PITT | SWANSON ENGINEERING

BIOENG 1320 – Biological Signals and Systems (Spring 2022)

MATLAB Project 1

Issued: January 26, 2022 Due: 1:00p, February 16, 2022 (via Canvas)

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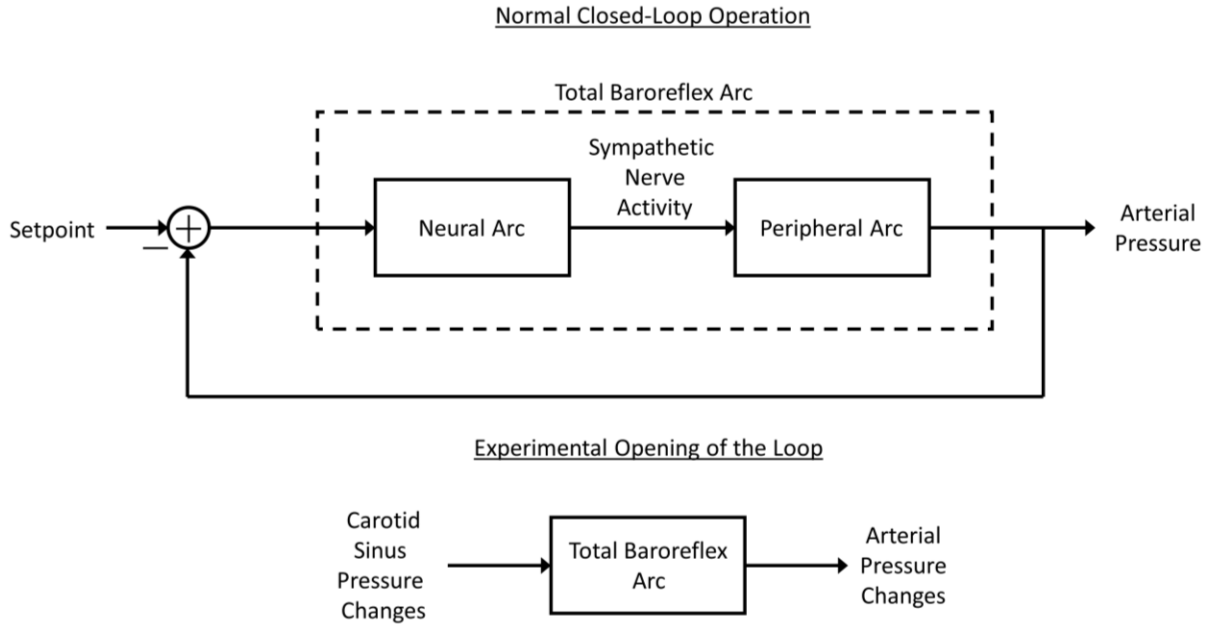
1. **Testing a biological system for linearity and time-invariance:** It is important for the body to keep arterial pressure within narrow limits. If arterial pressure is too low, tissue beds will not be adequately perfused with blood. If arterial pressure is too high, the tissue beds can be damaged. The baroreflex is a mechanism mediated by the autonomic nervous system for maintaining arterial pressure. Stretch receptors in the neck sense the arterial pressure in the carotid sinus region and relay this information to the brain. If the arterial pressure is above/below the desired level (i.e., setpoint), the brain responds by decreasing/increasing sympathetic nervous outflow to the circulation, which decreases/increases cardiac output and total peripheral resistance to restore the arterial pressure. The interaction between the baroreflex and circulation may be viewed as a negative feedback system as show in the figure.



This closed-loop system can be opened experimentally to investigate the total baroreflex arc, which relates changes in carotid sinus pressure to changes in arterial pressure. The total baroreflex arc will respond to an increase/decrease in carotid sinus pressure by decreasing/increasing the arterial pressure. The function **TotalBaroreflexArc** is a model of this system developed using experimental data from a rodent preparation. The function arguments are the carotid sinus pressure input and "n" for normotensive or "h" for

hypertensive, which developed after years of aging in the same subject. The function output is the resulting arterial pressure and corresponding time samples.

Use sinusoidal inputs with frequencies between 0.01 and 0.20 Hz, a sampling interval of 0.5 sec, and a duration of at least 50 sec to answer the following questions.

(a) Is the system linear or nonlinear?
(b) Is the system time-invariant or time-varying?
(c) If it is not linear and/or time-invariant, can it be approximated as LTI under certain conditions? If so, what are those conditions?
(d) What are the differences in classifying real biological systems versus mathematically-defined systems (e.g., from Lecture)?

Include properly labeled plots as supporting evidence.

2. **Filtering a biological signal to remove noise:** Action potentials (commonly referred to as spikes) are the electrical language that neurons use to communicate with one another. The first experiments to understand the mechanism of action potentials were performed on giant squid axons. These experiments involved stimulating the channels that control the movement of ions across the axon membrane with voltage pulses. The investigated ion channels were sodium, potassium and certain leak channels that allow the corresponding ions to flow in and out of the cell.

   A typical cell membrane has a negative resting membrane potential. When a voltage stimulus causes the axon to increase its membrane potential above a threshold, the sodium channels open causing an influx of sodium into the cell and depolarization to a peak potential (spiking). During this time, the potassium channels slowly open causing expulsion of potassium out of the cell and repolarization to the resting membrane potential. The resting, threshold, and peak membrane potentials are important parameters for characterizing axons. Measurement noise can be a practical problem in detecting these parameters.

   The file **apdata.mat** contains two computer-simulated giant squid axon action potential signals (spike trains) in units of mV and of 200 msec in duration with a "sampling interval" of 0.0796 msec each. One of the signals is artifact-free (vector labeled "clean"), while the other signal is contaminated with noise (vector labeled "noisy"). The file also includes the corresponding "time" vector for both signals (vector labeled "time"). The file **apfilter.mat** contains an impulse response for removing noise in the action potential signals while retaining information. The impulse response is given at the same sampling interval (vector labeled "h"). This discrete-time filter may be applied to originally continuous-time spike trains by approximating the convolution integral as follows:

$$y(t) = \int_{-\infty}^{\infty} h(\tau)x(t-\tau)d\tau \quad \rightarrow \quad y(nT_s) \approx \sum_{k=0}^{N-1} h(kT_s)x((n-k)T_s)T_s,$$

where $T_s = 0.0796$ msec and N is the impulse response length here.

a. Plot the two spike trains versus time and label the resting, threshold, and peak membrane potentials for the clean signal. Can the same information be readily seen for the noisy signal?
b. Apply the filter to both spike trains using the built-in **conv** function. Plot the two filtered signals versus time. The filtered signals are longer than the original signals and have some transients at the edges. What causes these edge effects and how should they be handled?
c. Describe the results of the filtering. Can you now better label the resting, threshold, and peak membrane potentials for the noisy signal? Has all the noise been removed from the noisy signal? Why or why not?
d. What do you still need to learn to be able to remove noise in other biological signals?

Deliverables: Submit a single pdf file containing answers to the questions, properly labeled plots, and the source code.