FITNESS FUNCTIONS – 1) POWER SPECTRUM AND 2) AMPLITUDE DISTRIBUTION

ALL SCRIPTS SHOULD APPLY THE CODING STANDARDS WE DISCUSS IN CLASS.
READABILITY, EFFICIENCY, MODULARLIZATION AND GENERALIZATION ARE IMPORTANT CONSIDERATIONS BEYOND FUNCTIONALITY

Useful functions for this assignment: `xlabel(), ylabel(), title(), text(), fft(), real(), imag() cart2pol(), histogram(), histcounts(), pwelch()`

Question 1a: Download the data file ex1.mat. This file contains a 1xN record of simulated EMG data sampled at 1000Hz. Plot 1 sec of the data. Be sure to use the correct time scale. In the same figure (ie use subplot), plot the power spectrum of the signal. Plot only the positive half of the spectrum, but scale it so that it represents all of the power in the signal. Be sure to use the correct frequency scale. You can use pwelch() to calculate the spectrum, but don't average any epochs.

Question 1b: Repeat part 1a using pwelch(), but this time, average with 0.5 sec square window epochs, no overlap. Don't forget that the frequency resolution of your power spectrum will change according to the duration of your epochs, so account for that in your new frequency scale.

Question 1c: Repeat part 1c and superimpose this output on a power spectrum that you create with your own averaging algorithm. Your algorithm should extract 0.5 sec square window epochs from the signal, calculate a power spectrum of each, and then average them to get the final output. You should use abs(fft(x))^2 to calculate the spectrum, but take into consideration any scaling necessary to ensure all the power in the signal is represented.

Question 2: Plot a 20-bin histogram of the amplitude of the signal you downloaded in question 1. Characterize the result (is the shape normal, bimodal, flat etc)?

NOTE: THE CODE YOU WRITE HERE SHOULD FORM THE BASIS FOR THE FITNESS
FUNCTIONS IN YOUR PROJECT GENETIC ALGORITHM