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BMEN 3302.501 Bioengineering Signals and Systems

Mini project 2

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Steps:

1. Load clean ECG and noisy ECG to be xClean and xNoisy.
2. Load the time of ECGs and set to be n.
3. Define yNoisy and yConv to be an array of zeros with 200 elements, initially.
4. Set N to be one of the values of 2, 3, 5, and 10 manually.
5. Use movmean() function of MATLAB to redefine yNoisy to be a trailing moving mean of xNoisy with N number of elements.
6. Find the impulse response of system.
   a. For N=2: $\frac{1}{2}(\delta[n] + \delta[n-1])$
   b. For N=3: $\frac{1}{3}(\delta[n] + \delta[n-1] + \delta[n-2])$
   c. For N=5: $\frac{1}{5}(\delta[n] + \delta[n-1] + \delta[n-2] + \delta[n-3] + \delta[n-4])$
   d. For N=10: $\frac{1}{10}(\delta[n] + \delta[n-1] + \delta[n-2] + \delta[n-3] + \delta[n-4] + \delta[n-5] + \delta[n-6] + \delta[n-7] + \delta[n-8] + \delta[n-9])$
7. Define impulse response h initially with zeros with N elements, and then redefine using a for loop looping N times with each element being 1/N.
8. Redefine yConv using conv(xNoisy,h).
9. Since the conv() function by definition outputs an array with size larger than original, the elements at the end exceeding the original array length were removed using for loop.
10. Plot each using stem() function.
11. For bio signal:
    a. Download and load the data into variables bio and t.
    b. Since the original data had 10 seconds of data with numerous elements, the data exceeding 2 seconds were removed.
    c. Plot original bio signal using stem() function.
    d. Redefine bio using movmean(bio,[N-1 0]) to redefine bio to be a trailing moving mean of itself.
    e. Plot the redefined bio using stem() function.

N = 2:
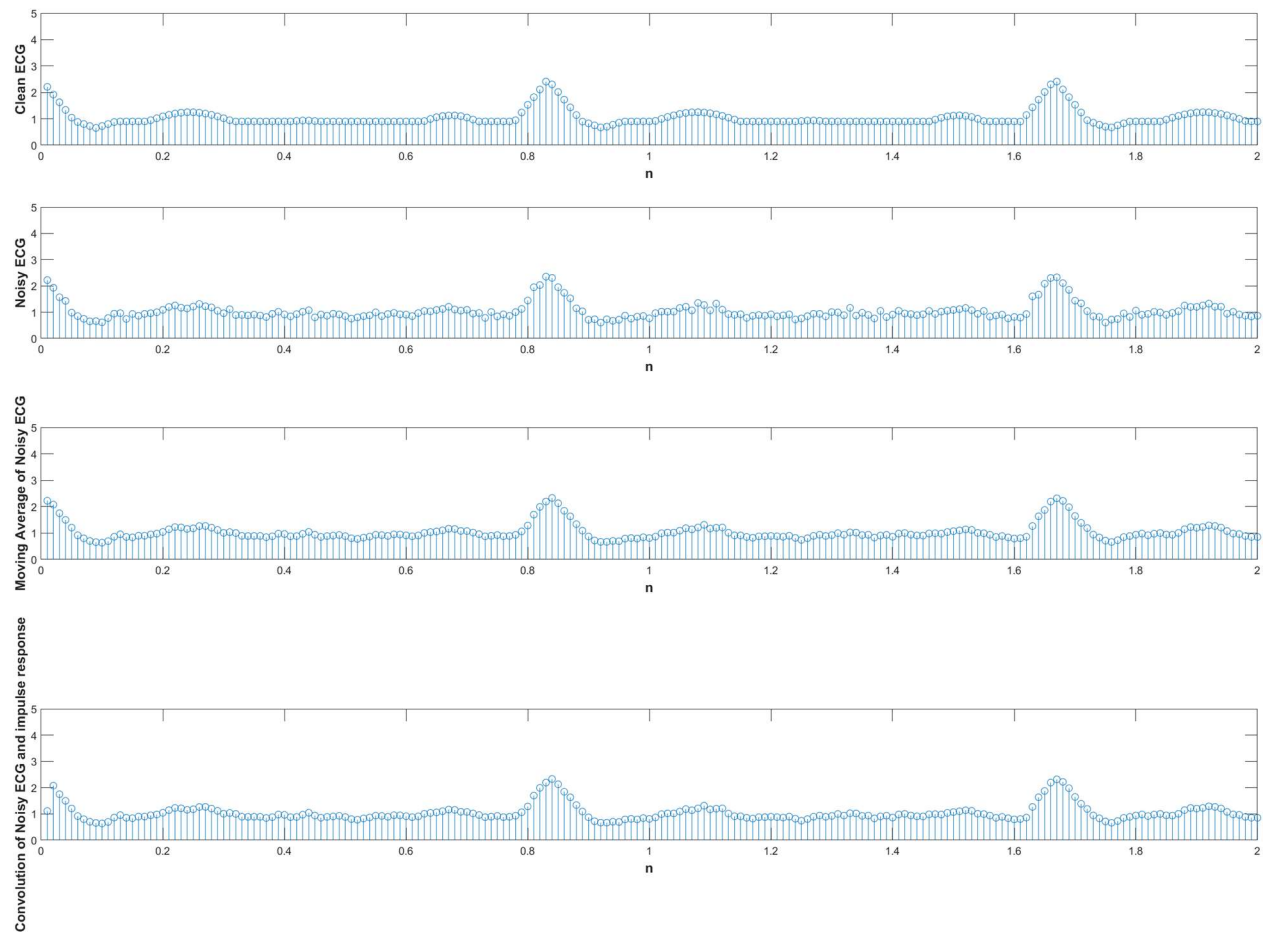


The moving average graph using N = 2 has the plots smoothed out, but the noise seen between the peaks is still very visible. The convolution outputted the same graph as the moving average, except for the initial data. This is because N = 2 and thus it takes 2 elements for the convolution to completely follow the moving average graph.

N = 3:
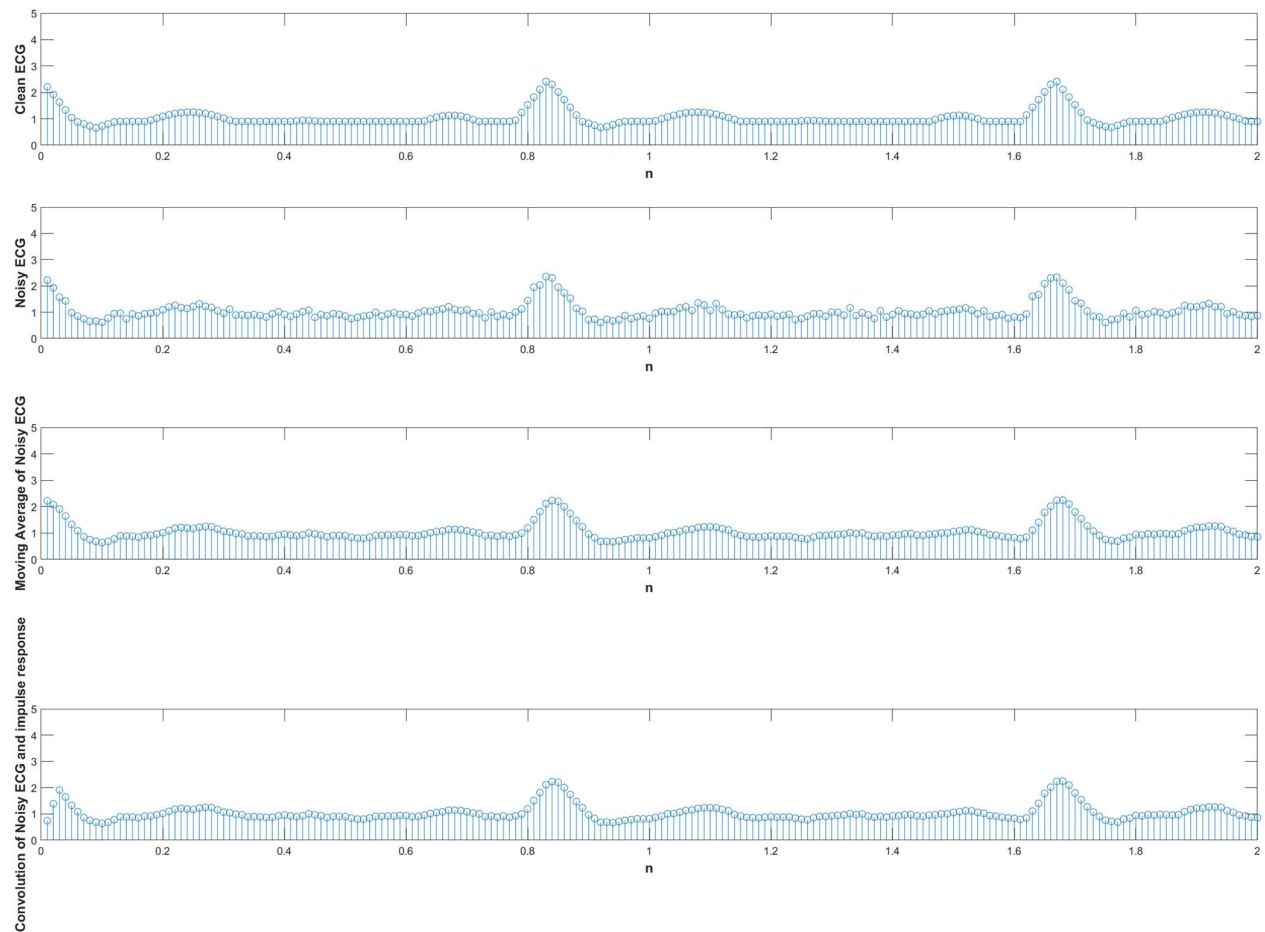


The moving average graph is even smoother, and the noise is flattened and seems very continuous. Similar to N = 2, the first 2 data points are off because N = 3 and thus takes 3 elements to follow the moving average.

N = 5:
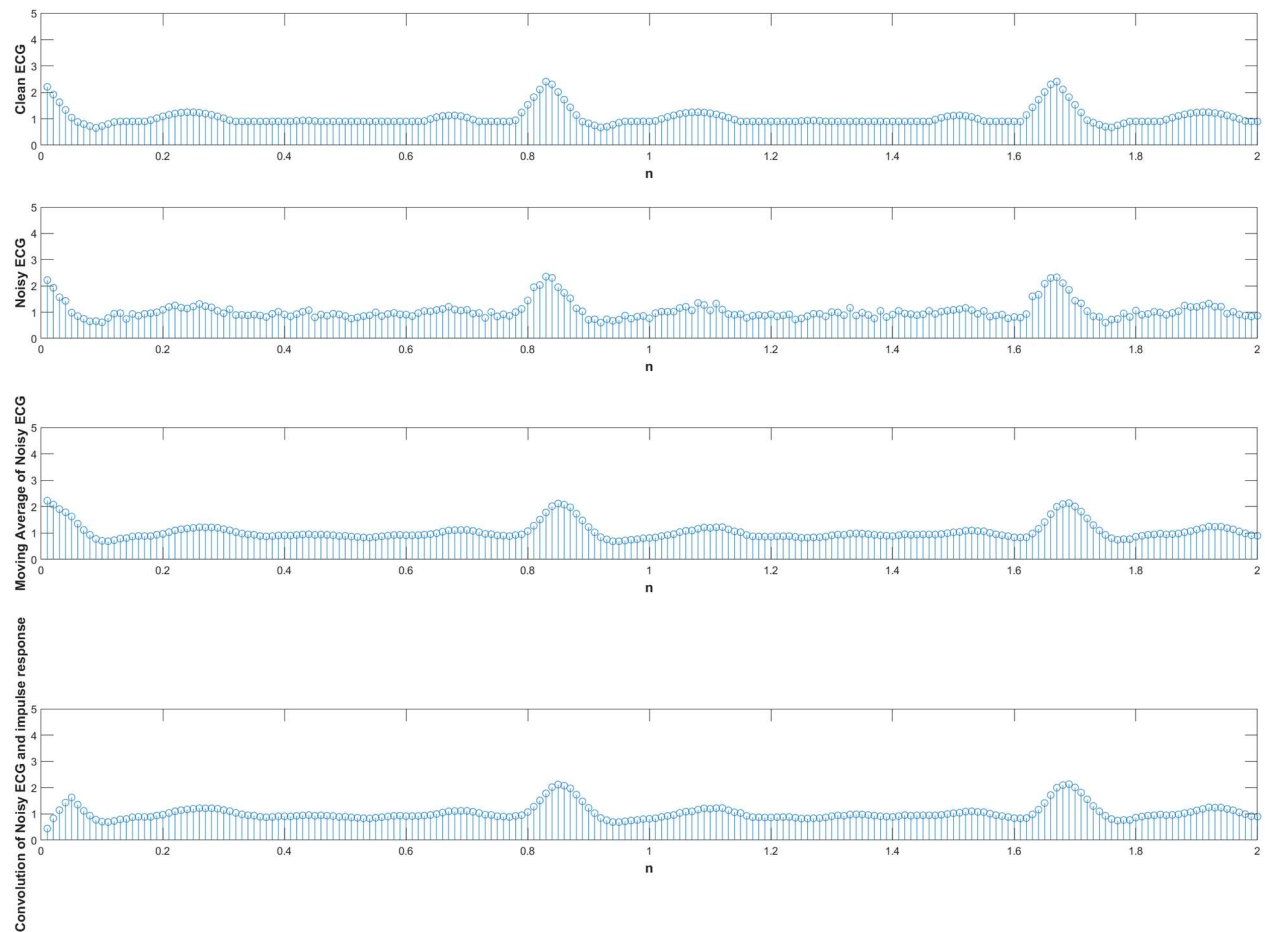


The mean average graph is flattened, making the maximum value of the peak lower than it actually is. The T wave of the ECG is also very difficult to differentiate from other noise, as they are all very similar. As expected, the convolution graph has its first 4 data much lower than actual, making the peak observed initially not noticeable.

N = 10:
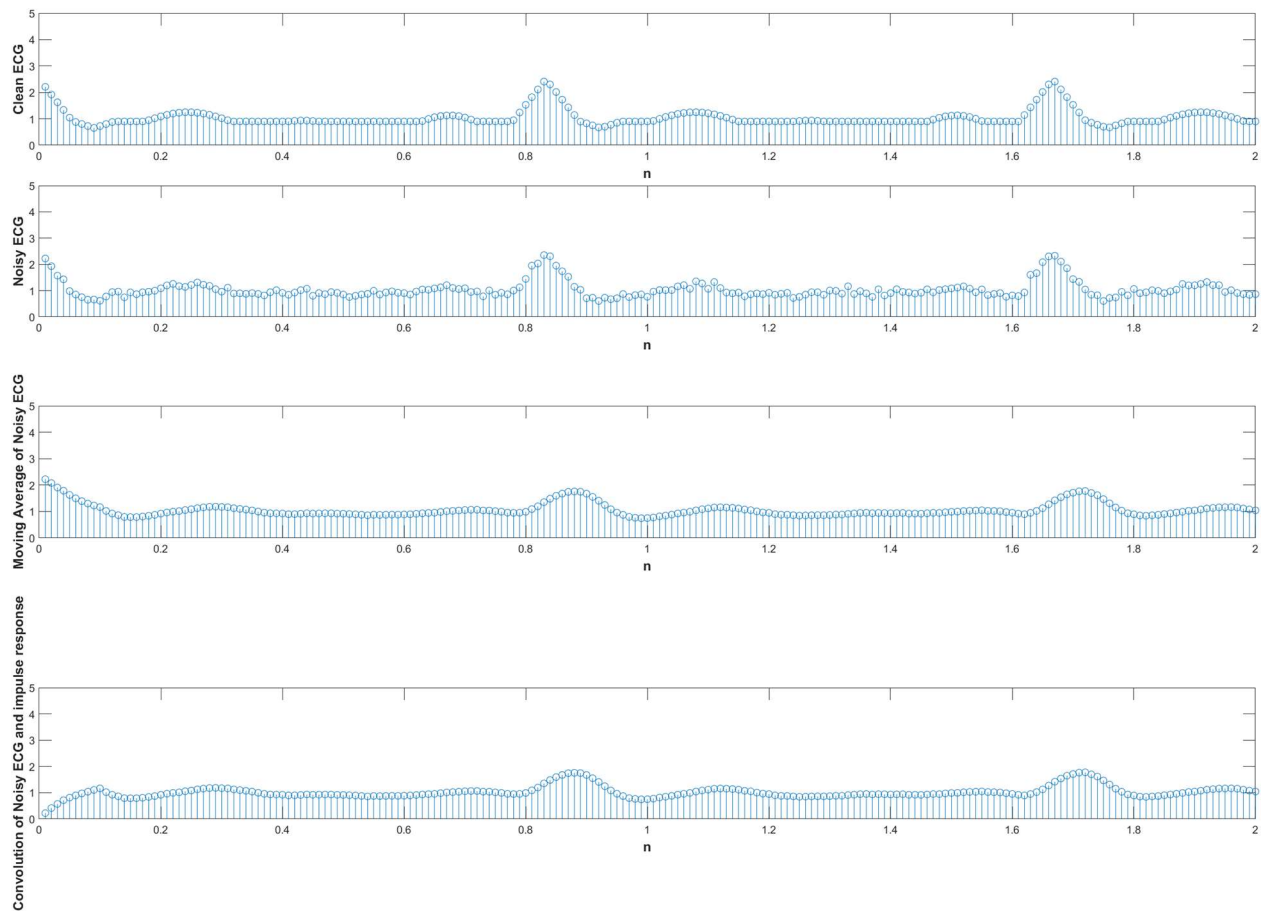


All of the data points are flattened out, making even the R wave almost indistinguishable from slightly larger T waves. In fact, it is impossible to determine if the T wave exists or not, as the data has been flattened so much. The convolution follows the moving average graph after the 9 initial rising data.

Bio signal:
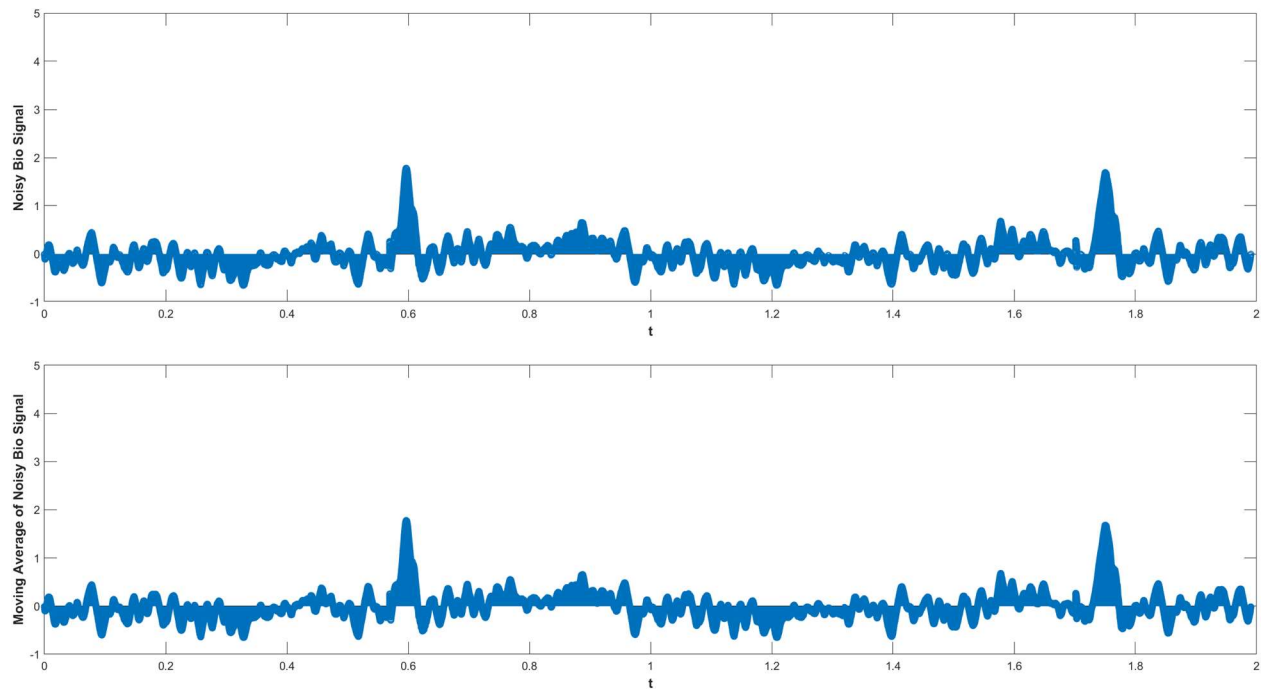




The moving average graph shown at the bottom is using N = 10. Even with N = 10, the graph seems almost identical, because the original signal has more than 1000 data points, and thus simply a mean of 10 was insufficient to be obvious. However, as seen below, the effect of N = 10 moving average becomes visible when zoomed in: the steps of the moving average graph are "smoothened" by making the jump less steep. From this, it can be concluded that N must be adjusted according to the number of data points that the signal has.
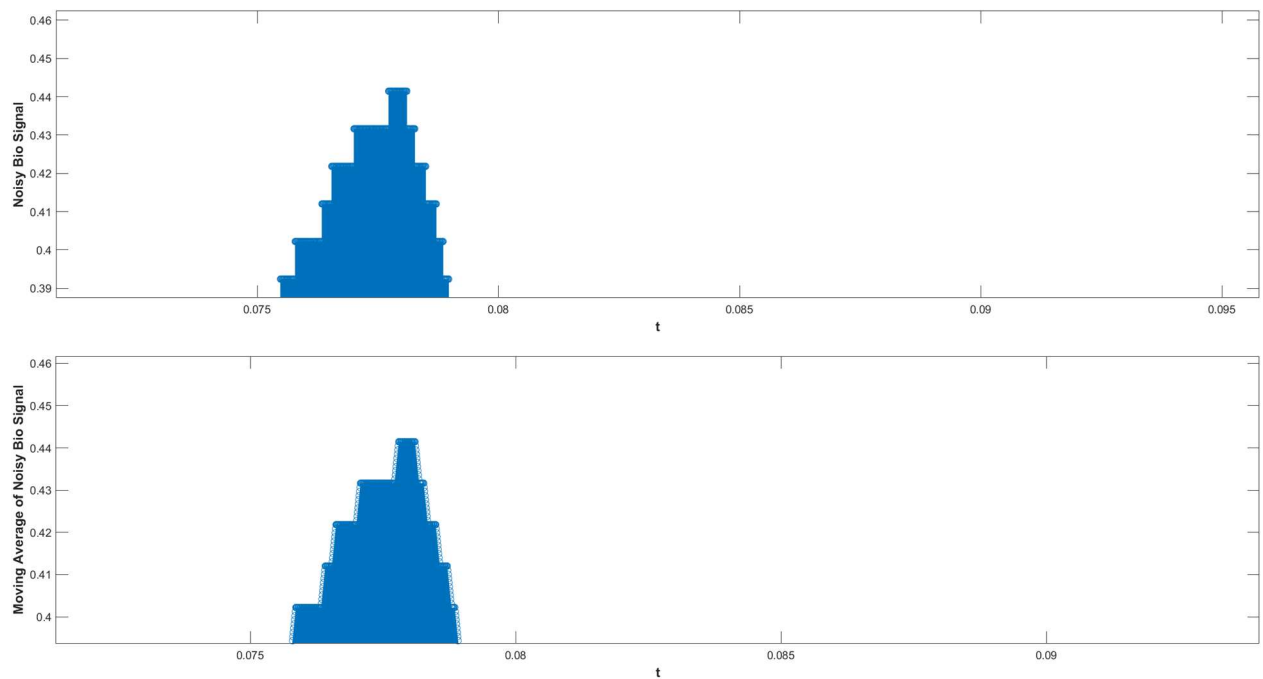
The advantage of increasing the N value is that the graph becomes smoother and thus becomes easier to interpret. However, the drawback is that increase in N value causes decrease in the detail of the graph. Thus, with N value that is too high, the graph loses significant shapes and only the rough estimation remains. With N values that is too low, the cleaned graph would appear the exact same as the original graph, similar to what I did for the bio signal. For the provided ECG, I would use N = 3, as the graph seemed smooth enough to ignore small noises, but still had enough details to differentiate between significant waves. For the bio signal, I would use N = 5000, as it has 254,782 elements.

Bio signal from downloaded from:

https://www.mathworks.com/matlabcentral/answers/383307-hi-i-am-trying-to-filter-this-noisy-ecg-signal-which-i-have-i-tried-many-of-the-filtering-metho