

Part I. ECG Artifact Removal

Motivation

In ECG, different noise sources can interfere with obtained signals in practice. The three main noise sources are baseline wander (in record 'bw'), muscle (EMG) artifact (in record 'ma'), and electrode motion artifact (in record 'em'). Electrode motion artifact is generally considered the most troublesome, since it can mimic the appearance of ectopic beats and also cannot be removed easily by simple filters, as can noise of other types. An active area of research in ECG is related to the design of filters that can improve the ECG recordings by removing such noise while keeping the ECG information intact.

Design Problem

Design suitable digital filters that allow removing ONE of the above noise sources from ECG recordings.

Design Input

- A set of ECG recordings containing baseline wander, EMG, or electrode motion artifacts.
- Original noise-free ECG signal as a reference (used as desired signal to compare your filtered output to).

Design Output

A report and documented Matlab code for a set of best three digital filter designs that handle ONLY ONE type of artifact of your choice (that is, either baseline wander, EMG, or electrode motion artifact should be considered).

Design Evaluation Criteria

- Qualitatively by comparing the output filtered signal to the noise-free record provided.
- Quantitatively by comparing the sum of absolute difference between the output filtered signal and the noise-free record provided.

References

[1] <http://physionet.org/physiobank/database/nstdb/>

- *Assigned:* Thursday July 2, 2015
- *Deadline:* Thursday August 6, 2015
- **Deliver project as a report and Matlab code “.m” to the instructors e-mail at ykadah@kau.edu.sa**

Part II. Genomic Signal Processing

Motivation

We hear about outbreaks of deadly diseases in different parts of the world all the time. Examples include Birds Flu, Ebola and MERS Coronavirus. It is interesting to think about what makes such viruses so unique and one way to investigate this is through genomic signal processing. The genome is the blueprint of life that contains all the information needed for all living beings to perform all their functions. Any genome consists of a unique long sequence of only four different proteins linked together. Such proteins are termed A, C, T and G. The genome of Coronavirus for example is given as [1]:

```
GATTTAAGTGAATAGCTTGGCTATCTCACTTCCCCTCGTTCTCTTGCAGAACTTTGATTTAAC  
GAACTTAAATAAAAAGCCCTGTTGTTTAGCGTATCGTTGCACTTGTCTGGTGGGATTGTGG ...
```

In genomic signal processing, we give each protein a number and consider the above sequence as an array of numbers (or practically a genomic “signal”) that can be processed using the available signal processing tools such as the Fourier transform.

Design Problem

Design a methodology to compare the Ebola virus to the MERS Coronavirus.

Design Input

- Genome sequences of both Ebola virus and the MERS Coronavirus.
- Matlab code to converts genome sequence to a numerical genomic signal.

Design Output

- A report and documented Matlab code for a method to characterize and differentiate between the two viruses by their Fourier transforms

Design Evaluation Criteria

- Qualitatively by comparing the spectra of their genomic signals.
- Quantitatively by stating the frequencies where they exhibit largest differences.

References

[1] <http://www.ncbi.nlm.nih.gov/nuccore/667489388?report=fasta&to=30119>

[2] <http://hgdownload.cse.ucsc.edu/goldenPath/eboVir3/bigZips/>

[3] <http://www.ncbi.nlm.nih.gov/genome/viruses/variation/MERS/>

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