BioE 105, Fall 2018
Homework Assignment 9
Assigned Wednesday November 9, 2018
Due Date: Monday December 3, 2018

Instructions: Make sure to list your name and the names of all people with whom you worked on this assignment. Don't submit matlab code for this assignment, just the results from below. Note that no two people should have identical results for question 1.

1. Time scaling property of convolution
If x(t) * g(t) = c(t) then show that x(at)*g(at) = |1/a|c(at). This is the time scaling property of convolution and states that if both x(t) and g(t) are time-scaled by a, their convolution is also time-scaled by a and multiplied by 1/a).

2. Image blurring/filtering example
In a few lectures we will get to filtering not just waveforms but also images. Filtering of images can make them look less 'grainy', but often times this can be accomplished by merely blurring your original image using the convolution of a Gaussian filter with your original image.

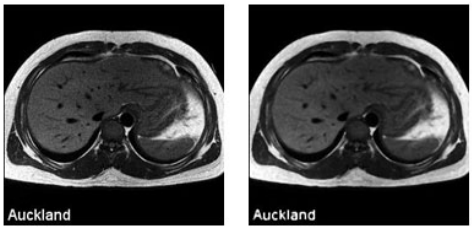
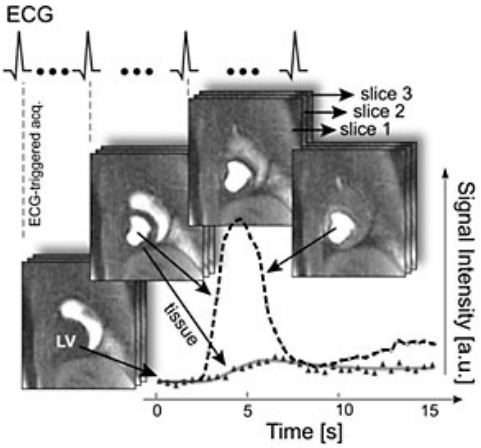


Fig8. (a)Poisson Noise (b) Filtered Poisson MRI image

To understand what this means, consider the function x(t) = u(t+3) – u(t-3). This is just a rectangle function at the origin with a width of 6s. Now, assume that your impulse response h(t) = exp[(t^2)/2] is a Gaussian function.

(a) What is the output of your system when y(t) = x(t) * h(t)?
(b) What do you notice about the width of y(t)?
(c) What happens at t = -3 and t = +3 that differs from x(t)

3. When imaging modalities are used to quantify blood flow to a tissue, this is based on the premise that a substance called a contrast agent that is injected into the blood stream will arrive at the location where you are imaging, fill the capillary beds, and change the signal intensity as a function of the concentration of the agent which is proportional to the blood flow through the capillaries. This is done with PET, CT, MRI, ultrasound, etc. Take a look at the figure below that comes from a cardiac perfusion MRI study.



The dashed curve represents the changes in signal intensity of the blood pool after this contrast agent is injected intravenously. As you can see, there is a rapid rise in the amount in the blood as the injected bolus arrives in the ventricular blood pool, and a rapid drop as it tapers off and moves elsewhere. This is effectively your input function x(t). The solid line connecting the individual symbols represents the signal intensity of the tissue, which has increased as the contrast agent enters the capillary beds and resides for 30 minutes or so in the extracellular tissue space. This is what you are directly measuring, and is your output y(t).

If your impulse response h(t) was just a delta function, then the signal intensity of the myocardium would just be a delayed and scaled version of the input waveform, but it is not. This happens because the contrast agent resides within the microvasculature and the surrounding extravascular space for some period before being drained out by the venous system. Subsequently, the impulse response can be described by a residue function as shown below.

$h(t) = F * \frac{1}{e^{(t-to-td)k}+1}\, u(t-t_d)$

In this equation F is blood flow, t_d is the delay in time between when the input function x(t) changes from baseline and the output function y(t) changes from baseline, t_o controls the width of the above Fermi function, and K is the decay rate of the residue impulse response. Based on this, the signal you measure in the tissue (y(t)) is the convolution of your input function (x(t)) and the residue function (h(t)).

Download the Matlab data set and accompanying code. Inside there are two variables

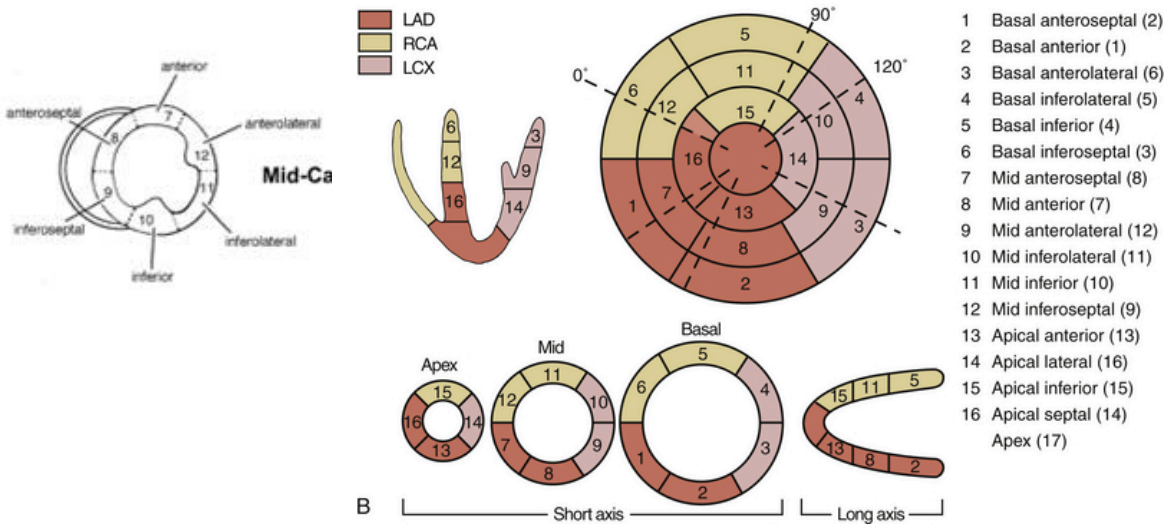
recon_AIF: array of images from first scan by which to characterize the arterial input function x(t)

recon_TF: array of images from second scan at much higher concentration of contrast agent from which to measure the tissue response y(t)

The code provided uses an iterative convolution approach to match the convolution of a Fermi function (see above) with your measured AIF to your measured TF. The Fermi

function with the best fit to the measured data provides you with the flow rate in units of ml of blood / g tissue /min.

Use the AIF data to define your input function. This will be the same for all subsequent measurements. Use the ROI for your tissue function code to calculate the tissue function for the six regions of myocardium as defined by the American Heart Association. These are two septal segments (#1 and 6) between the left and right blood pools, two anterior and two inferior segments. Your short axis imaging slice is somewhere between the mid ventricle and the base.



(1) Submit one graph showing the six different tissue responses on the same graph. Export the data to excel to do this, and clearly label/identify each region using different symbols and a clearly legible legend. For your graph make sure you also label all axes and provide units where appropriate.

(2) Provide the graph of your input function with all axis labeled.

(3) Submit one graph showing the best fit residue function for each of your regions (look at the last cell in the code to find the appropriate variable where this is stored). Use the same approach as before (q1) to show the six different residue functions you reconstructed.

(4) Submit a table with the calculated flow values for each tissue segment. What kind of spatial variability in flow did you calculate?