Quantitative and Functional Imaging

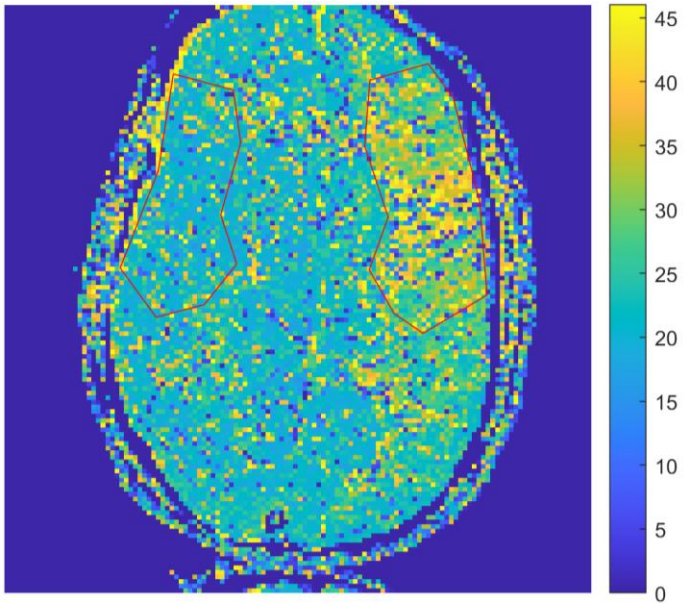
BME 4420/7450

Project #5

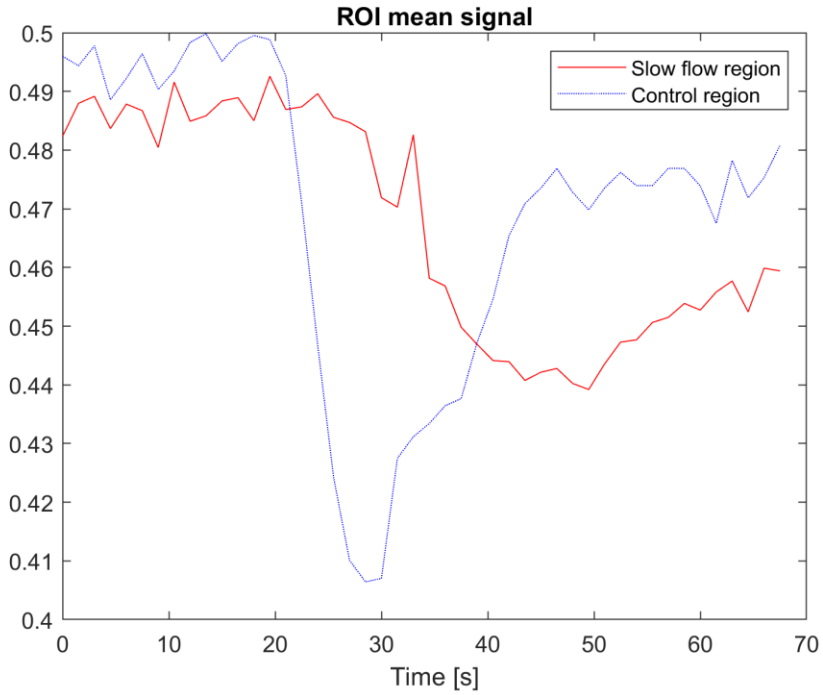
Measuring Cerebral Blood Volume

Deliverable Figures

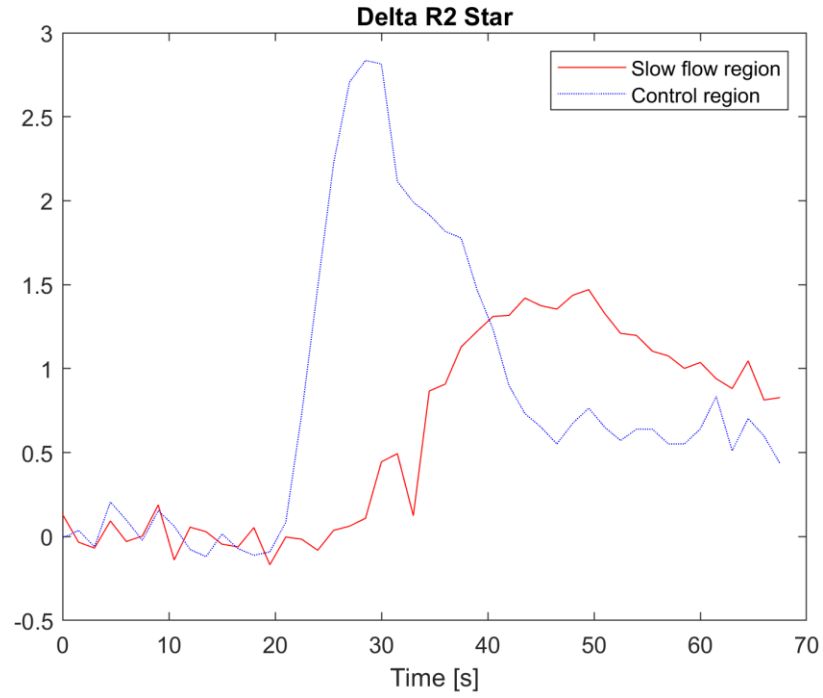
1. Figure showing the time-of-minimum map with your ROIs. Be sure to add a color bar to display numerical values



2. Your plot of signal intensity versus time for bone ROIs



3. Your plot of R2* change versus time for both ROIs



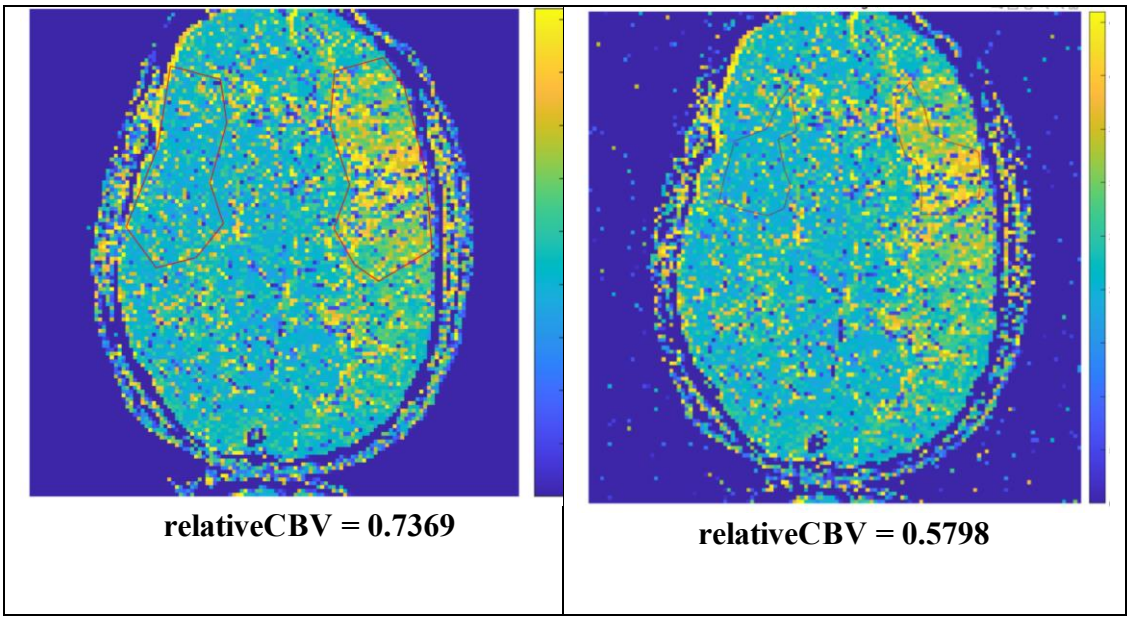
Questions

1. How does the R_2* curve differ between the two regions (in terms of amplitude, width, and time delay)? What physiological properties might these differences reflect?

- The amplitude of the peak for the slow-flow region is much smaller than for the control region. This is due to less contrast agent being delivered to the tissue due to obstruction of the vessels delivering blood to the region (due to stroke). Because less contrast is delivered, there is less dephasing and thus less change in the resulting relaxation rate, delta R2 star.
- Additionally, the peak for the slow-flow region appears to be delayed compared to the control region. The peak delay is also due to the vessel obstruction, which delays the time it takes for blood (carrying the contrast) to be delivered to the affected tissue. This in turn delays the effects of the contrast in changing R star for the tissue.
- The increased peak width is also due to the slower flow. The affected area has a lower mean transit time (MTT), which corresponds to the average time that red blood cells spend in capillary circulation. Because the flow is moving through the capillaries slower, the contrast in the blood will also move slower and therefore have a prolonged effect, increasing the width of the peak in the graph.

2. A stroke is a sudden brain injury caused by impaired blood supply (due to a blood clot blocking a vessel, for example). If the perfusion deficit is severe and prolonged, brain cells die due to *hypoxia* (insufficient oxygen). How could you use your measurements to evaluate the extent and severity of stroke?
   - Using our measurements, we can determine severity of stroke by looking at the rCBV value. A lower rCBV value would indicate higher severity stroke. In order to classify a patient's stroke as high, intermediate, or low severity, we would need to set threshold rCBV values that we can compare to the patient's rCBV. To obtain these threshold values, we would need to conduct a study in which we image a large population of stroke patients. We can determine their rCBV from these images and then evaluate the relationship between rCBV and stroke severity based on this study population. This study would therefore allow us to determine the range of rCBV values that typically correspond to a mild, intermediate, or severe stroke.
   - In order to standardize the drawing of the ROIs in our study, we can use a Sobel edge detection or similar algorithm to ensure that we are drawing consistent ROIs across patients. This is important to take into consideration because the size of the ROI will greatly affect the calculated rCBV value.

3. What is the relative CBV in the slow-flow region? Does this seem low enough to affect a patient?



relativeCBV = 0.7369

relativeCBV = 0.5798

- Yes, this value seems low enough to affect the patient, especially given the fact that our ROIs were drawn to be rather large. A smaller ROI that only included the most affected pixels would have a much lower rCBV value (~0.4 - 0.6). Thus, our rCBV value is likely on the higher side because we drew our ROIs to be larger. Nevertheless, our rCBV value still shows over a 25% decrease in CBV in our ROI, which indicates a significant reduction in blood flow to the area. The center of the stroke would have an even smaller rCBV value, indicating an even greater reduction in blood flow.

4. What are some possible sources of error in your measurement? Briefly describe what you could do to improve the accuracy of the relative CBV estimate.

- The ROI is a rough estimate of the stroke region. It is likely that the selected region includes tissue not affected by the stroke or excludes tissue affected by the stroke. We could have a better estimate of the stroke area by being stricter when drawing the ROI. One could also draw ROIs on several images/slices of the brain and take the average of the areas under the curve. We could also have an image with more contrast which will better differentiate precluded vasculature. However, both techniques would require more imaging time which can be detrimental when diagnosing a stroke.
- Another idea would be to use an edge detection algorithm, such as Sobel edge detection, in order to more precisely draw the ROIs around only the affected tissue.
- Moreover, in order to ensure that the two ROIs (one drawn in the affected hemisphere and the other drawn in the non-affected hemisphere) are perfectly symmetrical and of the same size, we could improve our MATLAB code by adding a line that reflects the first ROI across the midline of the brain.
- We could calculate the error associated with our measurements. A confidence interval can be created to give a range for the relative CBV estimate.

- We use trapezoidal numerical integration to approximate the area under the curve. The trapezoidal rule is $O(h^2)$, techniques like gaussian quadrature or Richardson extrapolation are more accurate and would decrease the truncation error.

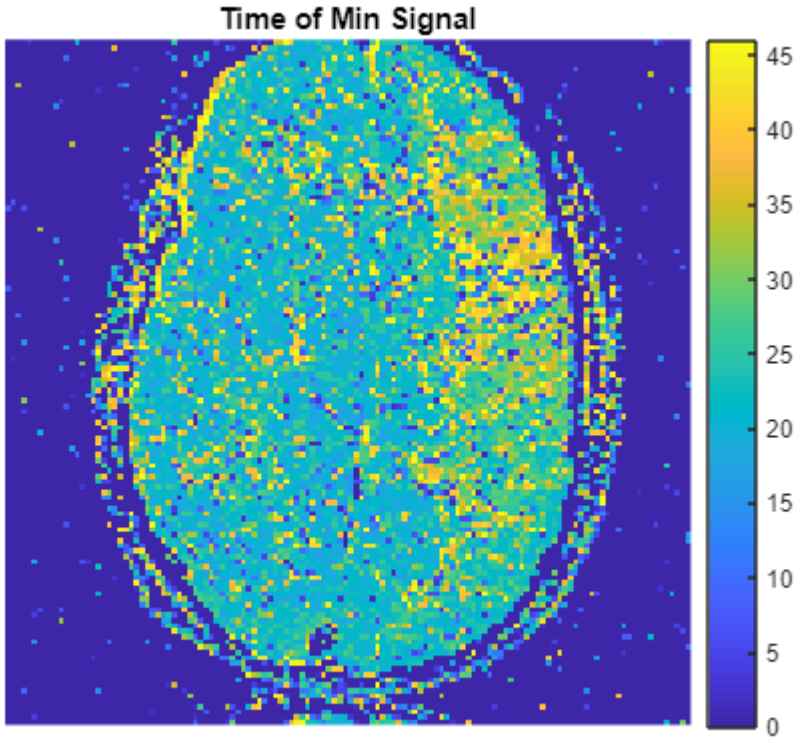
Code

```
load('proj5Data_qfi.mat');
```

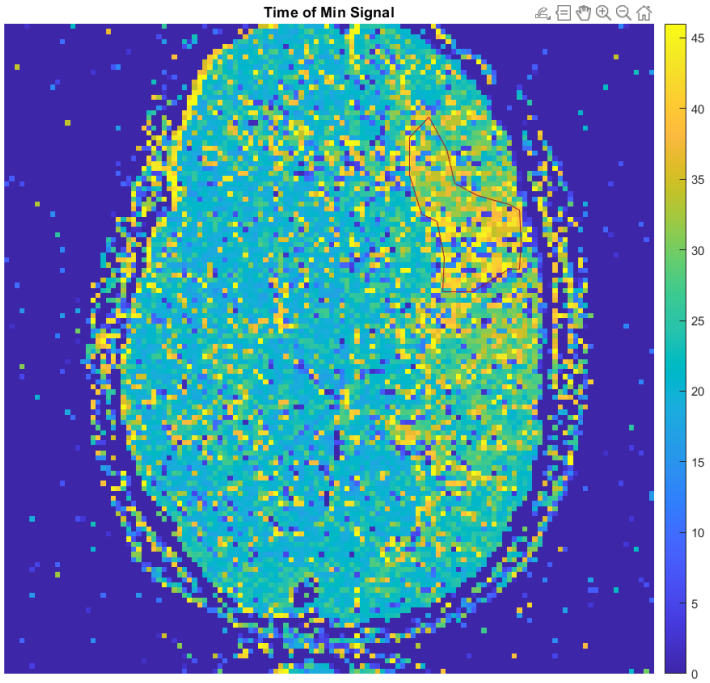
```
intLimits_v = [min(image_3d(:)), max(image_3d(:))];
figure
for index = 1:nTimes
    imagesc(squeeze(image_3d(:, :, index)),intLimits_v);
    axis image
    axis off
    colormap(gray)
    title(['Time points: ', num2str(index)])
    drawnow
    mov(index) = getframe;
end
fps = 8;          % frames per second.
nReps = 4;    % number of repetitions.
movie(mov, nReps, fps)
```

```
% Create head mask
imageMax = max(image_3d(:));
image_m = squeeze(image_3d(:, :, 1));
headMask_m = (image_m > 0.1*imageMax);
figure
imagesc(headMask_m)
colormap(gray)
axis image
axis off
title('Head mask')
```

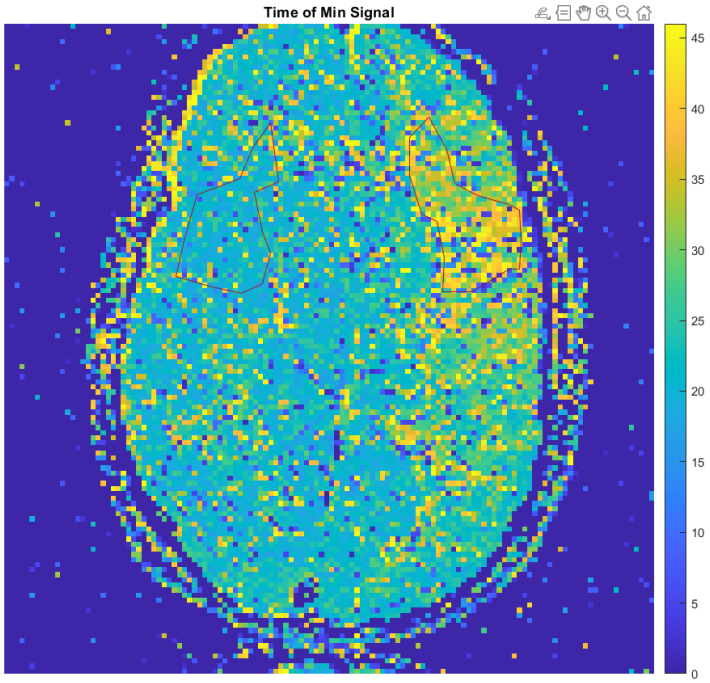

```
timeOfMin_m = zeros(nRows,nCols);
for row = 1:nRows
    for col = 1: nCols
        if (headMask_m(row, col) == 1)
            [minSignal, timeOfMin_m(row,col)] = min(image_3d(row, col, :), [], 3);
        end
    end
end
figure
imagesc(timeOfMin_m)
colorbar
axis image
axis off
title('Time of Min Signal')
```




```
[slowRoiMask_m, x_v, y_v] = roipoly ;
slowRoiMask_m = slowRoiMask_m .* headMask_m;
line(x_v, y_v, 'Color', '#A2142F') ;
```

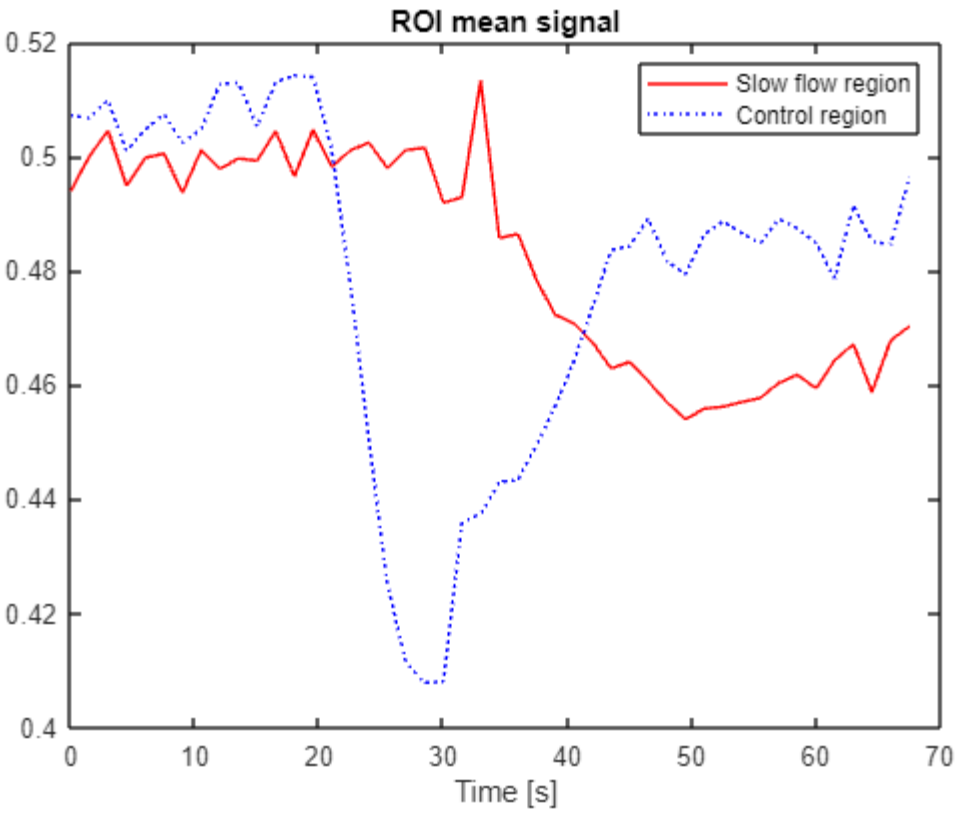



```
[controlRoiMask_m, xc_v, yc_v] = roipoly ;
controlRoiMask_m = controlRoiMask_m .* headMask_m;
line(xc_v, yc_v, 'Color', '#A2142F') ;
```



```
slowRoiMean_v = zeros(1, nTimes);
controlRoiMean_v = zeros(1, nTimes);
for timeIndex = 1:nTimes
    image_m = squeeze(image_3d(:, :, timeIndex));
    numelSlow = sum(sum(slowRoiMask_m));
    numelControl = sum(sum(controlRoiMask_m));
    slowRoi_m = image_m.* slowRoiMask_m;
    controlRoi_m = image_m.* controlRoiMask_m;
    % Enter your own code here to calculate the mean signal
    % in each ROI at the current time:
    slowRoiMean_v(timeIndex) =  sum(sum(slowRoi_m))./numelSlow;
    controlRoiMean_v(timeIndex) = sum(sum(controlRoi_m))./numelControl;
end
```

```
figure
time_v = tr * (0:(nTimes-1));
plot(time_v, slowRoiMean_v, 'r-', time_v, controlRoiMean_v, 'b:')
title('ROI mean signal')
xlabel('Time [s]')
legend('Slow flow region', 'Control region')
```

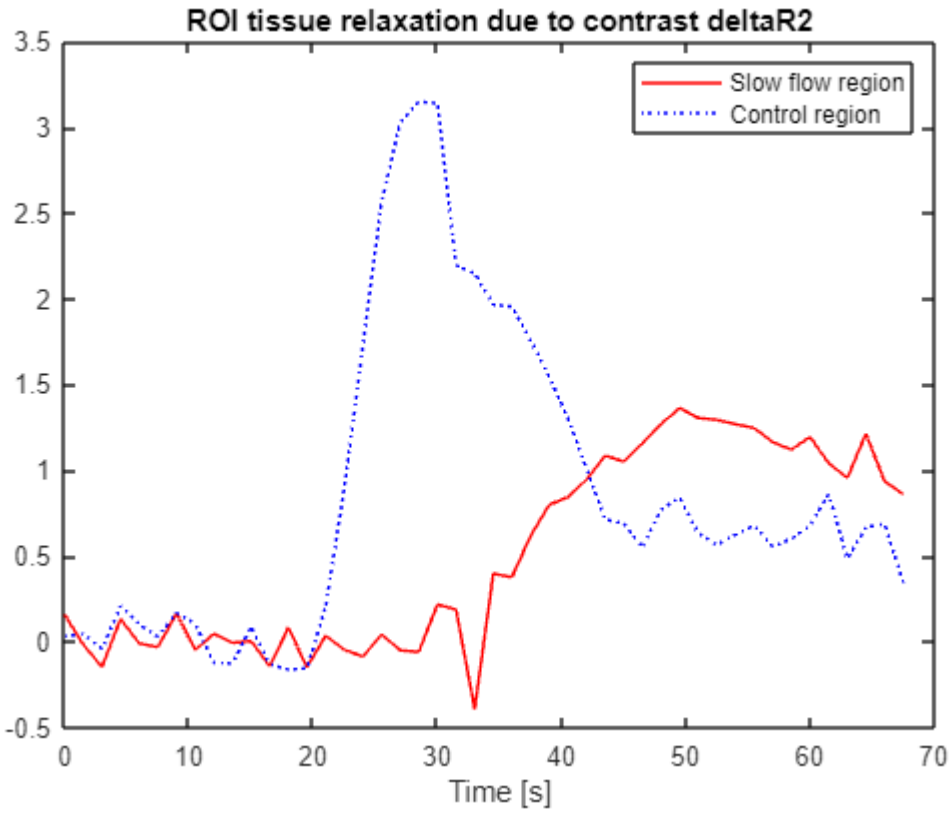



```
baselineTime = input('Enter the duration of the baseline (in seconds): '); %20s
baseIndex_v = find(time_v < baselineTime);
```

```
slowBaseSignal = mean(slowRoiMean_v(baseIndex_v));
controlBaseSignal = mean(controlRoiMean_v(baseIndex_v));
```

```
slowR2_v = -log(slowRoiMean_v/slowBaseSignal)/te;
controlR2_v = -log(controlRoiMean_v/controlBaseSignal)/te;

figure
time_v = tr * (0:(nTimes-1));
plot(time_v, slowR2_v, 'r-', time_v, controlR2_v, 'b:')
title('ROI tissue relaxation due to contrast deltaR2')
xlabel('Time [s]')
legend('Slow flow region', 'Control region')
```




```
slowCBV = trapz(time_v, slowR2_v);
controlCBV = trapz(time_v,controlR2_v);
relativeCBV = slowCBV/controlCBV
```

```
relativeCBV = 0.5798
```