Quantitative and Functional Imaging

BME 4420/7450

Project 8

**Dopamine receptor mapping with Positron Emission Tomography**

The goal of this project is to measure the distribution volume of fallypride, a radioactive tracer that binds with the dopamine D2 receptor. Using only PET image data, we can find the distribution volume in each image pixel relative to a reference tissue. Since the density of dopamine receptors in the cerebellum (CB) is negligible, we will use the CB as the reference tissue. The distribution volume ratio (DVR) is then the slope of the Logan plot, which we will calculate in each pixel. 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 cumsum*) or the Matlab Help pages for more details on any Matlab function.

1. Load the data file proj8Data.mat into your Matlab workspace. There are five variables in the file:

bgPetImage\_3d An array (64 x 64 x 18) of pixel values for 18 time points in the PET study. The image slice cuts through the basal ganglia (BG) near the center of the brain.

cbPetImage\_3d An array (64 x 64 x 18) of pixel values for 18 time points in the same study. The image slice cuts through the cerebellum (CB), which will be our reference region.

bgMrImage\_m A 2D array (64 x 64) of pixel values for an MRI image taken through the same plane as bgPetImage\_3d. The MRI and PET data have been registered so corresponding pixels coincide in space.

cbMrImage\_m A 2D array (64 x 64) of pixel values for an MRI image taken in the same plane as cbPetImage\_3d. Again, the MRI and PET images have been registered.

dTime\_v A 1D array (18 elements) giving the time (in minutes) used to acquire data for each image in the series. (PET images depend on detecting radioactive decay events in the subject—the longer the decay counts are summed, the less noisy the image will be. As the experiment goes on, the ‘exposure time’ is increased to try to compensate for the falling decay rates).

The indices of the array bgPetImage\_3d are (row, column, timeIndex). The individual images (the pages of the 3D array) are given in time order, i.e., bgPetImage\_3d(:,:,1) is the first image, bgPetImage\_3d(:,:,2) is the second, and so on.

1. Find the time (starting from the beginning of the experiment) when data collection stopped for each image. Use the cumulative sum function, *cumsum*, and put these times in the array time\_v:

*time\_v = cumsum(dTime\_v); % Time at the completion of each image.*

Loop through the time points, displaying the PET and MRI images of both slices:

*% Display PET (and MRI) images at each time point:*

*figure*

*bgImageMax = max(bgPetImage\_3d(:));*

*% Make 3D arrays of identical pages to display MR images in grayscale:*

*bgMrColor\_3d = cat(3, bgMrImage\_m, bgMrImage\_m, …*

*bgMrImage\_m)/max(bgMrImage\_m(:));*

*cbMrColor\_3d = cat(3, cbMrImage\_m, cbMrImage\_m, …*

*cbMrImage\_m)/max(cbMrImage\_m(:));*

*for timeIndex = 1:nTimes*

*% Show PET image of basal ganglia:*

*subplot(2, 2, 1)*

*bgPetImage\_m = squeeze(bgPetImage\_3d(:, :, timeIndex));*

*imagesc(bgPetImage\_m)*

*set(gca, 'CLim', [0, bgImageMax])*

*axis image; axis off*

*title(['Time index = ', num2str(timeIndex)])*

*% Show PET image of cerebellum:*

*subplot(2, 2, 2)*

*cbPetImage\_m = squeeze(cbPetImage\_3d(:, :, timeIndex));*

*imagesc(cbPetImage\_m)*

*set(gca, 'CLim', [0, bgImageMax])*

*axis image; axis off*

*% Show MR image of basal ganglia:*

*subplot(2, 2, 3)*

*image(bgMrColor\_3d)*

*axis image; axis off*

*% Show MR image of cerebellum:*

*subplot(2, 2, 4)*

*image(cbMrColor\_3d)*

*axis image; axis off*

*pause(1)*

*end*

1. Define a reference region of interest (ROI) in the cerebellum (this is the triangular structure inferior to the cerebral hemispheres in cbMrImage\_m) using *roipoly*. Name the ROI mask cbRoiMask\_m. Show the location of the ROI boundary on both cbMrImage\_m and the (temporal) mean of the PET images (in cbPetImage\_3d) using the *line* command.
2. Calculate the mean pixel intensity in the reference ROI as a function of time. Store this in the 1D array cbRoiMean\_v. Create a plot of cbRoiMean\_v versus time (from the beginning of the experiment).
3. To get an idea of the global time activity, define an ROI in the basal ganglia (a group of subcortical gray matter structures near the center of the brain). First, calculate the (temporal) mean intensity of the PET images in bgPetImage\_3d. Define an ROI around the hot spot(s) in the mean image using *roipoly*. Calculate the mean pixel intensity in the ROI as a function of time, and store these values in the elements of the 1D array bgRoiMean\_v. Create a plot of bgRoiMean\_v versus time.
4. Create a Logan plot for the basal ganglia ROI using the cerebellum ROI as a reference:

 [1]

where b is a constant. Defining



we have



which is the equation of a line with slope equal to the distribution volume ratio, , of the radiotracer. Calculate x(t) (naming the array bgRoiX\_v) and y(t) (naming it bgRoiY\_v) using a discrete approximation to the integrals. Draw your Logan plot:

*figure*

*plot(bgRoiX\_v, bgRoiY\_v, '-', bgRoiX\_v, bgRoiY\_v, '+')*

*title('Logan plot')*

The last several points on the curve should fall (approximately) on a straight line. Determine the number of these points—they will be used to calculate the slope of the linear part of the curve. Define a variable nFitPoints and set it equal to the number of points in the linear part of the curve.

1. Calculate a mask array for bgPetImage\_3d, indicating where the (temporal) mean PET pixel intensity is at least 5% of the maximum in the mean image. For every pixel that satisfies this condition, calculate the slope of the Logan plot (using the pixel intensity through time as the tissue concentration of interest and the cerebellum ROI mean as CCB(t) in eqn.[1]). You do not have to display the Logan plot for each pixel (that would take a long time). Use polyfit to calculate the slope of the last nFitPoints in the curve for each pixel. Store legal (i.e., positive) values for the slope in a dvr\_m array inside your pixel loop:

*% Check for legal values:*

*if (slope > 0)*

*dvr\_m(row, col) = slope; % DVR = slope.*

*else*

*dvr\_m(row, col) = 0;*

*end*

After you’ve calculated the DVR in each pixel, display the DVR values as a map and superimposed on the MRI anatomical image:

*% Display DVR map:*

*figure*

*imagesc(dvr\_m)*

*colorbar*

*axis image*

*axis off*

*title('Distribution Volume Ratio Map')*

*colorMap\_m = colormap;*

*nColors = size(colorMap\_m, 1);*

*% Show thresholded DVR on MRI:*

*figure*

*% Insert your code here to calculate a mask where the DVR values*

*% exceed half their maximum value. Name the mask dvrMask\_m:*

*…*

*% Render pixels inside dvrMask in color. Use same colormap as above:*

*colorIndex\_v = 1 + round((nColors-1) \* dvr\_m(:) / max(dvr\_m(:)));*

*redDvr\_m = dvrMask\_m .\* reshape(colorMap\_m(colorIndex\_v, 1), …*

*size(dvrMask\_m));*

*greenDvr\_m = dvrMask\_m .\* reshape(colorMap\_m(colorIndex\_v, 2), …*

*size(dvrMask\_m));*

*blueDvr\_m = dvrMask\_m .\* reshape(colorMap\_m(colorIndex\_v, 3), …*

*size(dvrMask\_m));*

*% Display the rest of the image in gray:*

*maskedMrImage\_m = (1-dvrMask\_m) .\* bgMrImage\_m / …*

*max(bgMrImage\_m(:));*

*color\_3d = cat(3, maskedMrImage\_m + redDvr\_m, ...*

*maskedMrImage\_m + greenDvr\_m, ...*

*maskedMrImage\_m + blueDvr\_m);*

*image(color\_3d)*

*%h = colorbar;*

*axis image*

*axis off*

*title('DVR map')*

See whether you can distinguish separate peaks in DVR within the basal ganglia in each hemisphere.

# Questions

1. The plot of mean pixel intensity versus time is called a *time-activity curve*. The time-activity curve for the cerebellum ROI rises and falls, but the curve for the basal ganglia rises to a plateau (and stays high). Why do these regions have such different behavior?
2. Why isn’t the Logan plot linear for all times? What determines the time at which it becomes linear? (You may want to refer to the lecture notes on Logan Plots).
3. Can you see any structure in the peak of the DVR maps (or is the peak a uniform blob)? If you can distinguish separate ‘hot spots’ in the basal ganglia (in each hemisphere), what anatomical structures do you think these correspond to?
4. What changes in the data acquisition or analysis would improve the accuracy of your results?

# Assignment

Create a Word document that includes

1. A figure showing the location of the cerebellum ROI on both MRI and mean PET images.
2. A plot of the cerebellum ROI mean pixel intensity versus time. Please label the axes.
3. A plot of the basal ganglia ROI mean pixel intensity versus time. Please label the axes.
4. Your Logan plot for the basal ganglia ROI data.
5. Your DVR map and thresholded DVR values in the MRI anatomical image.
6. Your answers to the questions above.
7. Your Matlab code.

Save your report (including your MATLAB code) in a single PDF document, name it “Project8\_…” (adding your name), and submit it by 11:59pm, Thursday, Dec. 8. Each group can submit one report—just make sure all group members are named on the report.