

Exploring Brain Anatomy

This week's exercises will let you explore the anatomical organization of the brain to learn some of its basic properties, as well as the location of different structures.

The human brain is the most complex object in the known universe. Although small, weighing only about 3 pounds (1.3kg) in the adult human, the brain contains approximately 100 billion neurons and perhaps several times as many supporting cells. While understanding the basic properties of these neurons and their connections is critical for neuroscience, MRI operates on too coarse of a spatial scale to study neurons directly. Instead, MRI investigates the gross anatomy of the brain, examining structure at the level of millimeters to centimeters. For comparison, neurons are on the order of a few tens of micrometers in size. In this laboratory, we will investigate the anatomical properties of a single brain captured using high-resolution imaging. You will learn techniques for loading and viewing MRI and fMRI data, the approximate size and shape of the adult human brain, the relation between gray and white matter, and the locations of some major anatomical landmarks.

Data Sets Used

This exercise uses one anatomical data set (ANAT1) and two functional data sets (FUNC1 and FUNC2).

The ANAT1 data set contains a single high-resolution anatomical image of the brain of a healthy young adult. The image was collected using an inversion-prepared 3D spoiled-grass (SPGR) pulse sequence, which provides excellent T_1 contrast (See Chapters 3 and 4 for details on this pulse sequence). The image dimensions are 256 (X) * 256 (Y) * 124 (Z), with voxel size of 0.9375mm * 0.9375mm * 1.5mm.

The FUNC1 and FUNC2 data sets contain time series of images of the same brain as ANAT1, collected using a gradient-echo spiral sequence, which provides BOLD contrast. The image dimensions are 64 (X) * 64 (Y) * 28 (Z), with voxel size of 3.75mm * 3.75mm * 4mm. There are 131 separate time points in each series, collected at a repetition time (TR) of 2s. Note that although these two data sets are of the same subject's brain as ANAT1, they have different voxel sizes from ANAT1 and thus the XYZ coordinates do not correspond. FUNC1 contains data collected using an event-related motor-visual task, and FUNC2 contains data collected using a blocked-design motor-visual task.

NOTE: All data and exercises for this course will be stored in the directory <\\huxley\data\class.01\Examples>. You have read-only access to this directory.

Exercise 1: Viewing the brain

1.1. Loading and viewing MRI data

Goals:

You should understand how to load and view two types of data, **anatomical images** and **functional images**. Anatomical images are high-resolution images that provide information about the organization of brain anatomy. They are usually sensitive to a tissue contrast parameter like T_1 or T_2 , or to the density of protons of a tissue type. Functional images are usually of lower resolution, but provide information about the changes in brain function over time. Most functional images generated by fMRI experiments are sensitive to blood-oxygenation-level-dependent (BOLD) contrast.

MATLAB:

There are several freely distributable or commercial programs available for viewing brain images collected from an MRI scan, and in this lab you will be introduced to one such program: ShowSrs2. ShowSrs2 is a program for MATLAB that can be used to display three-dimensional or four-dimensional data. It also allows overlaying of one image on top of another.

(Change to the data directory before beginning)

```
cd \\huxley\data\class.01\examples
```

- To load the ANAT1 dataset into MATLAB use the readmr command:

```
anat1 = readmr('ANAT_1\ANAT1_Whole_Brain.bxh')
```

- To load the FUNC1 dataset into MATLAB use the following command:

```
func1 = readmr('FUNC_1\FUNC1_V.bxh')
```

- To display the datasets using ShowSrs2 use the following commands:

```
ShowSrs2(anat1);  
ShowSrs2(func1);
```

You will be using ShowSrs2 frequently in future labs, so we will begin by describing its various features. First, running ShowSrs2 is simple: just call it as a function. It takes two arguments, a variable containing the data (e.g., func1) and an optional variable containing some configuration parameters (e.g., config_func1). The configuration parameters include information about the voxel size, orientation, and intensity scaling of the data.

We do not need the configuration parameters on these data sets because that information is included in the BXH header file.

NOTE: There is a guide to ShowSrs2 available on the BIAC website at:
<http://www.biac.duke.edu/education/>

ShowSrs2 allows data to be viewed in 3- or 4-dimensional space. The brain itself has three dimensions, usually expressed as X (left to right), Y (front to back), and Z (top to bottom). The fourth dimension is time. Anatomical data usually have 3 dimensions; functional data usually have 4 dimensions. To traverse the Z-dimension of the brain and view different slices, use the scrollbar at the right. To traverse the time-dimension and view the brain at different timepoints, use the scrollbar at the bottom of the image. You can also use the time controls at bottom left to scroll sequentially through the images in either direction, much like controlling a video or tape player. Remember that these buttons scroll through the data in *time*, not in space.

Questions:

Q1: While viewing the ANAT1 data set, quickly sketch axial slice 55.

Q2: While viewing the FUNC1 data set, quickly sketch axial slice 16.

Q3: These two slices are from approximately the same location within the brain. What differences are apparent in the visible anatomy?

1.1.1 Viewing the history of a single Voxel

Goals:

Because functional MRI data enable tracking of changes in voxel intensity, we can use relative change over time to identify areas of the brain associated with particular functions. This can be done in the FUNC1 data set.

MATLAB:

Evaluating the time course of a voxel can be done easily using ShowSrs2. Go to the window for the FUNC1 data set. Click on any voxel within the brain using your mouse, and a new window will pop up with a graph of the time course of fMRI activity in that voxel. At the top of the new window, you will see the coordinates of the specific voxel you just clicked on. If you click on a new voxel, a new time course will appear to replace the old one. Examine the time courses of a number of different voxels to get a feel for what time series data look like. As these data were collected in a motor/visual task, the best places to look for systematic changes will be in primary motor or visual cortices.

Questions:

Q4: Draw a quick sketch of the plot associated with the voxel at coordinates (43,35,8), which is within the anterior part of the central sulcus within the frontal lobe. Identify another voxel in the visual cortex and sketch its activation.

1.1.2 Viewing all three dimensions at once

Goals:

While MRI data are usually displayed as a collection of two-dimensional slices, it is important to recognize that the separate slices combine to form a three-dimensional object. By viewing data in more than one dimension at a time, or by viewing data as a three-dimensional surface, you can gain a better appreciation for important aspects of brain structure. The importance of looking at your data cannot be stressed enough. Take some time at this point in the lab to play with the different views of the brain. Ask yourself questions about its organization, and try to see what different views look like.

MATLAB: You should now use ShowSrs2 to explore different views of the ANAT1 data set.

From the “Orientation” menu, choose the option “3 Orthogonal Planes.” Now you can view the brain from three different angles! In the bottom left window, the brain appears as if you were looking at it from above, known as an **axial** view. In the top left window, the brain appears as it would from the front, known as a **coronal** view. And, in the top right, the brain appears as it would from the side, known as a **sagittal** view. As you click anywhere on one of the brains, the other two will update to match your new cursor position. Try clicking around in the various windows and getting comfortable with navigating between the three views. Note that once you have clicked on a voxel, you can navigate in one voxel increments using the ‘a’ & ‘d’, ‘w’ & ‘s’, and ‘q’ & ‘e’ keyboard letters.

This view, where you see all three brain orientations at the same time, will usually be the most helpful view.

Questions:

Q5: Why might brain researchers prefer one view of the brain or another? Can you think of any potential reasons?

1.1.3 Measuring the brain.

Goals:

An important use of MRI is measuring the brain. For example, researchers studying hippocampal changes with a given disorder may use MRI to measure its volume in patient and control groups. Anatomical images, like that in the ANAT1 data set, can have spatial resolution of about 1mm, so they can be very useful for fine measurement. Here, we will measure the brain’s maximal extent in each direction, and from those measurements we will estimate the volume of the brain in cubic centimeters.

MATLAB:

To measure the ANAT1 brain using ShowSrs2, first identify voxels that are at the very limits of its spatial extent. That is, find the voxel that is farthest forward, the one that is farthest back, and so forth. Remember that since the brain is rounded, these may be on different slices. You can click on voxels to find their coordinates, and you can find the distance between pairs of voxels by subtracting coordinate pairs.

Questions:

Q6: Approximate size of the ANAT1 brain (voxels): X _____ Y _____ Z _____

Now, we need to convert these values from voxels to millimeters. Each voxel represents a rectangular prism that is 0.9375mm (x) * 0.9375mm (y) * 1.5mm (z). Using this information, compute the size of the brain in millimeters.

Q7: Approximate size of the ANAT1 brain (mm): X _____ Y _____ Z _____

Q8: At the bottom of this lab you will find drawings of the brain in different views. On each drawing, write the maximum dimensions of the brain in each direction, on top of the provided arrows. Then, above each drawing, write that view's name.

Finally, estimate the total volume of the brain using these dimensions. (Hint: the brain is not rectangular, so simple multiplication of these values will result in overestimation. Assume some other shape for the brain to improve your estimate.)

Q9: Using the three values calculated in the question above, estimate an upper bound on the volume of the brain.

1.2 Finding the Gray / White Boundary

Goals:

A common distinction between types of tissue in the brain is between “gray matter” and “white matter”. Gray matter refers to a relatively thin (5mm) layer of cells on the outer surface of the brain. Most information processing is thought to occur in the gray matter. White matter refers to the axonal connections between different parts of the brain that transfer signals from one location to another. As their names imply, gray and white matter appear dark and light, respectively, on physical sections through the brain. They also appear dark and light on T₁-weighted images, like ANAT1. Here, you will use intensity-based segmentation to partition the brain into gray and white matter.

MATLAB:

Since gray matter appears darker than white matter on the ANAT1 images, we can estimate a cut-off value that will best separate the two types of tissue. There are two ways to do this in MATLAB.

First, you can do it easily (albeit roughly) using ShowSrs2. Select a number of points that should be in white matter, and a number of points that should be in gray matter (by visual appearance). Then, by clicking on these, determine what numerical range is typical for gray matter and what range is typical for white matter. A similar method is to select a point in gray matter and move the cursor voxel by voxel until you cross completely into white matter, making a note of what values are at the transition location.

Second, you can find the needed values by creating a histogram of the data from a single slice.

- First, you should select a slice that has good distributions of gray and white matter. If you selected slice 55, for example, you would could create a new variable:

```
slice=data(:,:,55);
```

[1.21]

- Next, you can plot all of the voxels in that slice using the `hist` command. You can specify how many bins you want to use in the histogram (e.g., 30).

```
hist(slice(:),30);
```

[1.1.2]

Depending on what slice you used, you are likely to see a plot that has several peaks. The very large peak near zero reflects the many voxels in the air around the head that have minimal signal. To the right will be a distribution with two much smaller peaks; these correspond to gray and white matter. Note that there are many voxels that have intermediate values between these peaks; these correspond to voxels that actually contain both gray and white matter (i.e., those on the boundary between them). You can estimate the cut-off value by finding the midpoint between these peaks.

Note that this cut-off value depends upon many factors, including scanners, subjects, pulse sequences, and reconstruction approaches. What is important is not the absolute number, but the relative difference between the tissues (i.e., their contrast).

Questions:

Q10: Looking over the numbers you have collected above, what value best separates gray and white matter in this data set? _____

1.3 Segmenting Gray and White Matter

Goals:

Now that you have separated gray and white matter, you can segment the brain into these tissue types. Segmentation is important for structural MRI, especially when comparing across groups. For example, a researcher may investigate whether volume changes associated with aging are more pronounced in gray matter or white matter. Segmentation is also often done in fMRI studies to help with preprocessing steps (such as image coregistration) or to improve analysis efficiency. We are going to do the simplest form of segmentation in this step: intensity-based.

MATLAB:

To partition the brain into two images representing voxels with intensity above and below your threshold, you can use the custom function “segment”, inserting your answer to the question above for `threshold`: (i.e., `segment(ANAT1,100)`).

```
addpath '\\huxley\data\class.01\examples\scripts
```

```
segment(anat1.data, threshold)
```

You can also do the segmentation manually using the “find” command. The `find` command lets you identify all voxels with values in a given range. For example, the below commands find all voxels whose values are greater than 100, and then creates a new brain with only those voxels included.

```
a=find(anat1.data > 100);
```

```
new_brain=zeros(size(anat1.data));
```

```
new_brain(a)=anat1.data(a);
```

The find command is also useful for counting the total number of voxels within a category. (Hint: this is very helpful for answering Q13 below).

Questions:

Q11: Compare your segmented brains to Based on these two views, do you think your original estimate was too high, too low, or about right? If too high or too low, what would your new estimate be?

Q12: What problems do you see with the intensity-based segmentation? That is, what sorts of mistakes were made by including the wrong type of tissue?

Q13: Approximately what percentage of the brain is gray matter?

1.4 Identifying Anatomical Locations

Goals:

Our final exercise will use identify key anatomical locations within the structural MRI image ANAT1. When doing fMRI studies, it is important to gain a working knowledge of brain anatomy, for several reasons. Researchers should be able to accurately and consistently identify areas of activity, to best develop and test brain-based hypotheses. Without a good knowledge of anatomy, it is difficult to read the neuroimaging literature or to converse with other investigators about experimental data. Nevertheless, learning neuroanatomy is hardly a simple task. We urge students to explore the suggested readings and other references provided in Chapter 2, as well as the online resources linked to on the CD-ROM, to help with identification of these locations.

The specific anatomical locations are listed at the bottom of these exercises.

MATLAB:

To identify brain regions using ShowSrs2, simply scroll through the slices as needed and click on the desired location to get its coordinates. We recommend using the “3 Orthogonal Planes” view, for best visualization of regions.

Suggested online atlases:

- o <http://www9.biostr.washington.edu/da.html>
- o <http://www.med.harvard.edu/AANLIB/home.html>

Summary of Exercises

Q1: While viewing the ANAT1 data set, quickly sketch the fifth slice of the brain.

Q2: While viewing the FUNC1 data set, quickly sketch the tenth slice.

Q3: These two slices are from approximately the same location within the brain. What differences are apparent in the visible anatomy?

Q4: Draw a quick sketch of the plot associated with the voxel at coordinates (43,35,8), which is within the anterior part of the central sulcus within the frontal lobe. Repeat for FUNC2, at the same voxel location.

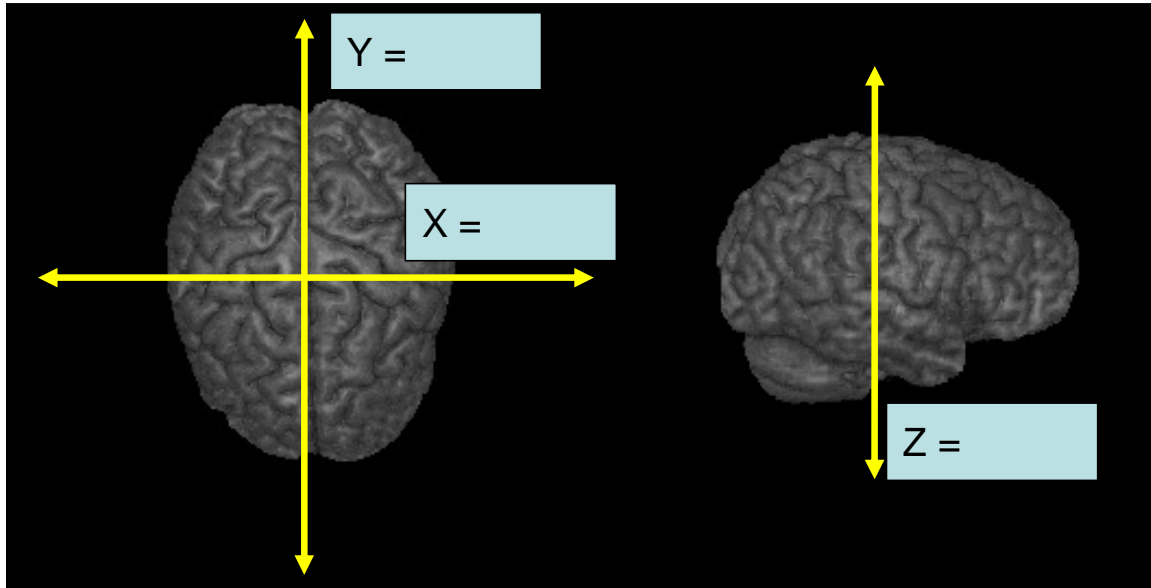
Q5: Why might brain researchers prefer one view of the brain or another? Can you think of any potential reasons?

Lab Exercises – Week 2

Q6: Approximate size of the ANAT1 brain (voxels): X ____ Y ____ Z ____

Q7: Approximate size of the ANAT1 brain (mm): X ____ Y ____ Z ____

Q8: At the bottom of this lab you will find drawings of the brain in different views. On each drawing, write the maximum dimensions of the brain in each direction, on top of the provided arrows. Then, above each drawing, write that view's name.



Q9: Using the three values calculated in the questions above, estimate an upper bound on the volume of the brain.

Q10: Looking over the numbers you have collected above, what value best separates gray and white matter in this data set? _____

Q11: Compare your segmented brains to Based on these two views, do you think your original estimate was too high, too low, or about right? If too high or too low, what would your new estimate be?

Q12: What problems do you see with the intensity-based segmentation? That is, what sorts of mistakes were made by including the wrong type of tissue?

Q13: Approximately what percentage of the brain is gray matter?

Lab Exercises – Week 2

Q14:

Approximate location of the Anterior Commissure:	X _____	Y _____	Z _____
... Posterior Commissure:	X _____	Y _____	Z _____
... genu (anterior pole) of Corpus Callosum:	X _____	Y _____	Z _____
... splenium (posterior pole) of Corpus Callosum:	X _____	Y _____	Z _____
... Thalamus:	X _____	Y _____	Z _____
... Caudate:	X _____	Y _____	Z _____
... Putamen:	X _____	Y _____	Z _____
... Hypothalamus:	X _____	Y _____	Z _____
... Pons:	X _____	Y _____	Z _____
... Gyrus Rectus:	X _____	Y _____	Z _____
... Inferior Frontal Gyrus:	X _____	Y _____	Z _____
... Cingulate Gyrus:	X _____	Y _____	Z _____
... Amygdala:	X _____	Y _____	Z _____
... Hippocampus:	X _____	Y _____	Z _____
... Central Sulcus:	X _____	Y _____	Z _____
... Fusiform Gyrus:	X _____	Y _____	Z _____
... Insular cortex:	X _____	Y _____	Z _____
... posterior extent of Sylvian Fissure:	X _____	Y _____	Z _____