ECG signal conditioning by Morphological Filtering

Project by Matteo Castagna (27366A)

This short document provides an explanation on how to run properly the MATLAB scripts and contains details on the implementation of the algorithms. Instructions on how to run the code, the meaning of the variables to tweak and adjustments I have made to the algorithm proposed in the paper are also embedded in the scripts themselves as comments.

1 Main scripts and How To Run

1.1 filterECG.m

The folder containing the project is called "project_matteo_castagna", the code need to be run from this folder. It contains two other folders, "Datasets" and "functions". "Datasets" has four .mat files; three of them are the datasets used to evaluate the proposed algorithms: "dataset_1.mat", "dataset_2.mat", "mit_bih_arrhythmia_database.mat". Those .mat files contain a variable "Fs", which is the sampling frequency of the ECGs, and a vector called "signals" which collects all the ECGs of the respective dataset. The fourth file, "mitbihQRSnumber.mat", contains a vector, "mitbihQRSnumber", which collects the number of QRS complexes for each subject in the MIT-BIH Arrhythmia Database. The "functions" folder contains the functions used in the main script.

The main script of the project is "**filterECG.m**". This script lets the user choose a dataset and a subject with the variables "**dataset**" (**line 16**) and "**i**" (**line 31**). "dataset" accepts as values 1, 2 and 3 (3 being the MIT-BIH Arrhythmia Database). "i" accepts values from 1 to 24 for dataset 1 and 2, and from 1 to 48 for the third dataset. The function "addNoise" is recalled to add noise and baseline drift to ECGs of dataset 1 and 2. The values given to the arguments of "addNoise", which control the slope, amplitude etc. of the drift, are the standard ones defined by Sun for dataset 1 and 2 (Paragraph 4.1.1 and 4.1.2 in [1]), so they don't necessarily need to be changed. For dataset 1 and 2, Baseline Correction Rate (BCR), Noise Suppression Rate (NSR) and Signal-Distortion Ratio (SDR) are evaluated and printed on the console. The clean ECG from the dataset, added baseline drift, detected baseline, added noise, detected noise and the filtered signal are plotted. For dataset 3 the Correct Detection Rate is evaluated for both the ECG before and after conditioning and printed on the console. Original ECG, conditioned ECG and detected QRS peaks are plotted.

Ultimately only "dataset" and "i" need to be tweaked, then the script can be run.

1.2 evaluateStatstichs.m

The other main script is "**evaluateStatstichs.m**". In this script the error metrics listed before are evaluated for all the ECGs of the selected dataset within a certain range for the parameters of the noise and baseline drift added, then their average is computed. The parameters to tweak are "**dataset**" (**line 32**) and "**stat**" (**line 45**). "dataset" accepts as values 1, 2 and 3. "stat" accepts as values 1, 2, 3 and 4:

- stat = 1, average BCR is evaluated for $\theta = 0$ and for A varying between 0.2 and 1 with a step width of 0.1, MMF and WF are considered;
- stat = 2, average BCR is evaluated for $A = 0$ and θ varying between 15 and 75 with a step width of 5, MMF and WF are considered;
- stat = 3, average NSR and SDR are evaluated for $K = 10$ and ϵ varying between 0.1 and 0.5 with a step width of 0.1, MMF and MF are considered ($K = \frac{\sigma_2}{\sigma_1}$);
- stat = 4, average NSR and SDR are evaluated for $\epsilon = 0.2$ and K varying between 10 and 25, with a step width of 5, MMF and MF are considered.

θ and A define the slope of the slanted line and the amplitude of the cosine used to generate the baseline drift. K is the rate between the variances of the two Gaussian used to generate the noise, ϵ is a scaling factor for the Gaussian. Those results are plotted and an overall mean of the metrics is printed on the console.

Once "dataset" and "stat" are tweaked the script can be run. As computing all the statistics may takes several minutes, the results and some graphs are reported at the end of this document.

2 Implementation details

Here changes in the algorithms implemented are presented.

2.1 MF and MMF

The project is based on Sun's Modified Morphological Filter (MMF)[1]. In the paper the MMF is tested with the MIT-BIH Arrhythmia Database and two other datasets made of simulated ECGs. The ECGs in the paper were hardware simulated, in the project they have been simulated with a MATLAB script available on PhysioNet[1]. The script lets the user control parameters such as the heart rate, the heights and anchor points of the ECG waves. Those parameters have been slightly randomized for each ECG by adding appropriately scaled values picked from a normal distribution. The first dataset contains 24 simulated ECGs with heart rate between 60 and 75 BPM. The second dataset contains 12 ECGs with heart rate between 45 and 55 BPM to simulate bradycardia and 12 ECGs with heart rate between 99 and 119 BPM to simulate tachycardia. ECGs have been simulated at a sample rate of 360 Hz as the ECGs recorded in the MIT-BIH Arrhythmia Database. ECGs in the latter have been exported and saved in a MATLAB variable with the help of the WFDB Toolbox[2].

The MMF differs from Chu's MF [2] in both the baseline detection and noise suppression stages. While in Chu's work the baseline detection stage is conduct after the noise suppression, Sun et al. swap the operations. Also Chu's baseline detection technique is divided in two branches, performing opening and closing alternately. Chu himself explain that one branch can be ignored. In Sun's work, baseline drift removal is performed using only one branch. In order to produce comparable results, both MMF and MF baseline drift removal have been implemented with one branch only in my project. The second difference is that MF uses only one structuring element $(0, 1, 5, 1, 0)$ while MMF uses two. As Sun and I both use the same dataset and sampling frequency, the length of ECGs' waves are comparable, so the length of the structuring elements used in the project hasn't been changed.

[1] `https://physionet.org/content/ecgsyn/1.0.0/`

[2] `https://archive.physionet.org/physiotools/matlab/wfdb-app-matlab/`

The height of the structuring element is related to the amplitude of the signal, as can be seen in the implementation of erosion and dilation operators in [2] and [1]. In Chu's work QRS peaks reach up to 5 milliVolts, but in both MIT-BIH Arrhythmia Database and the the two simulated datasets the amplitude of the QRS peaks does not go beyond 2. In the project the structuring element $(0, 1, 5, 1, 0)$ has been changed to $(0, 1, 2, 1, 0)$ for the MMF and $(0, 1, 1, 1, 0)$ for the MF in order to oimprove performances.

The noise added to the ECGs of datasets 1 and 2 is scaled with a 0.3 coefficients to produce a noise which amplitude is comparable with the one in real ECGs such as the ones in the MIT-BIH Arrhythmia Database, otherwise it would have been too high. The frequency of the cosine used to create the baseline drift was not specified in any of the paper on MMF and MF, so in the project it was fixed to 0.5 Hz.

2.2 WF

In [1] the MMF is compared with a Wavelet Filter (WF). I decide to implement one myself in order to make more comparable results. The WF has been implemented following Dai et al. work [3], cited by Sun. In [3] a 13 levels wavelet transform is performed on the ECGs, the level m_B where the baseline drift is dominant is detected and the wavelet coefficients from level m_B to 13 are put to 0, then reconstruction is performed. Dai use a non-orthogonal wavelet. The MATLAB function which performs wavelet transform only allows built-in MATLAB wavelet, which are orthogonal and bi-orthogonal, so the wavelet that I used was the Daubechies 3, "db3". After some testing, the wavelet levels have been set to 20 instead of 13 due to better performances. To detect the level where the baseline drift is dominant first the number of local maximum for the coefficients of each level is computed. A rate between those values for adjacent levels is computed, m is the level which has the maximum rate, and $m_B = m + 1$.

2.3 QRS complexes detection

In [1] MMF performances on MIT-BIH Arrhythmia Database ECGs are evaluated by computing the CDR on ECGs before and after conditioning, in the paper the QRS detection algorithm used is the one described by Trahanias[4].

Trahanias describe a procedure in which the ECG is first filtered through morphological operations similar to Chu's, then QRS complexes are detected using an adaptive threshold. Filtering has been implemented following exactly Chu's procedure, including both the branches. Instead of using the paper Trahanias cites to implement the adaptive threshold I choose to use a much recent procedure described by Lu et al.[5] in 2018. The filtered ECG is differentiated and squared, so that the slope of the peaks is emphasized. The result is integrated to unify the peaks. The integration has been performed with a moving window summation, the size of the window is set to be 33 milliseconds long. Before performing peak detection I decide to put to 0 small residual peaks under an amplitude of 0.01, this lead to better performances. The signal is now traversed, each time a new sample has a bigger amplitude than the previous one, the amplitude and the index of the sample are recorded as the maximum. When the amplitude of a sample drops by 25% of the maximum and the last peak is further then a certain number of samples, the last recorded maximum is saved as a peak. The resulting vector is traversed again and peaks are preserved accordingly with a threshold which is adapted using the amplitude of the latest peak.

3 Results

Here results of the filtering procedures are presented and compared.

Tab. 1, 2 and 3 refers respectively to the average BCR, NSR and SDR values computed for all the observations in both datasets 1 and 2, while in Tab. 4 are presented the BCR, NSR and SDR evaluated for the 1^{st} subject of both datasets. Sun does not tell to which data his results refers to, if are an average of all the ECGs or one picked randomly, so the results are not really comparable. Still the metrics in Tab. 5 are similar to Sun's.

Referring to Tab. 5 (results on a single ECG), MMF and MF perform better then WF in detecting the baseline distortion, the latter especially performs poorly with unusual heart rate (dataset 2). Despite Sun's results, MMF is able to suppress noise better then the MF. By looking at the plots of the filtered ECGs, despite the noise being efficiently suppress, Q and S valleys are not always preserved, this may be the cause of an SNR higher then Sun's one.

Referring to Tab. 1, considering A varying between 0.2 and 1, BCR is bigger then one, this result can be interpret as the introduction of new artifacts while correcting the cosine of the baseline drift. When A is set to 0, so the baseline drift consists of only the slanted line, performances are good, with MMF and MF performing better then WF. Considerations already made on NSR and SDR for Tab. 5 are still valid for Tab. 2 and 3.

Tab. 4 shows average CDR percentages evaluated on all the ECGs in the MIT-BIH Arrhythmia Database. Despite the percentages being generally lower then Sun's ones, which depends on the QRS peaks detection algorithm used, results confirm MMF and MF being able to clean the ECGs correctly, with a better precision in detecting QRS peaks after the conditioning, especially after filtering using the MMF.

	MMF / MF	WF
$\theta = 0, \quad 0.2 \leq A \leq 1$		
Dataset 1	1.0395	0.9086
Dataset 2	1.1325	1.6895
$15 \leq \theta \leq 75, \quad A = 0$		
Dataset 1	0.99890	0.57726
Dataset 2	0.99918	0.56639

Table 1: BCR

	MMF	MF
$K = 10, \quad 0.1 \leq \epsilon \leq 0.5$		
Dataset 1	0.95369	0.7403
Dataset 2	0.96666	0.73844
$5 \leq K \leq 25, \quad \epsilon = 0.2$		
Dataset 1	0.95106	0.74207
Dataset 2	0.96247	0.73983

Table 2: NSR

	MMF	MF
$K = 10, \quad 0.1 \leq \epsilon \leq 0.5$		
Dataset 1	0.48482	0.48568
Dataset 2	0.76003	0.75544
$5 \leq K \leq 25, \quad \epsilon = 0.2$		
Dataset 1	0.48519	0.4806
Dataset 2	0.75186	0.74851

Table 3: SDR

	Conditioning	
No Conditioning	MF	MMF
92.9669	93.1332	93.7787

Table 4: CDR

	BCR		NSR		SNR	
	MMF / MF	WF	MMF	MF	MMF	MF
Dataset 1	0.95489	0.89397	0.96208	0.72882	0.38994	0.3834
Dataset 2	0.97272	0.50253	0.92282	0.71363	0.60802	0.60203

Table 5: Metrics evaluated for the first ECG of both datasets 1 and 2.

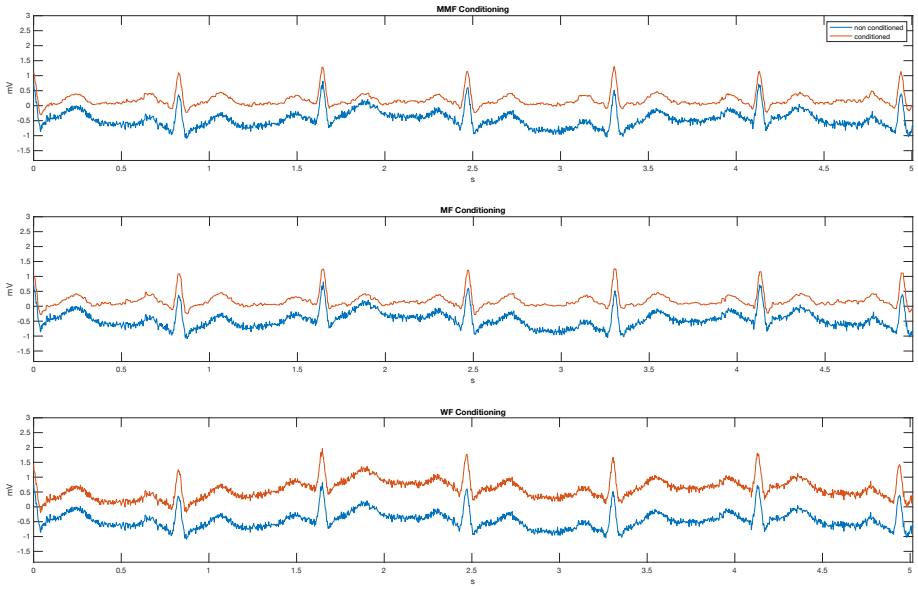


Figure 1: Corrupted ECG and conditioned one are plotted. Plots refer to the first ECG from dataset 1.

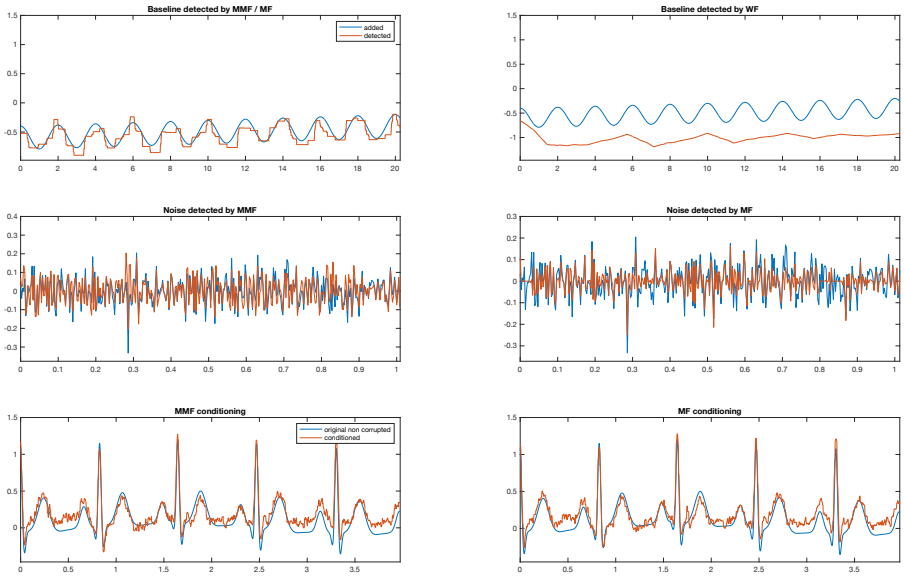


Figure 2: In the first row baseline added to the signal and detected baseline are plotted. In the second row added noise in detected noise are plotted. In the third row the original clean signal and corrupted signal after conditioning are plotted. Plots refer to the first ECG from dataset 1.

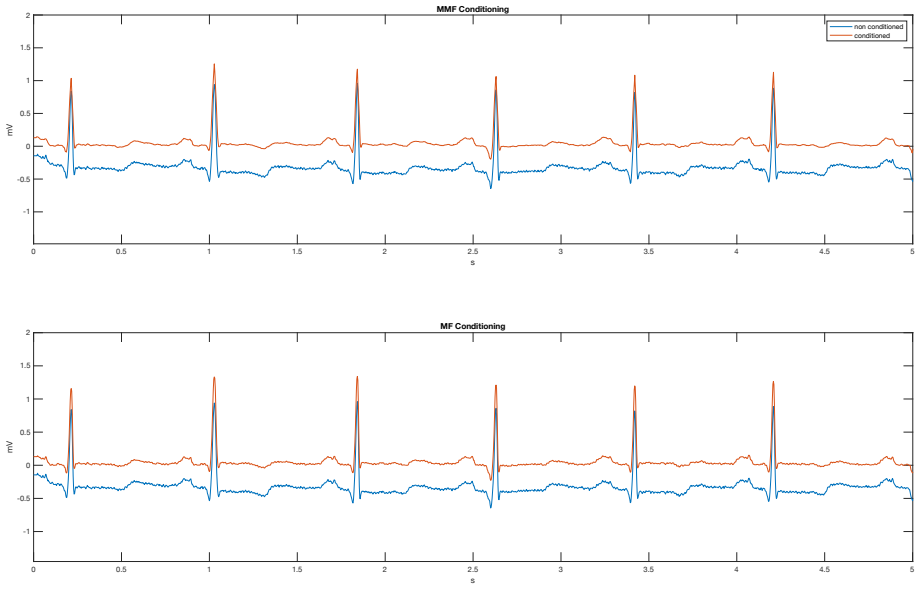


Figure 3: Corrupted ECG and conditioned one are plotted. Plots refer to the first ECG from MIT-BIH Arrhythmia Database.

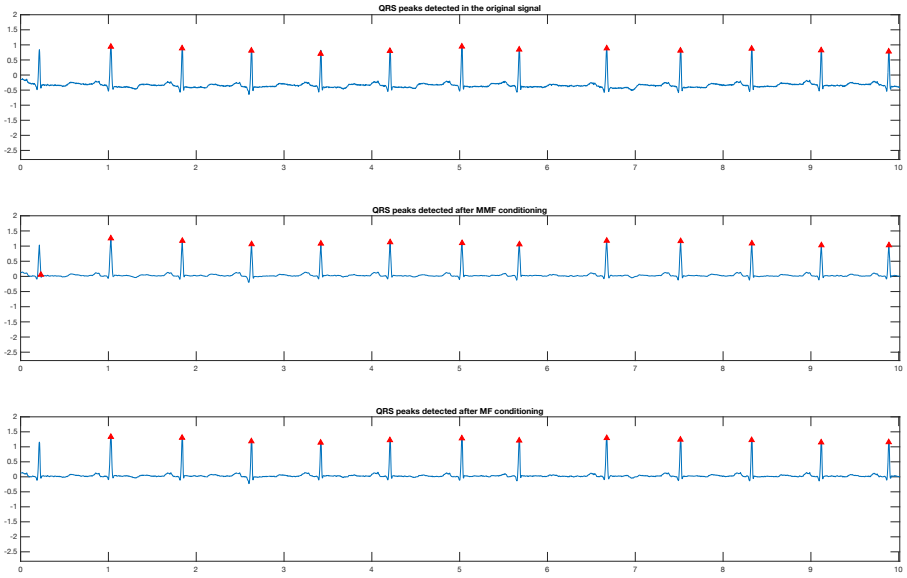
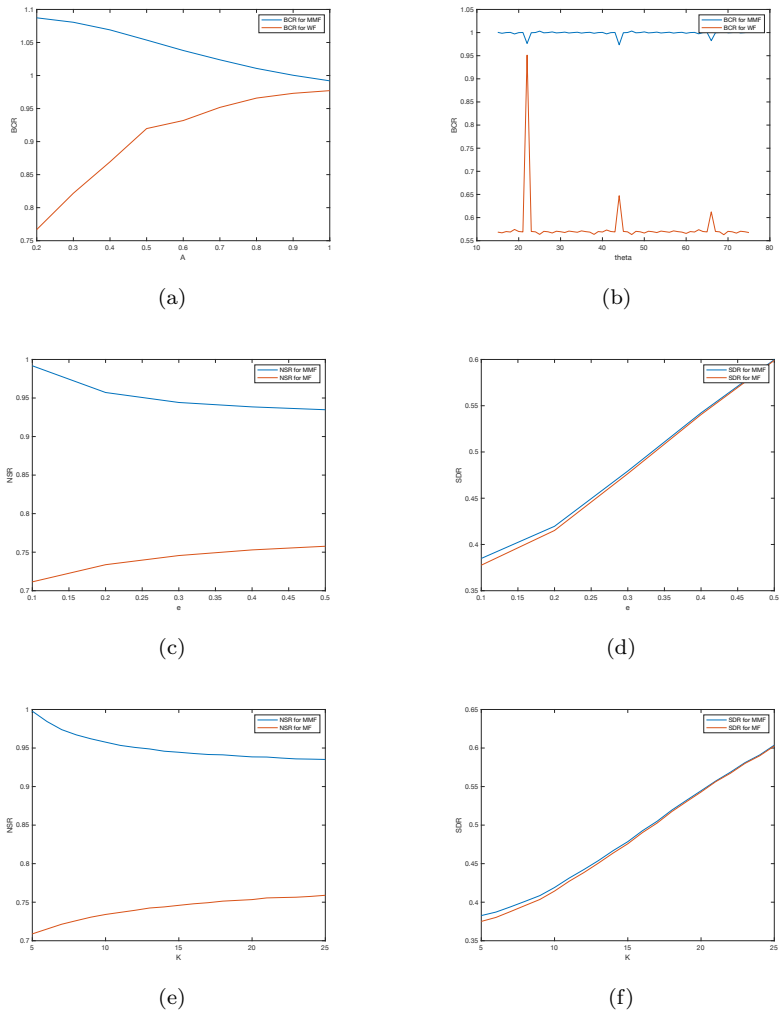


Figure 4: Detected QRS complexes and the respective signal from which are detected. Plots refer to the first ECG from MIT-BIH Arrhythmia Database.



(a) (b) (c) (d) (e) (f)

Figure 5: (a) BCR evaluated for $\theta = 0$ and A varying. (b) BCR evaluated $A = 0$ and θ varying. (c) and (d) NSR and SDR evaluated for $K = 10$ and ϵ varying. (e) and (f) NSR and SDR evaluated for $\epsilon = 0.2$ and K varying. Results refer to the first dataset. All the metrics have been evaluated singularly for each ECG in the dataset in the defined range of parameters, then averaged along the ECGs. Metrics computed for dataset 1

References

[1] Yan Sun, Kap Chan, and Shankar Krishnan. Ecg signal conditioning by morphological filters. *Computers in biology and medicine*, 32:465–79, 12 2002.

[2] C.-H.H. Chu and E.J. Delp. Impulsive noise suppression and background normalization of electrocardiogram signals using morphological operators. *IEEE Transactions on Biomedical Engineering*, 36(2):262–273, 1989.

[3] Wei-Wen Dai, Zhen Yang, Soon Lee Lim, O. Mikhailova, and J. Chee. Processing and analysis of ecg signal using nonorthogonal wavelet transform. In *Proceedings of the 20th Annual International Conference of the IEEE Engineering in Medicine and Biology Society. Vol.20 Biomedical Engineering Towards the Year 2000 and Beyond (Cat. No.98CH36286)*, pages 139–142 vol.1, 1998.

[4] P.E. Trahanias. An approach to qrs complex detection using mathematical morphology. *IEEE Transactions on Biomedical Engineering*, 40(2):201–205, 1993.

[5] Xuanyu Lu, Maolin Pan, and Yang Yu. Qrs detection based on improved adaptive threshold. *Journal of Healthcare Engineering*, 2018:1–8, 03 2018.