BME 790: Engineering Programming and Signal Processing
Fall 2013

Homework Assignment #5
Assigned Wednesday, November 13, 2013
Due: Wednesday, December 1, 2013

Read Chapter 6 from Haykin, 2nd edition, and then complete the following problems. For this homework you only have special problems, no book problems, but if you're looking for good practice problems check out 6.29, 6.30, 6.32, and 6.40:

1. Let's look at BME applications of Linear Differential Equations (LDEs). The ingestion and metabolism of a drug in a human is modeled by the equations

$$\frac{dq(t)}{dt} = -k_1 q(t) + x(t)$$
$$\frac{dy(t)}{dt} = k_1 q(t) - k_2 y(t)$$

where $x(t)$ is the ingestion rate of the drug, the output $y(t)$ is the mass of the drug in the bloodstream, and $q(t)$ is the mass of the drug in the gastointestinal tract. Suppose that $k_1 = 0.05$, $k_2 = 0.02$, $y(0) = 0$, $q(0) = 10$ milligrams (mg), and $x(t) = 0$ for $t \geq 0$. This corresponds to a person having recently ingested a drug that resulted in a 10 mg amount in the gastrointestinal tract at time $t = 0$.

   (a) What is the zero state response (ZSR) of q? Calculate both H(s) and h(t), the transfer function and impulse response function for the gastrointestinal system.

   (b) Using the relationship between Laplace and Fourier Transform, calculate $H(j\omega)$ and plot both the magntiude and phase. What kind of filter is this?

   (c) Calculate the ZSR for y and the zero input response (ZIR) for y leaving it without substituting in for the constants.

   (d) Calculate the transfer function H(s)=Y(s)/X(s) of the bloodstream and h(t) the overall impulse response function of the bloodstream for this particular drug. What kind of filter is your overall digestive track?

   (e) This time, convert the differential equations from time-domain into s-domain and solve for $y(t)$ for $t > 0$.

   (f) Try it again, but this time have $q(0) = 0$ and $x(t) = u(t)$. Now you have a way to solve these problems that makes life (and differential equations) so much more fun!

2. A long time back we looked at a negative feedback loop in class while we were covering control systems in convolutions. You might remember unlike other examples, we had trouble calculating the overall impulse response function with the toolbox we had at the time. Let's revisit this problem and see if we are better equipped to handle it now! Consider the positive feedback loop shown below:
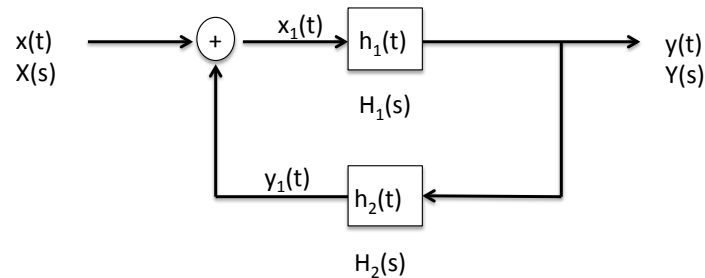
(a) In the time domain calculate $x_1(t)$, $y_1(t)$, and $y(t)$. Rememember to solve for h(t) we needed it in the form $y(t) = x(t) * h(t)$. Can you calculate h(t) this way? Why or why not?

(b) Now let's see if Laplace can help. Calculate the Transfer function, $H(s) = \frac{Y(s)}{X(s)}$, for the control system in terms of $H_1(s)$ and $H_2(s)$.

(c) Assume $H_1(s) = k$ and $H_2(s) = s$. Explain what these control systems do to their inputs.

(d) Calculate $H(s)$ for the given values in (b).

(e) Calculate h(t) for this system. Is this system stable? What does this mean about positive feedback loops?

(f) Keep everything the same except change it from a positive feedback loop to a negative feedback loop and recalculate the overall h(t). Is this system stable? What does this say about negative feedback loops?

3. Let's look at how gene expression is regulated in the body. It turns out that there is a negative feedback loop that alerts the RNA of the presence of other RNA, as well as the concentration of the protein the RNA creates, thus ensuring that you don't make 'too much' of a given protein. Let's take a closer look. (Thanks to Inka Johnson, Frank Lee, and Kelsey Tarzia for bringing this problem to my attention)

$$\frac{dC_{protein}}{dt} = k_p C_{RNA}(t) - \gamma_p C_{protein}$$
$$\frac{dC_{RNA}}{dt} = k_R u(t) - \gamma_R C_{RNA}$$

(a) Convert the above equations from the time domain into the s-domain. Solve the equation for $C_{protein}(s)$.

(b) Let's assume $k_p = 10^{-1}$, $k_R = 0.4$, the initial concentration of protein in the system is $c_p(0) = 0$, the initial concentration of RNA in the system is $c_R(0) = 0$, the degradation rate of the RNA is $\gamma_R = 5$, and the degradation of the protein is $\gamma_p = 10$. Use MATLAB's residue command, and the constants provided, solve for $c_{protein}(t)$ and plot the response as a function of time.

(c) Keep everything the same only change $c_p(0) = .1$, that is there is an initial concentration of protein. Solve for $c_{protein}(t)$ and plot the response as a function of time. How did having an initial concentration of protein change the solution? Does the system produce more protein or does it attempt to remove protein and how do you know?

(d) Make $c_p(0) = 0$ and this time change $c_R(0) = .5$ and calculate the solution. How did having an initial concentration of RNA affect the solution?

(e) Lastly have $c_p(0) = .01$ and $c_R(0) = .5$ and calculate the solution. Plot all four solutions on the same graph in MATLAB and explain how changing the intial conditions affected the result.

(f) How did the different intial conditions affect the intial response of the system?

(g) How did the different initial conditions affect the steady state response? Doesn't Laplace rock for solving these problems?

4. The figure below is a filter commonly used in BME applications. Find the transfer function, H(s) for the circuit presented in Figure 1 and describe qualitatively what it is doing to an input signal X(s). Then take the input x(t)=u(t)-u(t-2) and in MATLAB present a plot output y(t). Is this what you would expect? Convert from X(s) to $X(\omega)$, using your knowledge of the relationship between Laplace Transforms and Fourier Transforms. What kind of filter is this?