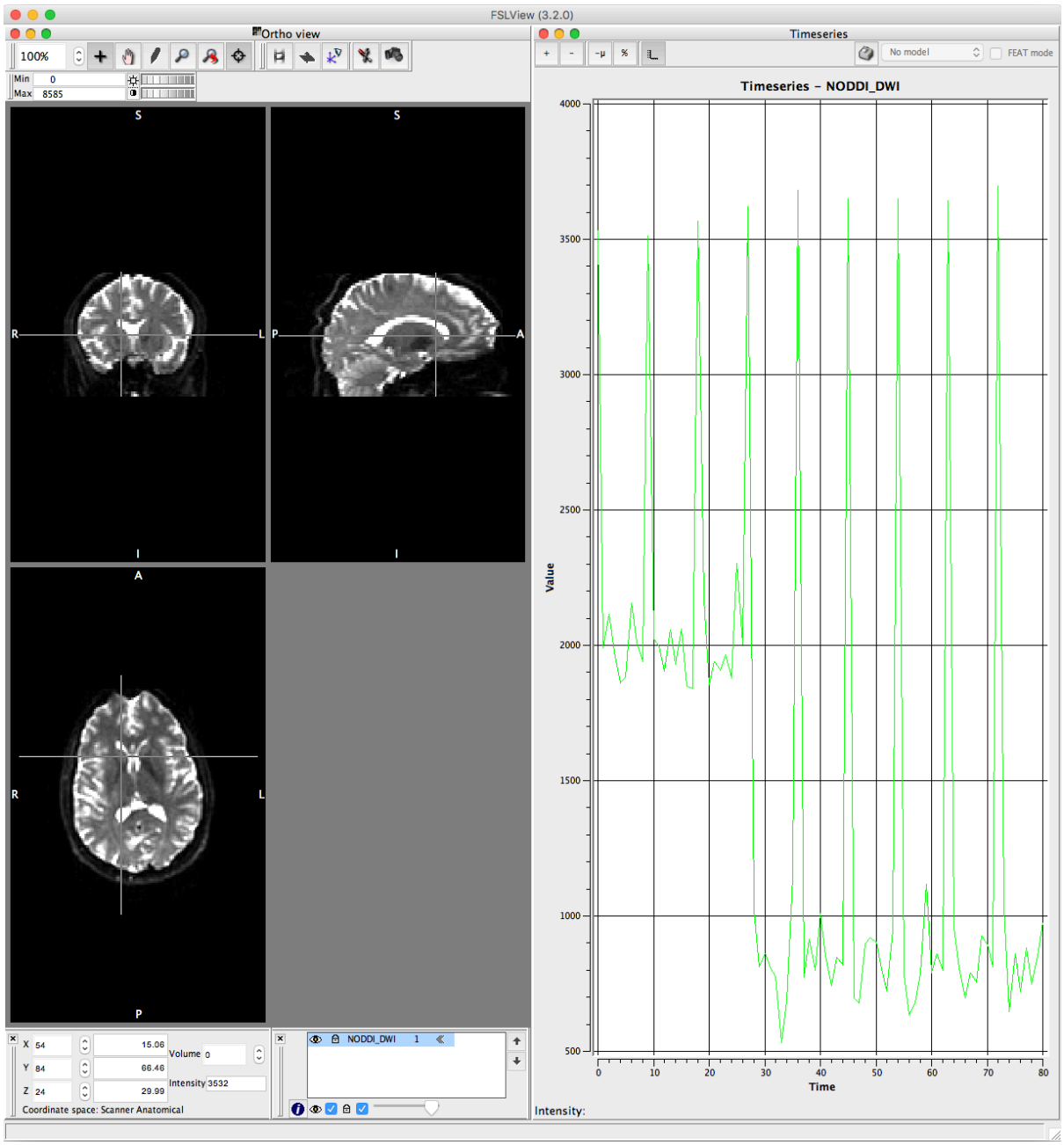
The first example looks at a voxel in the cortex. Observe how the diffusion anisotropy is dramatically reduced compared to the WM examples I have shown above, reflecting the highly dispersed orientational organisation of dendrites in GM.




The sharp-eyed among the readers may have noted the b=0 measurements appear to be more variable here. This is often seen for voxels that are near the edge of the brain.

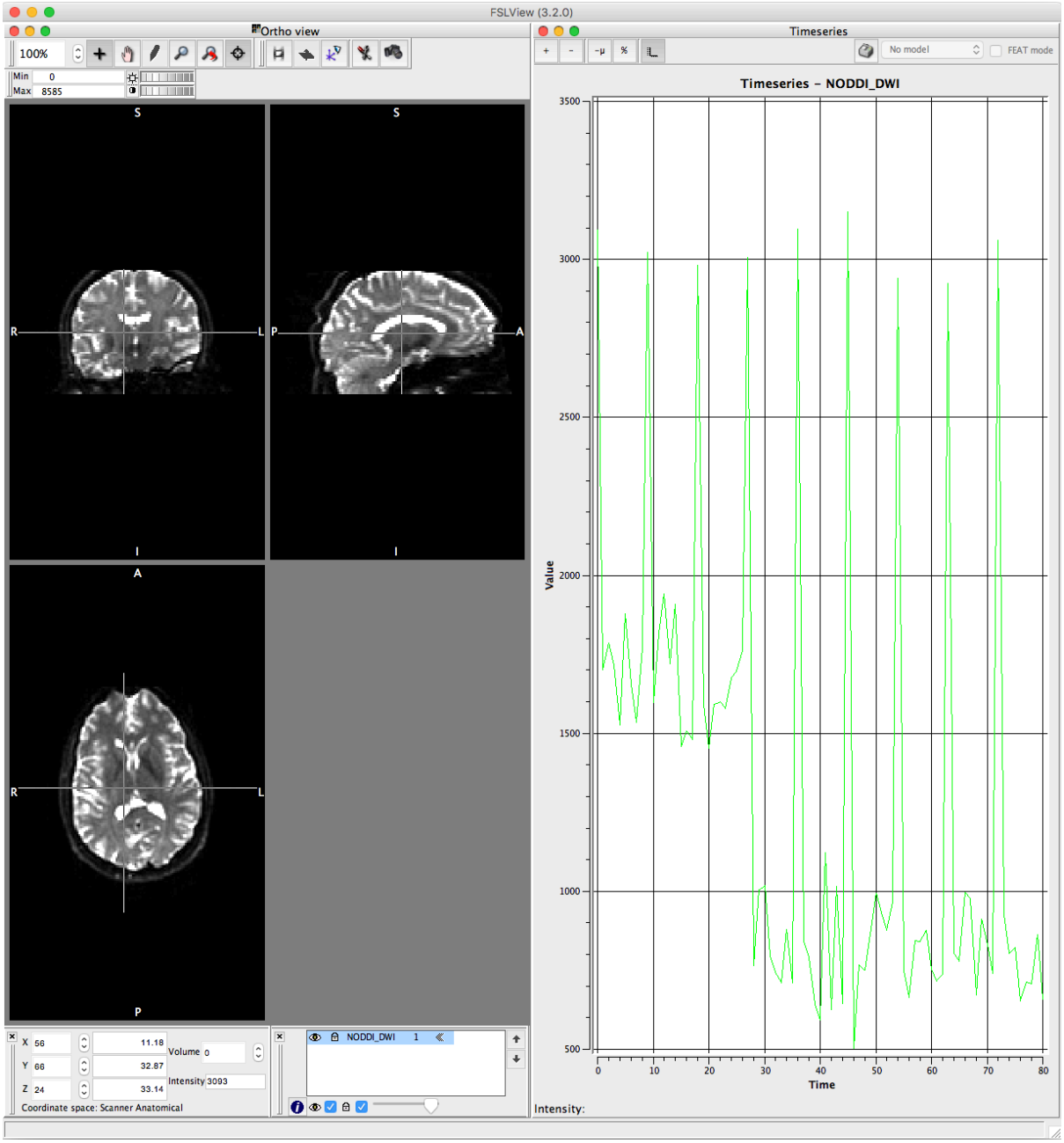
### 4.2.2 Caudate

The second example comes from a voxel in the Caudate, a deep-lying GM structure. It exhibits a low diffusion anisotropy as the cortex example, which is consistent with what neuroanatomists know about the structure.




### 4.2.3 Thalamus

The final example is a voxel from the Thalamus, also a deep-lying GM structure but with a difference. It is divided into distinct sub-structures each of which contains coherently aligned axons together with orientationally dispersed dendrites. As a result, one expects to see higher diffusion anisotropy than other GM structures. The data clearly bears this out.




## 5. Summary

To summarise, this tutorial shows how to inspect DWI data meaningfully with FSLview, the time series view of which, designed originally for functional MRI data, is well suited for the purpose illustrated here.

I have illustrated the expected signal behaviours for a set of common anatomical structures. When working with one's own data, it is very important to review the data in a similar fashion to ensure that the data is acquired correctly and is organised properly. Doing so ensures that subsequent analysis, such as fitting a diffusion model like NODDI, can give sensible result.