Quantitative and Functional Imaging

BME 4420/7450

Project #4

**Imaging tissue microstructure with diffusion tensor imaging**

The goals of this project are to visualize the orientation of axon fibers in the brain and track fibers between gray matter regions in opposite hemispheres. As in the previous projects, you are free to get your results in some other way—these procedures are just one (not necessarily optimal) method. Matlab commands are given in *italics* for easy reference. Use *help <command>* (for example, *help line*) or the Matlab Help pages for more details on any Matlab function.

1. Load the data file proj4data.mat into your Matlab workspace. There are three arrays in the file:

anat\_m A matrix (256 x 256) of pixel values for a **T2 weighted image**. This is the ‘anatomical’ image.

eigValues\_3d A 3D array (256 x 256 x 3) of diffusion coefficients (tensor eigenvalues). For each pixel there are **three diffusion coefficients** (one for each of the orthogonal ‘principal’ directions). (Lamdas)

fastDiffVector\_3d A 3D array (256 x 256 x 3) of (x, y, z) vector components. For each pixel there are **three components of a unit vector** parallel to the fast diffusion direction.

**Magnitude**: The dimensions of eigValues\_3d are (row, column, principal axis number), **where the principal axis number is 1, 2, or 3**. The corresponding diffusion coefficients (eigenvalues of the diffusion tensor) are 1, 2, and 3. The **diffusion coefficient** parallel to the fiber (i.e., the ‘**fast diffusion’ direction**) is **1**. The diffusion coefficients perpendicular to the fiber are 2 and 3 (3 is the diffusion coefficient in the ‘slowest diffusion’ direction, and 2 is the (intermediate) diffusion coefficient in the direction perpendicular to both the ‘fast’ and ‘slow’ directions).

**Direction** The dimensions of **fastDiffVector\_3d** are (row, column, component), where the component index can have the value 1, 2, or 3 (corresponding to x, y, and z, respectively). The fast diffusion direction is given by the **eigenvector corresponding to 1.** Note that x is in the column direction (left to right) of the image, and y is in the row direction (top to bottom).

1. Create a map of diffusion anisotropy. To do this, calculate the fractional anisotropy (FA) of diffusion **in every pixel in the head** (use a binary mask based on anat\_m to define **which pixels are in the head**). The FA measures how strongly diffusion depends on orientation, and reflects the directional preference of cell membranes in the tissue. The FA is defined as the **ratio of the standard deviation** to the root-**mean-square of the three eigenvalues:**

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where



FA is a number between 0 (no directional preference of diffusion) and 1 (diffusion in one dimension only**). Create a matrix of FA values, fa\_m,** **and display it as a gray scale map.** FA is high in the white matter where nearly-parallel axons, bundled into large fibers, ­­carry information **between widely separated synapses**.

1. The FA map you’ve created tells you where the axon bundles are in the brain, but there is more information in the diffusion tensor. The direction that corresponds to the fastest diffusion (1) is stored in fastDiffVector\_3d. Use the x, y, and z components of this vector to color-code the FA map with direction information. Display a color map by passing *imagesc* a 3D array with red, green, and blue intensities on page 1, 2, and 3, respectively:

*% Display color-coded FA map:*

*red\_m = fa\_m .\* abs(fastDiffVector\_3d(:, :, 1));*

*green\_m = fa\_m .\* abs(fastDiffVector\_3d(:, :, 2));*

*blue\_m = fa\_m .\* abs(fastDiffVector\_3d(:, :, 3));*

*color\_3d = cat(3, red\_m, green\_m, blue\_m);*

*imagesc(color\_3d)*

*axis image*

*axis off*

*title('Red = R/L, Green = A/P, Blue = S/I')*

Red shows where fibers run right/left in the image, green shows anterior/posterior and blue shows superior/inferior fibers.

1. Prompt the user to identify (click on) a seed point in a white matter fiber that passes through the corpus callosum. Find the coordinates of the seed point:

*imagesc(anat\_m)*

*axis image*

*colormap(gray)*

*hold on*

*disp('Define seed point...')*

*[x0, y0] = ginput(1);*

The *hold on* command will keep the image in the current figure, even when you draw other graphics in the figure. This allows you to draw fiber paths on the anatomical image.

1. Create variables to hold the **current x (column**) and y (row) positions of the fiber path and use arrays x\_v and y\_v to hold all fiber coordinates (starting from the seed to the current point). **The tracking algorithm should advance the path** in the local fast diffusion direction, repeating until **a stopping criterion is met**. Use a *while* loop, stepping in the **fast diffusion direction** as long as the variable ‘stepFlag’ is 1.

**X0y0 poiting where – add**

**One reason to stop a path is that no direction has faster diffusion than any other (diffusion is isotropic). In this case the calculated path is likely to take random steps**—the angle between consecutive steps would be relatively large in this case. Hence, for each step we’ll **calculate cosAngle, the cosine of the angle between the previous and the next step**.

A second reason to stop the path is that the fast diffusion direction points too far out the plane of the image.

Initialize the variables

*x = x0;*

*y = y0;*

*x\_v = x0;*

*y\_v = y0;*

*stepFlag = 1;*

*cosAngle = 1;*

*stepSize = 1;*

1. Create a *while* loop that executes as long as stepFlag = 1:

*while (stepFlag == 1)*

*% Insert code here to find* ***the fast diffusion direction******at the nearest***

***% integer values of row and col:***

*% We want to track fibers in the plane of the image, so insert code*

*% here to find the component of the* ***fast diffusion direction*** *in the*

*% image plane. Call this* ***fast\_v*** *(it should have just two elements,*

*% the x and y components of the fast diffusion direction):*

*% Break out of the while loop if the in-plane component of the*

*% vector is too small:*

*if (sum(fast\_v.^2) < 0.5)*

*disp('In-plane component of fast\_v is too small')*

*break*

*end*

*% If this is not the first step away from the seed point, calculate*

*% cosAngle, the cosine of the angle between the* ***previous step*** *and*

*% fast\_v. If cosAngle is negative, reverse the direction of fast\_v*

*% (add code here):*

*% Step a distance* ***stepSize in the direction of fast\_v***

*% (i.e., update x\_v and y\_v):*

*% Add a line segment to the image to show the current step:*

*line([x\_v(length(x\_v)-1), x], [y\_v(length(y\_v)-1), y])*

*drawnow*

*% Add code here to set stepFlag = 0 if abs(cosAngle) is too small:*

*% End of while loop:*

*end*

1. Repeat (i.e., copy and paste) your code for **parts 5** and 6 to track in the opposite direction from the seed point. You need to change/add only one or two new lines to start in the opposite direction.
2. Freeze the figure for the next graphics command:

*hold off*

1. Using your program, try to **track fibers** from one hemisphere to the other through the **genu** of the corpus callosum. You may need to try a few different seed points to do this.
2. Plot the **FA as a function of position** along the fiber track you created in part 9. Be sure to order your data to show FA starting at one end of the track and ending at the other. Note the variations of FA along the fiber.

# Questions

1. **How accurate do you think your fiber path is? If there are points where the path took a wrong turn, indicate these on your figure.**
2. **Can you think of simple ways to improve the tracking algorithm? If so, briefly describe them.**
3. **What is the total length of the fiber path (the path that you show in your report)? The width of each pixel is 1 mm.**
4. **What tissue properties might account for the variation of FA along the fiber?**

# Assignment

Create a Word document that includes

1. **Your gray-scale and color-coded FA maps.**
2. **A figure showing the anatomical image with a fiber path connecting gray matter regions in the two hemispheres.**
3. **Your plot of FA as a function of position along the fiber.**
4. **Your answers to the questions above.**
5. Your Matlab code.

Please save your report as a PDF file, name it “Project4\_<your name(s)>” (adding your name), and submit it on Brightspace by Tuesday, Nov. 1. Each group can submit one report—just make sure all group members are named on the report.