

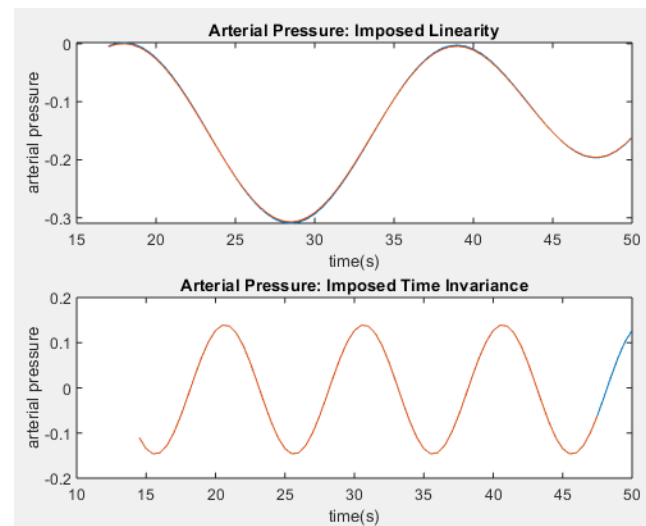
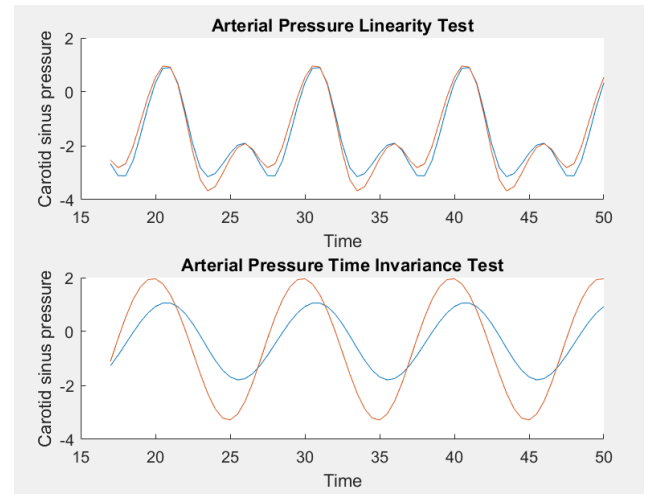
Part 1

A) **Not linear** – if the system was linear, linearly combining the inputs would have the same plotted output as if we linearly combined the outputs & plotted that result. Also, for the system to be linear, this would have to be true for all sinusoidal inputs. As you can see in the ‘Arterial Pressure Linearity Test’ plot, that is not the case.

B) **Time-varying** – if the system was time invariant, outputs of functions with either normotensive arguments or hypertensive arguments would be the same if the input was the same. As you can see in the ‘Arterial Pressure Time Invariance Test’ plot, this is not the case.

C) Linearity can be imposed by restricting both input functions amplitude to be less than 1 (See “Arterial Pressure: Imposed Linearity”). The system can be approximated as time invariant when the function arguments are the same (‘n’ vs. ‘h’), or the function is applied within a reasonably similar time window (within seconds/minutes of each other instead of years, see “Arterial Pressure: Imposed Time Invariance”). So the system can be approximated as LTI when input function amplitudes are <1 and when the Baroreflex function is applied to two signals within a similar time period.

D) Real biological systems are typically not perfect LTI systems, so it can be difficult to mathematically approximate them using LTI systems. Additionally, biological systems have an unknown number of external variables impacting them at any one time, making accurate mathematical approximations (even with a non-linear, time varying system) difficult.



Part 2

A) No, it is not very clear where the peak, threshold, and resting AP values are in the noisy signal.

B) The zero-padded edges in the plots result from the convolved signal being a different length than the time vector. They can be handled by using the MATLAB command `conv` with the shape input 'same.' Use of this shape argument is included in the comments on the MATLAB code.

C) The noisy signal is still not as clean as the provided filtered signal, but now it is a lot easier to visually identify the resting, threshold, and peak membrane potentials. Not all of the noise has been removed because the filter does not categorize signals by frequency and efficiently distinguish desirable frequencies/signals from unwanted noise.

D) We don't know how to filter signals in the frequency domain yet, so it's difficult to filter out higher frequency noise in a way that keeps the signal identifiable.

