

# **DETERMINATION OF R-PEAK OF ECG SIGNAL AND HEART RATE USING EMPIRICAL MODE DECOMPOSITION**

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This Report Presented in Partial Fulfilment of the Requirements for  
the Degree of Bachelor of Science in Electronics and Telecommunication  
Engineering.

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## **APPROVAL**

This Project titled “DETERMINATION OF R-PEAK OF ECG SIGNAL AND HEART RATE USING EMPIRICAL MODE DECOMPOSITION”, submitted by Md. Shoaib Farhan, Md. Kamal Hossen and Ashker Ibnea Shaikh to the Department of Electronics and Telecommunication Engineering, Daffodil International University, has been accepted as satisfactory for the partial fulfilment of the requirements for the degree of B.Sc. in Electronics and Telecommunication Engineering and approved as to its style and contents. The presentation has been held on 12<sup>th</sup> December, 2010.

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## **DECLARATION**

We hereby declare that, this project has been done by us under the supervision of **Tahsina Farah Sanam, Lecturer, and Department of ETE** Daffodil International University. We also declare that neither this project nor any part of this project has been submitted elsewhere for award of any degree or diploma.

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## Abstract

The project has been inspired by the need to find an efficient method for ECG Signal Analysis which is simple and has good accuracy and less computation time. The initial task for efficient analysis is the removal of noise. It actually involves the extraction of the required cardiac components by rejecting the background noise. Enhancement of signal is achieved by the use of Modified Morphological Filtering method. The second task is that of boundary detection which is achieved by the use of Empirical Mode Decomposition (EMD). Efficiency of the method is measured in terms of detection error rate. Then We determined the R-peak by summing 1<sup>st</sup> three IMF from EMD operation and later compute the heart rate. The simulation is done in MATLAB environment. The experiments are carried out on MIT-BIH database. The results show that our proposed method is very effective and an efficient method for fast computation of R peak detection.

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## Summary of Thesis

The report is organized into the following chapters:

**Chapter 1** gives an introduction regarding the project and the various methods used in ECG signal analysis and our proposed method.

**Chapter 2** is dedicated to description of ECG signal and the other biomedical aspects.

**Chapter 3** describes the process of enhancement of ECG signal by the use of modifies morphological filtering method.

**Chapter 4** describes R peak detection using empirical mode decomposition, EMD method have been covered in the initial sections of this chapter to give an insight into different approaches for R peak detection.

**Chapter 5** is dedicated to the data analysis and result and comparison.

**Chapter 6** gives a conclusion and lays out some ideas for future work.

## **Chapter 1**

### **Introduction**

#### **1.1 Background**

Electrocardiogram (ECG) is a nearly periodic signal that reflects the activity of the heart. A lot of information on the normal and pathological physiology of heart can be obtained from ECG. However, the ECG signals being non-stationary in nature, it is very difficult to visually analyze them. Thus the need is there for computer based methods for ECG signal Analysis.

A lot of work has been done in the field of ECG signal Analysis using various approaches and methods. The basic principle of all the methods however involves transformation of ECG signal using different transformation techniques including Fourier Transform, Hilbert Transform, Wavelet transform etc. Physiological signals like ECG are considered to be quasi-periodic in nature. They are of finite duration and non stationary. Hence, a technique like Fourier series (based on sinusoids of infinite duration) is inefficient for ECG. On the other hand, EMD, which is a very recent addition in this field of research, provides a powerful tool for extracting information from such signals. The determination of QRS complex duration and heart rate is an essential task in automated ECG analysis. QRS complex duration is an important marker of different kinds of heart diseases. Normal limit for time duration of QRS complex is 0.08-0.12 sec. QRS complex time duration greater than 0.12 sec results from different heart diseases. To diagnose these diseases, QRS complex duration is a very important marker. Many algorithms have been used for automated detection of the reference points of the ECG characteristics waves; for example, algorithms from the field of artificial neural networks (Y. H. Hu and Afonso, 1993), genetic algorithms (R. Poli and Valli, 1995), wavelet transforms (M. Bahoura and Hubin, 1997), filter banks (V. X. Afonso and Luo, 1999) as well as heuristic methods mostly based on nonlinear transforms (Suppappola and Sun, 1994). Most of these techniques are filtering or adaptive threshold based, which has many limitations in real time application. The main problems of filtering based approach are that frequency variations in the characteristics waves often adversely affect its performance. The frequency distribution of QRS complex generally overlaps with that of the noise,

resulting in both false positive and false negative detections. The main problems of threshold techniques are their high noise sensitivity. Therefore, more sophisticated signal processing techniques are needed to facilitate the development of new detection schemes with higher detection accuracy. As Empirical Mode Decomposition (EMD) decompose the signal into different Intrinsic Mode Functions (IMFs), different characteristic waves of ECG signal can be achieved from different IMFs. The EMD is a powerful tool for analysing nonlinear and non-stationary data. The aim of EMD is to decompose the signal into a sum of Intrinsic Mode Functions (IMFs). An IMF represents the oscillatory mode embedded in the data. The reason behind using the EMD lies in the fact that lower order IMFs capture fast oscillation modes while higher order IMFs typically represent slow oscillation modes. The lower order IMFs of ECG can be used to distinguish the QRS complex in the ECG signal from high P or T waves, noise, and baseline drift. A smooth ECG signal can be obtained from the higher order IMFs from which the P and T waves can be detected. The algorithm consists of two basic parts: preprocessing and detection.

## 1.2 Algorithm

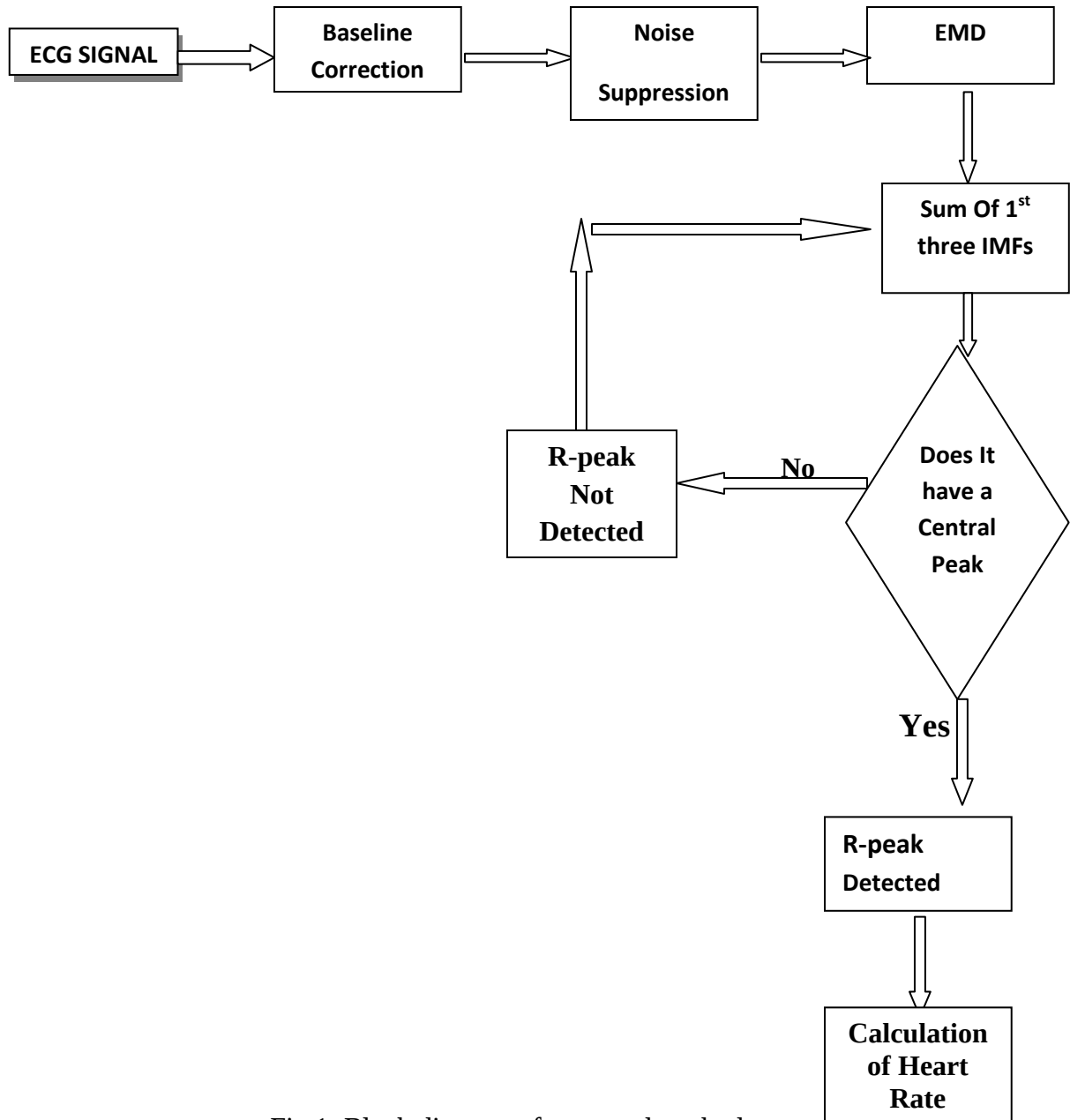


Fig 1: Block diagram of proposed method

## Chapter-2

### THEORETICAL ASPECTS OF ECG

#### 2.1 Heart

The heart, located in the mediastinum, is the central structure of the cardiovascular system. It is protected by the bony structures of the sternum anteriorly, the spinal column posteriorly, and the rib cage.

Sinoatrial (SA) node is the dominant pacemaker of the heart, located in upper portion of right atrium. It has an intrinsic rate of 60–100 bpm.

Atrioventricular(AV) node is a part of AV junction tissue. It slows conduction, creating a slight delay before impulses reach ventricles. It has an intrinsic rate of 40–60 bpm.

Table 1: Electrophysiology

| Action         | Effect                                                                                                                     |
|----------------|----------------------------------------------------------------------------------------------------------------------------|
| Depolarization | Shifting of electrolytes across the cell membrane causes change in electric charge of the cell. It results in contraction. |
| Repolarization | Internal negative charge is restored and the cells return to their resting state.                                          |

Table 2: Conduction System Structure and Functions

| Structure                  | Function and Location                                                                                                             |
|----------------------------|-----------------------------------------------------------------------------------------------------------------------------------|
| Sinoatrial (SA) Node       | Dominant pacemaker of the heart, located in upper portion of right atrium. Intrinsic rate 60–100 bpm.                             |
| Internodal Pathways        | Direct electrical impulses between SA and AV nodes.                                                                               |
| Atrioventricular (AV) node | Part of AV junction tissue. Slows conduction, creating a slight delay before impulses reach ventricles. Intrinsic rate 40–60 bpm. |
| Bundle of His              | Transmits impulses to bundle branches. Located below AV node.                                                                     |
| Left bundle Branch         | Conducts impulses that lead to left ventricle.                                                                                    |
| Right bundle Branch        | Conducts impulses that lead to right ventricle.                                                                                   |
| Purkinje system            | Network of fibers that spreads impulses rapidly throughout ventricular walls. Located at terminals of bundle branches.            |

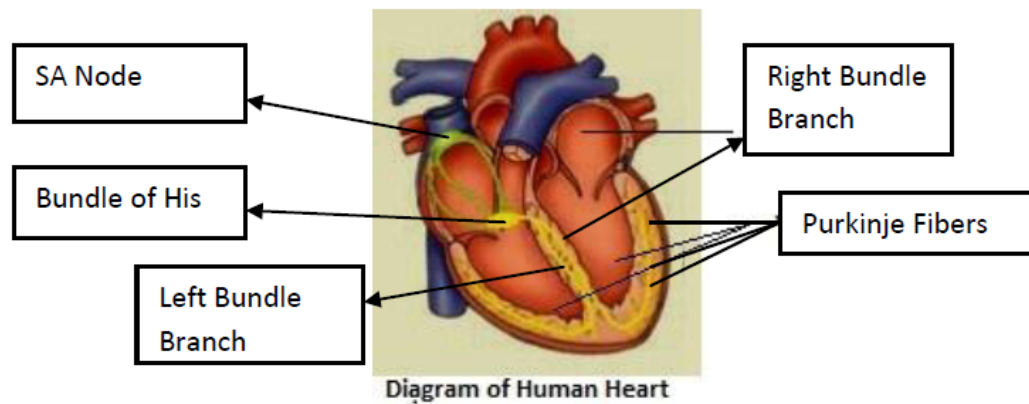


Fig.2 Conduction System structure

## The Heart: Phases

There are two phases of the cardiac cycle.

**Systole:** The ventricles are full of blood and begin to contract. The mitral and tricuspid valves close (between atria and ventricles). Blood is ejected through the pulmonic and aortic valves.

**Diastole:** Blood flows into the atria and through the open mitral and tricuspid valves into the ventricles.

## 2.2 Electrocardiogram (ECG)

An ECG is a series of waves and deflections recording the heart's electrical activity from a certain "view". Many views, each called a lead, monitor voltage changes between electrodes placed in different positions on the body.

Each cardiac cell is surrounded by and filled with solutions of Sodium ( $\text{Na}^+$ ), Potassium ( $\text{K}^+$ ), and Calcium ( $\text{Ca}^{++}$ ). The interior of the cell membrane is considered to be negative with respect to outside during resting conditions. When

an electric impulse is generated in the heart, the interior part becomes positive with respect to the exterior. This change of polarity is called depolarization. After depolarization the cell comes back to its original state. This phenomenon is called repolarization. The ECG records the electrical signal of the heart as the muscle cells depolarize (contract) and repolarize.

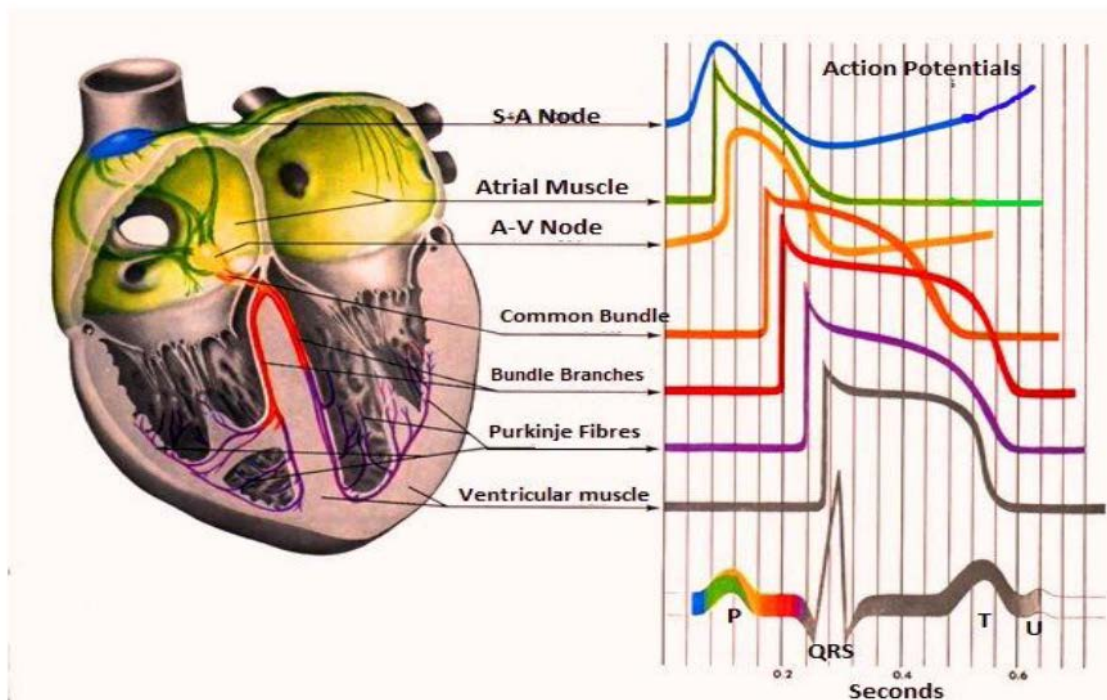


Fig.3The various views of ECG

A normal ECG signal is shown in Fig.4.

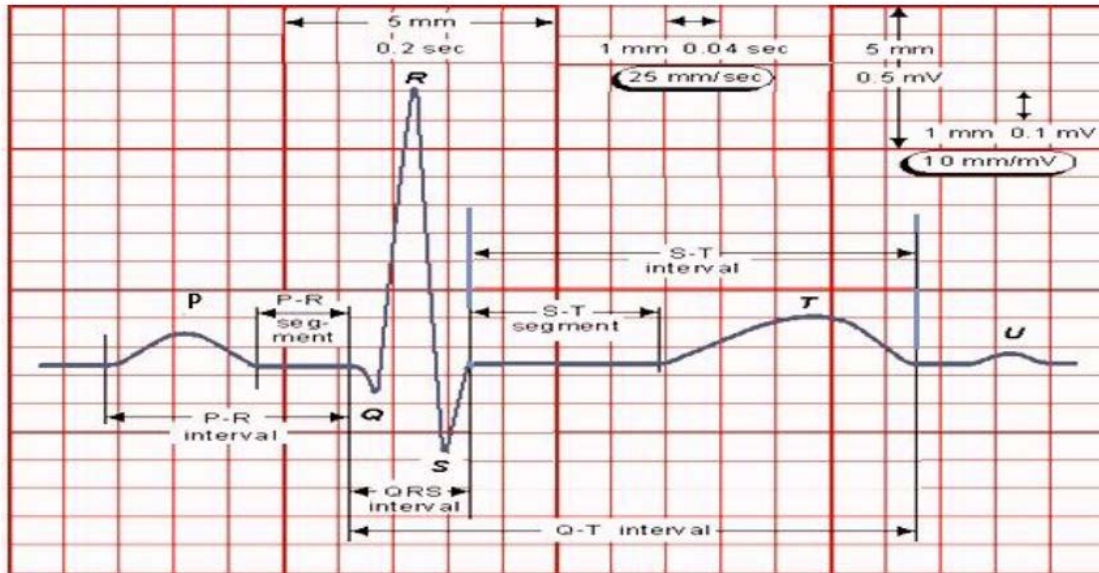


Fig.4. Normal ECG Signal and its various components

The impulses of the heart are recorded as waves called P-QRS-T deflections.

The following is the description and significance of each deflection and segment.

**P wave** indicates atrial depolarization (and contraction).

**PR Interval** measures time during which a depolarization wave travels from the atria to the ventricles.

**QRS Interval** includes three deflections following P wave which indicates ventricular depolarization (and contraction). Q wave is the first negative deflection while R wave is the first positive deflection. S wave indicates the first negative deflection after R wave.

**ST Segment** measures the time between ventricular depolarization and beginning of repolarization.

**T wave** represents ventricular repolarization.

**QT Interval** represents total ventricular activity.

### 2.3 Typical Parameter Values

Table 3: Typical amplitude of ECG characteristic waves

| Characteristic Waves | Amplitude (mV) |
|----------------------|----------------|
| P wave (%)           | 0.25           |
| R wave (%)           | 1.60           |
| Q wave (%)           | 25% of R wave  |
| T wave (%)           | 0.1 to 0.5     |

Table 4: Typical duration of ECG characteristic waves

| Intervals           | Duration (sec) |
|---------------------|----------------|
| P-R interval (%)    | 0.12 to 0.20   |
| Q-T interval (%)    | 0.35 to 0.44   |
| S-T interval (%)    | 0.05 to 0.15   |
| P wave interval (%) | 0.11           |
| QRS interval (%)    | 0.09           |

## 2.4 Arrhythmia

Normally, the SA Node generates the initial electrical impulse and begins the cascade of events that result in a heart-beat. For a normal healthy person the ECG comes off as a nearly periodic signal with depolarization followed by repolarization at equal intervals. However, sometimes this rhythm becomes irregular.

**Cardiac arrhythmia** (also **dysrhythmia**) is a term for any of a large and heterogeneous group of conditions in which there is abnormal electrical activity in the heart. The heart beat may be too fast or too slow, and may be regular or irregular.

Arrhythmia comes in varieties. It may be described as a flutter in chest or sometimes “racing heart”. The diagnosis of Arrhythmia requires Electrocardiogram. By studying ECG, Doctors can diagnose the disease and prescribe the required medications

## **Chapter-3**

### **Signal Pre-processing**

ECG provides information regarding the state of heart i.e. it gives us useful data regarding diseases. Thus ECG analysis is an important method for monitoring patients. However, the efficiency of diagnosis relies heavily upon accurate analysis of the signal. But the ECG signal that we obtain for analysis is not free from noise. The most important job for a coder is to denoise the ECG i.e. to extract the valid cardiac components and reject the rest of the background noise.

Transmission of ECG often results in the corruption of signal due to introduction of noise. Various factors responsible for introduction of noise include poor channel conditions, Baseline wander (caused by respiration), 50 or 60 Hz power line interference, motion artifact from the electrode–skin interface, muscle activities etc. Analyzing such a noisy signal is bound to give erroneous results. In addition, baseline drift caused by the respiration, radio frequency surgical noise and motion of the subject degrades ECG signals significantly. Therefore, signal conditioning for baseline correction and noise suppression is typically the first step in the analysis of ECG signals. The objective of ECG signal conditioning is to produce an output that can facilitate the subsequent processing, such as ECG episode characterization for life-threatening arrhythmia recognition, or the characteristic wave detection for non-life-threatening ECG signals. It is important to minimize the distortion of the ECG signal caused by signal conditioning algorithms so that analysis on the conditioned signal can be performed to give reliable results.

#### **3.1 Morphological Operation**

Conventionally used techniques for noise suppression are often based on band-pass filtering. However, band-pass type of linear filtering techniques has a fixed cut-off frequency which distorts the ST segment as well as the QRS complex significantly. It is also not adaptive and hence cannot track the changing characteristics of the time-varying

ECG signals, which tend to vary quasi periodically, with each period corresponding to one heart beat. Recently, adaptive filtering techniques have been developed for the purpose of noise suppression in ECG signals. Most adaptive noise-removal methods are based on the least mean squares principle or on the recursive least squares principle. They gradually reduce the mean squared error between the input signal and some reference signal. However, in some cases, these techniques experience the difficulty of not being able to obtain a suitable reference signal, which limits the wide application of this kind of approach. Wavelet transform, being a very promising technique for joint time–frequency analysis, provides an interesting solution to ECG signal conditioning .By decomposing signals into transform domains, a number of coefficients at different scales can be obtained. By selecting suitable scales and disregarding the coefficients below predefined thresholds, additive noise and baseline drift can be separated from the ECG signal components. However, in this kind of techniques, the scales and the thresholds for the non-stationary baseline correction and noise suppression cannot be selected adaptively.

Morphological operators have been widely used in the signal- and image-processing fields because of their robust and adaptive performance in extracting the shape information in addition to their simple and quick sets computation. Chu and Help used the combined opening and closing operators for baseline correction and noise suppression of ECG signals and good filtering performance was obtained. However, their morphological filtering (MF) algorithm distorts the characteristic points in ECG signal. This makes it difficult for the subsequent processing to reliably detect the significant ECG components or intervals. In this paper, a modified morphological filtering (MMF) algorithm is proposed for baseline correction and noise suppression of ECG signals. For baseline correction, the same operators are used in the MF algorithm and the MMF algorithm. For

noise suppression, modified morphological operators are used in the MMF algorithm. Better signal conditioning performance has been obtained.

Mathematical morphology (MM), which is based on sets operations, provides an approach to the development of non-linear signal processing methods, in which the shape information of a signal is incorporated. In MM operations, the result of a set transformed

by another set depends on the shapes of the two sets involved. The shape information of a signal can be extracted by using a structuring element to operate on the signal. A specific structuring element has to be designed depending on the shape characteristics of the signal that is to be extracted.

There are two basic morphological operators: erosion and dilation. Opening and closing are derived operators defined in terms of erosion and dilation. These operators are described in detail below with corresponding mathematical expressions. Here  $f(n); \{n = 0; 1; \dots; N - 1\}$ , denotes a discrete signal consisting,  $N$  points, and  $B(m); \{m = 0; 1; \dots; M - 1\}$ , is a symmetric structuring element of  $M$  points:

**Erosion:**

$$(f \ominus B)(n) = \min_{m=0, \dots, M-1} \left\{ f \left( n - \frac{M-1}{2} + m \right) - B(m) \right\}$$

$$\text{for } n = \left\{ \frac{M-1}{2}, \dots, N - \frac{M+1}{2} \right\}.$$

**Dilation :**

$$(f \oplus B)(n) = \max_{m=0, \dots, M-1} \left\{ f \left( n - \frac{M-1}{2} + m \right) + B(m) \right\}$$

$$\text{for } n = \left\{ \frac{M-1}{2}, \dots, N - \frac{M+1}{2} \right\}.$$

**Opening:**

$$A \circ B = (A \ominus B) \oplus B$$

Opening generally smoothes the contour of an object breaks narrow isthmuses, and eliminates thin protrusions.

**Closing:**

$$A \bullet B = (A \oplus B) \ominus B$$

Closing tends to smooth sections of contours, but fuses narrow breaks and long thin gulfs, eliminates small holes, and fills gaps in the contour.

The opening of a data sequence can be interpreted as sliding a structuring element along the data sequence from beneath and the result is the highest points reached by any part of the structuring element. Similarly, the closing of a data sequence can be interpreted as sliding a ‘Nipped-over’ version of the structuring element along the data sequence from above and the result is the set of lowest points reached by any part of the structuring element. In most applications, opening is used to suppress peaks, while closing is used to suppress pits.

### 3.2 MMF algorithm for ECG signal Preprocessing

The proposed MMF algorithm, viz., the MF algorithm with modified opening and closing operators, for baseline correction and noise suppression in the conditioning of the ECG signal, is shown in Fig.4. ECG signal is conditioned through a sequence of opening and closing operations. Based on the different characteristics of the baseline drift and the noise contamination in the ECG signals

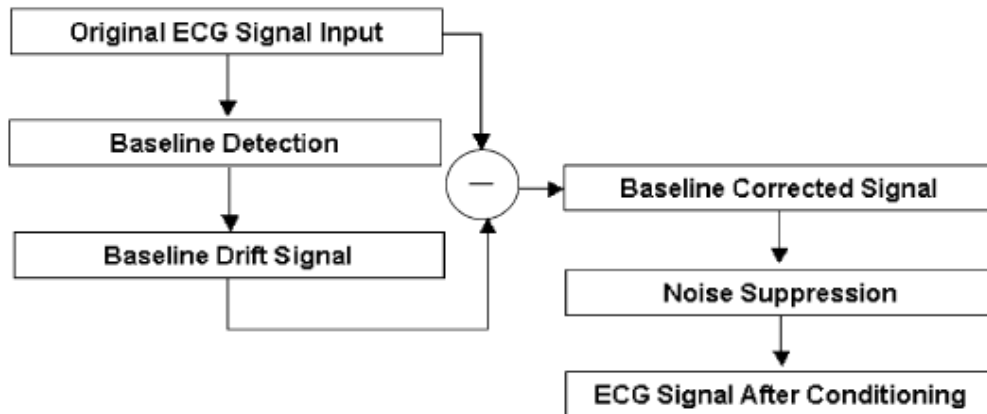


Fig 5. Block diagrams for MMF ECG signal conditioning algorithm.

Different structuring elements and different morphological operators are used. For baseline correction, an opening operator followed by a closing operator is defined; for noise suppression, modified opening and closing operators are used. They are described in detail in the following subsections.

### 3.2.1 Baseline correction

The correction of baseline is performed by removing the drift in background from the original ECG signal. It follows Chu's method. This is given below-

$$f_b = f_o \circ B_o \bullet B_c$$

The signal is first opened by a structuring element  $B_o$  for removing peaks in the signal. Then the resultant waveforms with pits are removed by a closing operation using the other structuring element  $B_c$ .  $B_o$  and  $B_c$  are selected as two horizontal line segments of zero amplitude, but with different lengths. The final result is then an estimate of the baseline drift  $f_b$ . The correction of the baseline is then done by subtracting  $f_b$  from the original signal  $f_o$ . The reasons for using different lengths in  $B_c$  and  $B_o$  are as follows. The baseline drift signal is estimated by removing the ECG signal from the test signal. Hence, the construction of the structuring element for baseline correction depends on the duration (or width) of the characteristic wave and the sample frequency ( $F_s$ Hz) of the ECG signal. If the width of a characteristic wave is  $T_w$  (s), the number of samples of the wave is  $T_w F_s$ . In order to extract the characteristic wave, the structuring element  $B_o$  should have a length larger than  $T_w F_s$ . Since the subsequent closing operation is used to remove the pit left by the opening operation, the length of the structuring element  $B_c$  must be longer than the length of  $B_o$ . The width of the characteristic wave in the ECG signal, such as the P wave, the T wave, and the QRS complex, is generally less than 0.2 s. Hence,  $L_o$ , the length of  $B_o$ , is selected as  $0.2 F_s$ , and  $L_c$ , the length of  $B_c$ , is typically selected to be longer than  $B_o$ , at about  $1.5 L_o$ .

### 3.2.2 Noise suppression

After baseline correction, noise suppression is performed by processing the data through an opening and a closing operation concurrently, and then the results are averaged. In this study, the opening and closing operations for noise suppression use a structuring element pair,  $B_{pair}$ , not a single structuring element as in Chu's MF algorithm.  $B_{pair}$  is defined as  $B_{pair} = \{B_1; B_2\}$ , where  $B_1 \neq B_2$ , i.e., different in shape but the same in length. The

sequence of B1 and B2 corresponds to the order of dilation and erosion in the opening and closing operations. The process of signal conditioning is described by the following equation:

$$\begin{aligned} f &= \frac{1}{2}(f_{bc} \bullet B_{\text{pair}} + f_{bc} \circ B_{\text{pair}}) \\ &= \frac{1}{2}(f_{bc} \oplus B_1 \ominus B_2 + f_{bc} \ominus B_1 \oplus B_2), \end{aligned}$$

where  $f$  is the resultant signal after noise suppression, and  $f_{bc}$  is the signal after baseline correction. The  $B_{\text{pair}}$  is selected by considering the purpose of analysis and the morphological properties of the ECG signal.  $B_1$  is selected to be a triangular shape and  $B_2$  is a line segment. A triangular structuring element is used to retain the peaks and valleys of the characteristic waves, such as the QRS complex, the P and T waves, while a short line segment structuring element is used for removing noise in the ECG signal. In order to minimize the distortion to the ECG signal, the length of  $B_1$  is selected to be the same as that of the  $B_2$ . Since the processing is discrete; the selection of the structuring element length is related to the bandwidth of ECG signal, and the sampling rate. Given that the sampling frequency is fixed, a shorter structuring element can be used to reduce the distortion of the waveform. Based on the sample frequency  $F_s$ , the lengths of  $B_1$  and  $B_2$  are selected as 5 sample units each, with values of  $B_1 = (0, 1, 5, 1, 0)$ ;  $B_2 = (0, 0, 0, 0, 0)$ . Using the proposed structuring element pair, noise can be suppressed while reducing the smoothing of the significant peaks and valleys in the ECG signal, which are essential characteristic singularities for the subsequent reliable detection of the characteristic waves.

### 3.3 Results

#### Example: 1

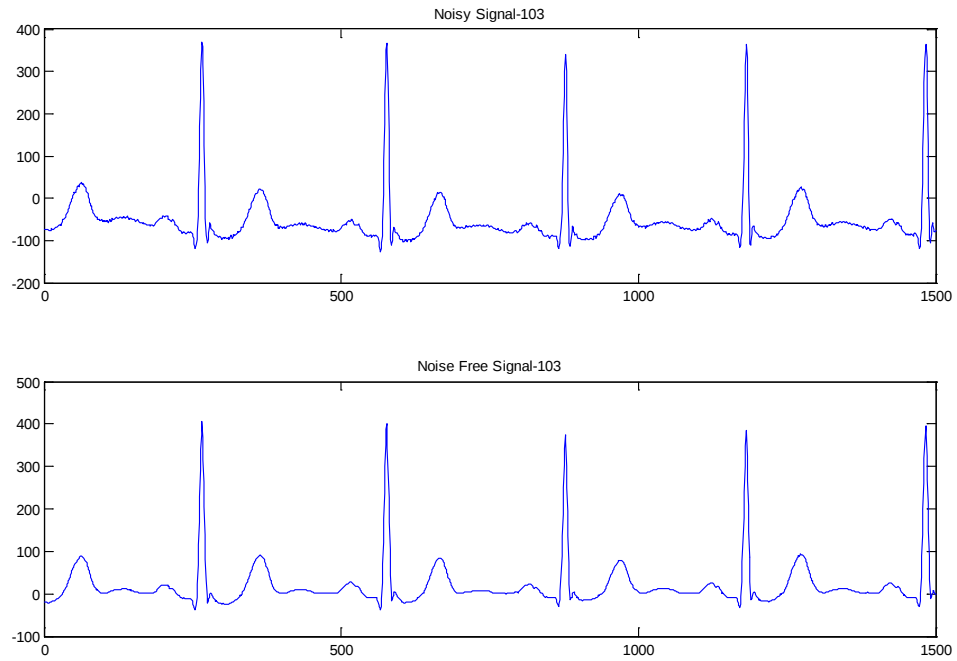


Fig 6: Noisy & noise free ECG signal (Record No.103)

### Example: 2

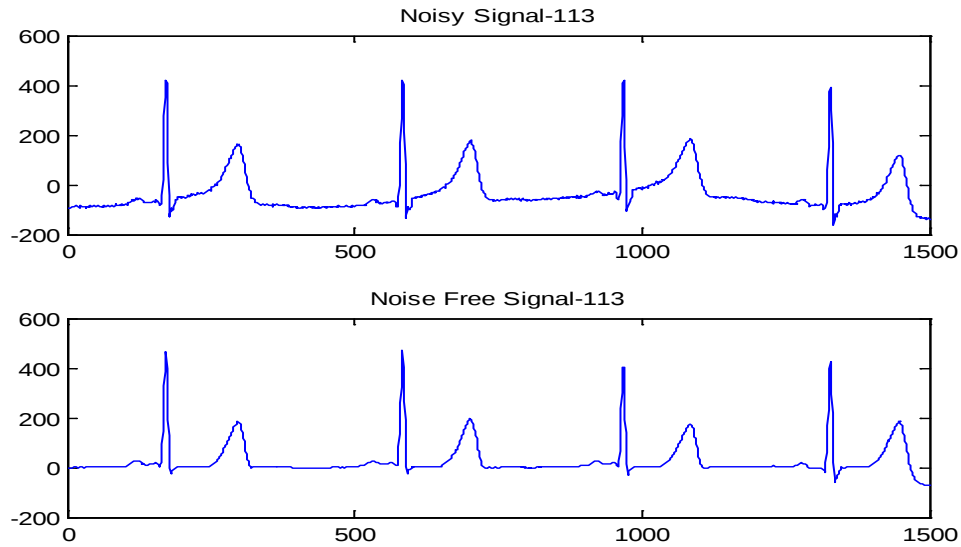


Fig 7: Noisy & Noise free ECG signal (Record No.113)

### **3.4 Conclusion**

In conclusion, a morphological filtering algorithm using modified morphological operators, called the MMF, is proposed for baseline correction and noise suppression in ECG signals. By using a structuring element pair in closing and opening operations, signal distortion rate in ECG signal can be decreased by sacrificing the noise suppression rate a little and the corresponding computational burden is lessened. The MMF algorithm can retain the significant characteristic waves and intervals in the ECG signal, which is more important for subsequent processing, such as the ECG characteristic wave or interval detection, or arrhythmia recognition. The performance of the proposed algorithm for signal conditioning was evaluated by using simulated signals and clinically acquired ECG data from a standard set. Results were compared with those obtained by other ECG conditioning techniques. In addition, a comparison of the QRS complexes detecting from the original signal, from the signal after conditioning using Chu's morphological filtering algorithm as well as using the proposed MMF algorithm, was performed. The results show that the proposed MMF algorithm is more suitable for the conditioning of the ECG signal, in view of the subsequent processing.

## Chapter-4

### R-Peak Detection Using EMD

#### 4.1 Empirical Mode Decomposition

A new non-linear technique, called Empirical Mode Decomposition method, has recently been developed by N.E.Huang *et al* for adaptively representing non-stationary signals as sums of zero mean AM-FM components. EMD is an adaptive, high efficient decomposition with which any complicated signal can be decomposed into a finite number of Intrinsic Mode functions (IMFs). The IMFs represent the oscillatory modes embedded in the signal, hence the name Intrinsic Mode Function. These IMFs are based on and derived from the data and can serve as basis of an expansion that can be linear or non-linear as dictated by the data.

The starting point of EMD is to consider oscillations in signals at a very local level. It is applicable to non-linear and non-stationary signal such as ECG signal.

#### 4.2 Intrinsic Mode Functions

An intrinsic mode function (IMF) is a function that satisfies two conditions:

- (1) In the whole data set, the number of extrema and the number of zero crossings must either equal or differ at most by one;
- (2) At any point, the mean value of the envelope defined by the local maxima and the envelope defined by the local minima is zero.

The first condition is obvious; it is similar to the traditional narrow band requirements for a stationary Gaussian process. The second condition is a new idea; it modifies the classical global requirement to a local one; it is necessary so that the instantaneous frequency will not have the unwanted fluctuations induced by asymmetric wave forms. Ideally, the requirement should be 'the local mean of the data being zero'. For non-stationary data, the 'local mean' involves a 'local time scale' to compute the mean, which

is impossible to define. As a surrogate, we use the local mean of the envelopes defined by the local maxima and the local minima to force the local symmetry instead. This is a necessary approximation to avoid the definition of a local averaging time scale. Although it will introduce an alias in the instantaneous frequency for nonlinearly deformed waves, the effects of nonlinearity are much weaker in comparison with non-stationary. With the physical approach and the approximation adopted here, the method does not always guarantee a perfect instantaneous frequency under all conditions. Nevertheless, even under the worst conditions, the instantaneous frequency so defined is still consistent with the physics of the system studied.

The name 'intrinsic mode function' is adopted because it represents the oscillation mode imbedded in the data. With this definition, the IMF in each cycle, defined by the zero crossings, involves only one mode of oscillation, no complex riding waves are allowed. With this definition, an IMF is not restricted to a narrow band signal, and it can be both amplitude and frequency modulated. In fact, it can be non-stationary. As discussed above, purely frequency or amplitude modulated functions can be IMFs even though they have finite bandwidth according to the traditional definition.

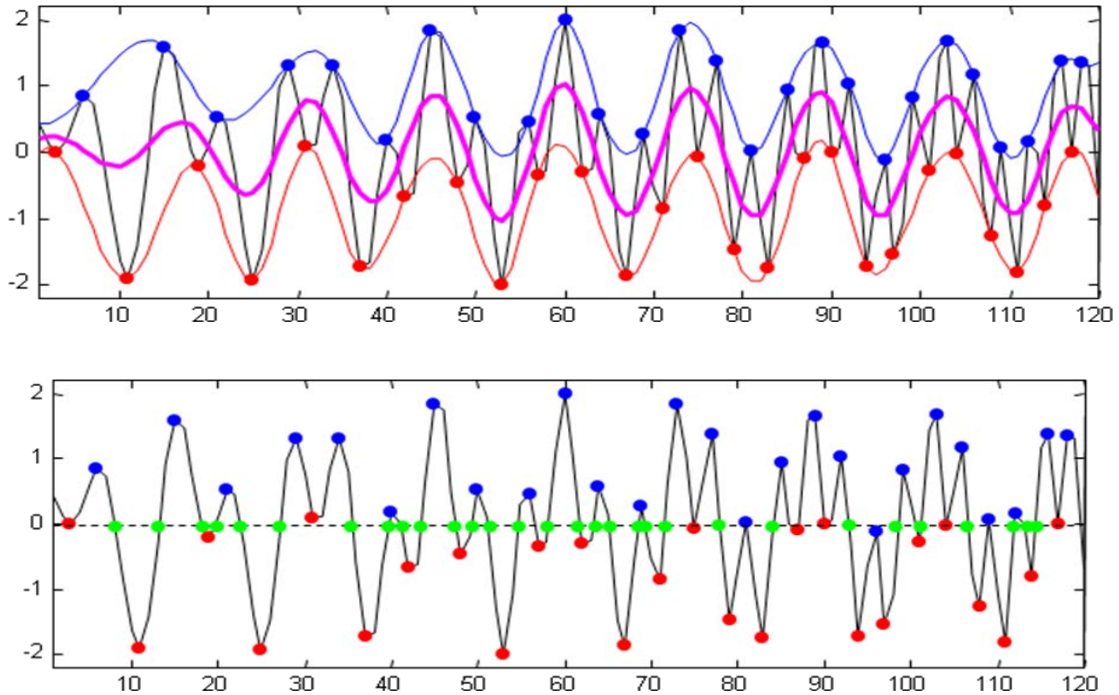


Fig 8: Example of Intrinsic Mode Function (IMF)

### 4.3 EMD: Shifting Process

Some of the assumptions made for decomposition are:

- (1) The signal has at least two extrema: one maximum and one minimum
- (2) The characteristic time scale is defined by the time lapse between the extrema.
- (3) If the signal has no extrema but has inflection points, then the signal can be differentiated one or more times to find the extrema.

The basic principle of this method is to identify the intrinsic oscillatory modes by their characteristic time scales in the data empirically and then decompose the data.

A systematic way to extract the IMFS is called the Sifting Process and is described below:

**Step1:** Calculate the upper and lower envelopes of the signal  $x(t)$  and their mean value  $m_1(t)$ .

**Step2:** Calculate  $h_1(t) = x(t) - m_1(t)$

**Step3:** Check if  $h_1(t)$  satisfies the IMF properties.

**Step4:** If not, use  $h_2(t) = h_1(t) - m_2(t)$  to obtain new  $h$ , where  $m_2(t)$  is found from  $h_1(t)$  as in step1.

**Step5:** Continue until an  $h_k(t)$  satisfies the IMF properties. When done,  $c_1(t) = h_k(t)$  is the first IMF.

**Step6:** Considering the  $r(t) = x(t) - c_1(t)$  as the new signal, continue from Step1 to get the higher IMFs, up to  $c_n(t)$ .

Process is continued until the residue becomes a monotonous function.

An example of EMD is given in the following figure:

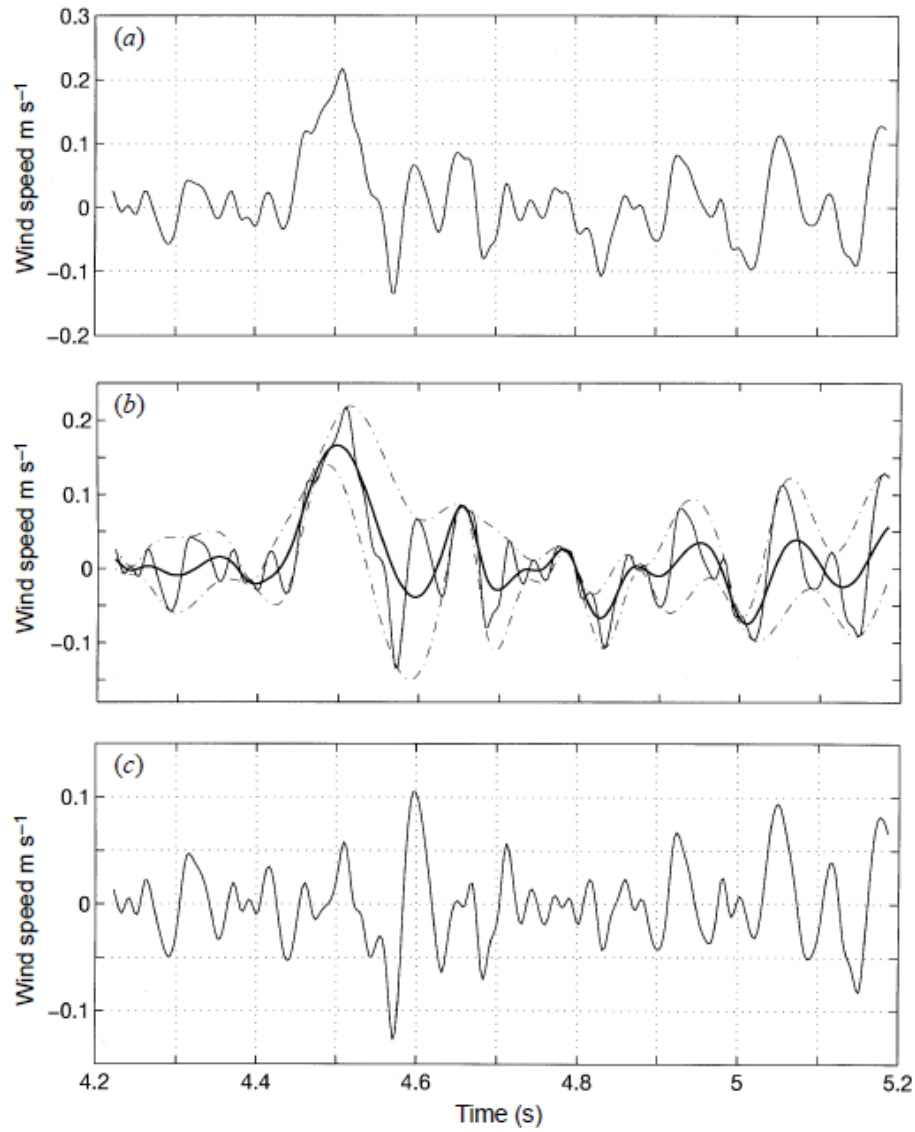


Fig 9: Illustration of the sifting processes: (a) the original data; (b) the data in thin solid line, with the upper and lower envelopes in dot-dashed lines and the mean in thick solid line; (c) the difference between the data and  $m_1$ . This is still not an IMF, for there are negative local maxima and positive minima suggesting riding waves.

#### **4.4 Benefits of EMD**

- > Does not assume a prior basis function for the decomposition and thus is fully adaptive.
- > Can separate non-stationary oscillations.
- > Does not require spurious harmonics to represent non-linear data.
- > Can give meaningful instantaneous frequency representation using Hilbert transform.

#### **4.5 Limitations of EMD**

- > EMD does not have an analytic mathematical expression, which makes its processing very difficult.
- > The definition of an IMF is not unique because it depends on the envelope estimation.
- > The sifting process is iterative, so computation of EMD is time consuming.
- > Real time implementation is still not available.

#### **4.6 R-PEAK DETECTION OF ECG SIGNAL**

ECG signal can be expressed as repetitions of P-QRS-T waves. The basic principle behind the analysis of ECG signal is finding the QRS complex. R peak detection is the 1st and foremost step in finding the QRS complex. Various methods have been implemented in the recent past for R peak detection including Fourier Transform, Hilbert Transform, Difference Operation Method, Wavelet Transform etc. We use the IMFs which is extract from the EMD described earlier.

#### 4.6.1 Decomposing ECG into IMFs

Now, the EMD is applied on  $x(t)$  and the IMFs are obtained to locate the fiducial points in the ECG signal. The EMD of  $x(t)$  is given by

$$x(t) = \sum_{i=1}^n c_i(t) + r_n(t)$$

Where  $c_i(t)$  is the  $i$ th IMF and  $r_n(t)$  is the residue.

#### 4.6.2 R peak detection

An important criterion of EMD is that the higher the order of the IMF, the lower is its frequency. For this reason, the first three IMFs contribute mainly to the QRS complex as the QRS complex is the highest frequency portion in ECG signal and the IMFs of the order above three not only contribute to the QRS complex but also to the lower frequency P and S waves. In our analysis, we have also found similar results. We denote the sum of first three IMFs as fine to coarse three,  $f2c_3(t)$  given by

$$f2c_3(t) = \sum_{i=1}^3 c_i(t)$$

The oscillations associated with QRS complex in  $f2c_3(t)$  are much larger than those due to noise. Here  $f2c_3(t)$  with  $x(t)$  for a single ECG beat. It reveals that the R-peak in the ECG signal is detected by the peak of  $f2c_3(t)$ . Therefore, the R-peak detection comprises the following steps which are also illustrated in Fig. 2 for a series of ECG beats:

- (i) Sum the first three IMFs to get  $f2c_3(t)$  and take its absolute value as  $a(t)$ .
- (ii) Retain the amplitudes of  $a(t)$  larger than a threshold,  $T$ , where  $T$  is statistically selected to be half of the maximum value of  $a(t)$  and make others zero. This eliminates the noise.
- (iii) Find the position of the maximum of a segment of time duration  $t_R$  starting from the first non zero value of  $a(t)$ .

This is the first R-peak position. Similarly, find all other R-peak positions until the end of  $a(t)$  is reached. According to the width of QRS complex which is normally 100 ms with variation of  $\pm 20$  ms [6], we select  $t_R$  to be about 200 ms. We have considered the absolute value of  $f2c3(t)$  since R-wave, and thus  $f2c3(t)$ , give a negative peak in some ECG leads. After finding the R-peak position,  $t_o$ , we can find whether the peak is positive or negative from the value of  $f2c3(t_o)$ . If  $f2c3(t_o)$  is positive, then the R-peak is positive since the base of  $f2c3(t)$  is zero. Central maxima of each oscillatory segment represents R peaks of QRS complex.

#### 4.7 Heart Rate

The heart rate calculation R peak position is required. The Heart rate is defined as

$$\text{Heart rate} = (60 * f_s) / d_R$$

Where  $d_R$  denotes average index difference between two consecutive R peaks. The R peak location in the ECG signal is detected by the index given by the central maxima of the chosen IMF. Though for some cases the IMF central maxima fails to detect the exact R-peak location but this does not effect the heart rate calculation as the index difference remains the same.

## CHAPTER 5

### Data Analysis and Results

#### 5.1 Data Analysis

The proposed EMD based algorithm for the detection of characteristic wave boundaries in ECG signal was tested using the MIT-BIH arrhythmia database. The records were taken from existing ECG databases, including the MIT-BIH Arrhythmia Database, the MIT-BIH ST Change Database, the MIT-BIH Supraventricular Arrhythmia Database, the MIT-BIH Normal Sinus Rhythm Database, the MIT-BIH Long-Term ECG Database, the European Society of Cardiology ST-T Database, and from “sudden death” patients from BIH. The MIT-BIH arrhythmia database contains 48 two-channel records (each 30 minutes long) with a sampling frequency of 360 Hz.

More than 10000 normal ECG beats randomly selected from the MIT-BIH arrhythmia database were used to test the performance of the new algorithm for the detection of ECG wave boundaries.

To reduce the processing time required by EMD, we put a limit on the maximum number of iterations in the EMD MATLAB routine (for an example, 400 for a 10 s ECG signal).

For each input ECG signal, the following procedures were performed: (i) signal preprocessing; (ii) empirical mode decomposition of the preprocessed signal; (iii) summing the 1st three IMF for detecting R-peak ; (iv) detection of R-peak; (v) Calculating heart rate.

#### 5.2 Results on R-Peak detection

We have presented a preprocessed ECG signal in Fig. 7 and Fig.8. The signal is then decomposed into IMFs by performing EMD. The 1<sup>st</sup> three IMFs are then sum and taken the absolute value. The detected R-peak is presented in Fig 10.

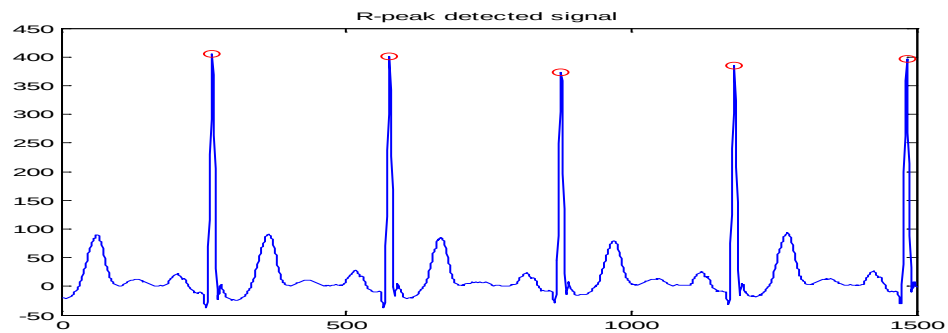


Fig 10: R-peak detected Signal (Record No.103)

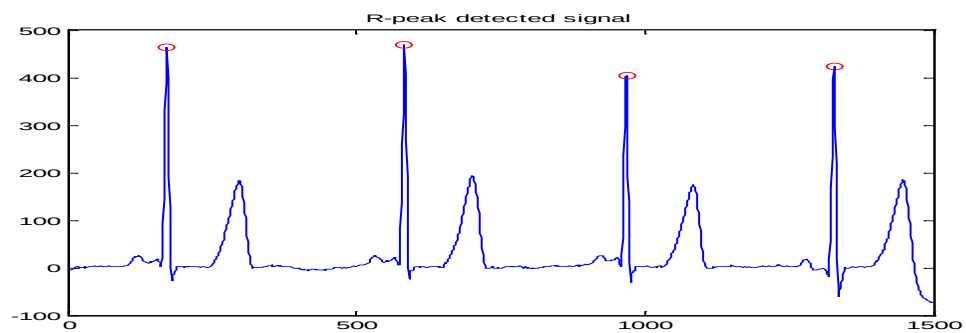


Fig 11: R-peak detected Signal (Record No.113)

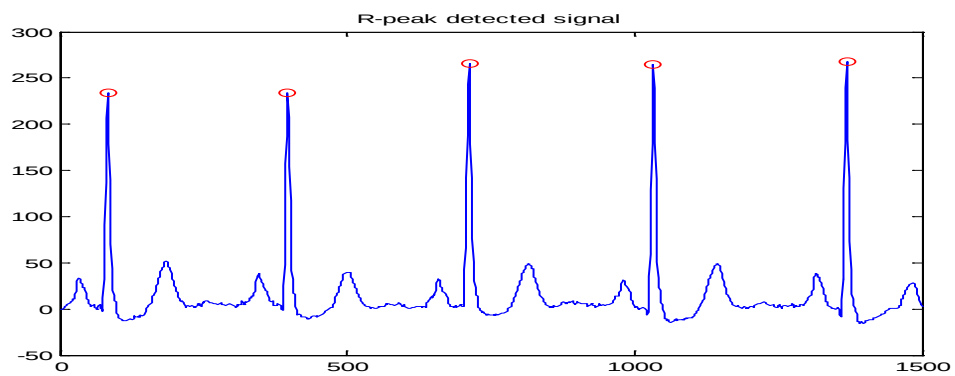


Fig 12: R-peak detected Signal (Record No.101)

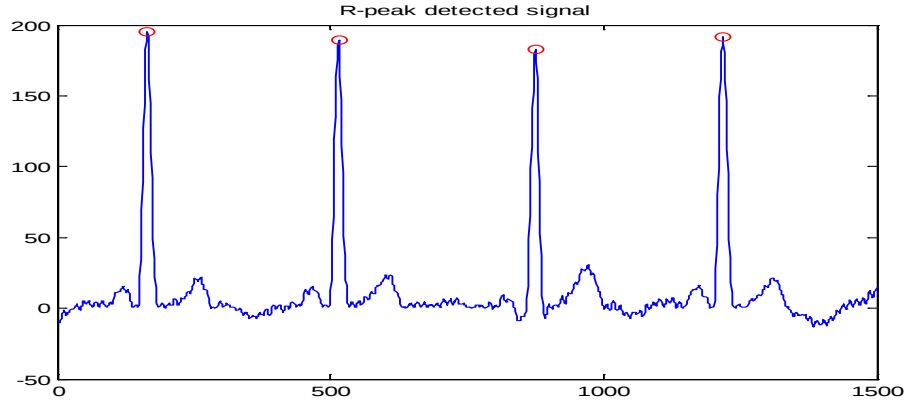


Fig 13: R-peak detected Signal (Record No.121)

Heart rate is calculated from the position of the central maxima in the chosen IMF by using . Table 5 provides R peak positions, calculated Heart rate as obtained by the proposed method.

Table 5: Determination of Heart rate

| Record No | R-peak position       | Heart rate |
|-----------|-----------------------|------------|
| 101       | 83,397,712,1033,1369  | 67.55      |
| 103       | 266,577,877,1181,1483 | 70.99      |
| 113       | 172,584,968,1328      | 56.05      |
| 121       | 165,515,875,1219      | 60.44      |

The average percent error in determining heart rate is 0.0195% which is negligible in heart rate calculation. Therefore, the proposed EMD-based algorithm is a preferred technique considering algorithm simplicity, robustness and detection accuracy.

## **CHAPTER 6**

### **CONCLUSION AND FUTURE WORK**

#### **6.1. CONCLUSION**

Our sole objective of this project was to develop a method for efficient analysis of ECG signal. In this piece of work, we have used a method of detecting R peaks of ECG signal using Empirical Mode Decomposition. Then compute the heart rate. The functionality of this EMD based algorithm was tested using the full set of MIT-BIH arrhythmia database. For 30% signals our proposed method showed better performance in terms of detection accuracy and for the rest of the signals this method showed similar performance to the MMD based technique. The EMD method works not only for lead II but also for other leads. Only three lower order IMFs are needed to completely identify the fiducially points in the ECG signal. Given these locations, features of clinical importance such as the RR interval may be measured readily.

#### **6.2. FUTURE WORK**

Empirical Mode Decomposition is very recent techniques. Hence a lot of research needs to be done on the properties so that we can come up with still simpler methods for ECG signal Analysis.

Feature extraction is yet another field in ECG signal Analysis untouched by us. But it is very important for classification of Arrhythmia. Hence our future work will be dedicated to feature extraction and classification.

The process of enhancement can be modified using more evolved techniques. Research needs to be done for finding more efficient methods for signal enhancement.

## Appendix A

### MATLAB Code

```
% ***** Automatic detection of R-peaks of ECG signal *****

% *****

% This is a program which converts the .DAT file into .MAT file..
% Here ECG .DAT files are given as input...
% 3 files are needed - 1) attribute file,
% 2) Header file and 3) .DAT file.....

clc
clear all;
close all;

PATH= 'G:\Thesis\1.3.10\datfile_diu'; % path, where data are saved

ATTRFILE= '100.atr'; % attributes-file in binary format
HEADERFILE= '100.heg'; % header-file in text format
DATAFILE= '100.dat'; % data-file
SAMPLES2READ=1500;
    % 650000; %MAX
    % number of samples to be read
    % in case of more than one signal:
    % 2*SAMPLES2READ samples are read

%----- LOAD HEADER DATA -----
fprintf(1,'\n WORKING ON %s ...\n', HEADERFILE);
signalh= fullfile(PATH, HEADERFILE);
fid1=fopen(signalh,'r');
z= fgetl(fid1);
A= sscanf(z, '%*s %d %d %d', [1,3]);
nosig= A(1); % number of signals
sfreq=A(2); % sample rate of data
clear A;
for k=1:nosig
    z= fgetl(fid1);
    A= sscanf(z, '%*s %d %d %d %d %d', [1,5]);
    dformat(k)= A(1); % format; here only 212 is allowed
    gain(k)= A(2); % number of integers per mV
    bitres(k)= A(3); % bitresolution
```

```

        zerovalue(k)= A(4);      % integer value of ECG zero point
        firstvalue(k)= A(5);    % first integer value of signal (to test for errors)
end;
fclose(fid1);
clear A;

%----- LOAD BINARY DATA -----
if dformat~= [212,212], error('this script does not apply binary formats different to 212.');
```

```

end;
signalid= fullfile(PATH, DATAFILE);      % data in format 212
fid2=fopen(signalid,'r');
A= fread(fid2, [3, SAMPLES2READ], 'uint8'); % matrix with 3 rows, each 8 bits long,
= 2*12bit
fclose(fid2);
M2H= bitshift(A(:,2), -4);
M1H= bitand(A(:,2), 15);
PRL=bitshift(bitand(A(:,2),8),9);  % sign-bit
PRR=bitshift(bitand(A(:,2),360),5); % sign-bit
M( : , 1)= bitshift(M1H,8)+ A(:,1)-PRL;
M( : , 2)= bitshift(M2H,8)+ A(:,3)-PRR;
if M(1,:) ~= firstvalue, error('inconsistency in the first bit values'); end;
switch nosig
case 2
    M( : , 1)= (M( : , 1)- zerovalue(1));%/gain(1);
    M( : , 2)= (M( : , 2)- zerovalue(2));%/gain(2);
    TIME=(0:(SAMPLES2READ-1))/sfreq ;
case 1
    M( : , 1)= (M( : , 1)- zerovalue(1));
    M( : , 2)= (M( : , 2)- zerovalue(1));
    M=M';
    M(1)=[];
    sM=size(M);
    sM=sM(2)+1;
    M(sM)=0;
    M=M';
    M=M;%/gain(1)
    TIME=(0:2*(SAMPLES2READ)-1)/sfreq;
otherwise % this case did not appear up to now!
    % here M has to be sorted!!!
    disp('Sorting algorithm for more than 2 signals not programmed yet!');
end;
clear A M1H M2H PRR PRL;
fprintf(1,'\n LOADING DATA FINISHED');
P=M(:,1);
Q=M(:,2);

```

```

save('NEW.mat');

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

Y=P';      %This is the noisy ECG signal!

%% *****Baseline Correction*****

B0 = strel('line', 72, 0);
Op = imopen(Y,B0);      %Opening Operation
Bc = strel('line', 108, 0);
Ybd = imclose(Op,Bc);   %Closing Operation
Ybc=Y-Ybd;              %Baseline Corrected ECG signal

%% *****Noise Suppression*****

B1 = strel('arbitrary', 5, 300);
B2 = strel('line', 5, 0);
I1 = imdilate(Ybc,B1);   %dilation
I2 = imerode(I1,B2);     %erosion
I3 = imerode(Ybc,B1);
I4 = imdilate(I3,B2);
Y_nfree=(I2+I4)/2;       %This is the Noise Free Signal

% Plot ECG signal and Noise free ECG Signal

Figure(1);
subplot(111),plot(Y);
subplot(112),plot(Y_nfree);

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

% EMD function

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

function [imf,ort,nbits] = emd(varargin)
[x,t,sd,sd2,tol,MODE_COMPLEX,ndirs,display_sifting,sdt,sd2t,r,imf,k,nbit,NbIt,MAXI
TERATIONS,FIXE,FIXE_H,MAXMODES,INTERP,mask] = init(varargin{:});
if display_sifting
    fig_h = figure;
end
%main loop : requires at least 3 extrema to proceed

```

```

while ~stop_EMD(r,MODE_COMPLEX,ndirs) && (k < MAXMODES+1 ||
MAXMODES == 0) && ~any(mask)
    % current mode
    m = r;
    % mode at previous iteration
    mp = m;
    %computation of mean and stopping criterion
    if FIXE
        [stop_sift,moyenne] = stop_sifting_fixe(t,m,INTERP,MODE_COMPLEX,ndirs);
    elseif FIXE_H
        stop_count = 0;
        [stop_sift,moyenne] =
stop_sifting_fixe_h(t,m,INTERP,stop_count,FIXE_H,MODE_COMPLEX,ndirs);
    else
        [stop_sift,moyenne] = stop_sifting(m,t,sd,sd2,tol,INTERP,MODE_COMPLEX,ndirs);
    end
    % in case the current mode is so small that machine precision can cause
    % spurious extrema to appear
    if (max(abs(m))) < (1e-10)*(max(abs(x)))
        if ~stop_sift
            warning('emd:warning','forced stop of EMD : too small amplitude')
        else
            disp('forced stop of EMD : too small amplitude')
        end
        break
    end
    % sifting loop
    while ~stop_sift && nbit<MAXITERATIONS
        if(~MODE_COMPLEX && nbit>MAXITERATIONS/5 &&
mod(nbit,floor(MAXITERATIONS/10))==0 && ~FIXE && nbit > 100)
            disp(['mode ',int2str(k),', iteration ',int2str(nbit)])
            if exist('s','var')
                disp(['stop parameter mean value : ',num2str(s)])
            end
            [im,iM] = extr(m);
            disp([int2str(sum(m(im) > 0)), ' minima > 0; ',int2str(sum(m(iM) < 0)), ' maxima < 0.'])
        end
        %sifting
        m = m - moyenne;
        %computation of mean and stopping criterion
        if FIXE
            [stop_sift,moyenne] = stop_sifting_fixe(t,m,INTERP,MODE_COMPLEX,ndirs);
        elseif FIXE_H
            [stop_sift,moyenne,stop_count] =
stop_sifting_fixe_h(t,m,INTERP,stop_count,FIXE_H,MODE_COMPLEX,ndirs);

```

```

else
    [stop_sift,moyenne,s]
stop_sifting(m,t,sd,sd2,tol,INTERP,MODE_COMPLEX,ndirs);
end
% display
if display_sifting && ~MODE_COMPLEX
    NBSYM = 2;
    [indmin,indmax] = extr(mp);
    [tmin,tmax,mmin,mmax] = boundary_conditions(indmin,indmax,t,mp,mp,NBSYM);
    envminp = interp1(tmin,mmin,t,INTERP);
    envmaxp = interp1(tmax,mmax,t,INTERP);
    envmoyp = (envminp+envmaxp)/2;
    if FIXE || FIXE_H
        display_emd_fixe(t,m,mp,r,envminp,envmaxp,envmoyp,nbit,k,display_sifting)
    else
        sxp=2*(abs(envmoyp))./(abs(envmaxp-envminp));
        sp = mean(sxp);
        display_emd(t,m,mp,r,envminp,envmaxp,envmoyp,s,sp,sxp,sdt,sd2t,nbit,k,display_sifting,stop_sift)
    end
end
mp = m;
nbit=nbit+1;
NbIt=NbIt+1;
if(nbit==(MAXITERATIONS-1) && ~FIXE && nbit > 100)
    if exist('s','var')
        warning('emd:warning','forced stop of sifting : too many iterations... mode ',int2str(k),'. stop parameter mean value : ',num2str(s))
    else
        warning('emd:warning','forced stop of sifting : too many iterations... mode ',int2str(k),'.')
    end
end
end % sifting loop
imf(k,:) = m;
if display_sifting
    disp(['mode ',int2str(k), ' stored'])
end
nbits(k) = nbit;
k = k+1;
r = r - m;
nbit=0;
end %main loop
if any(r) && ~any(mask)
    imf(k,:) = r;

```

```

end
ort = io(x,imf);
if display_sifting
    close
end
end
%-----
% tests if there are enough (3) extrema to continue the decomposition
function stop = stop_EMD(r,MODE_COMPLEX,ndirs)
if MODE_COMPLEX
    for k = 1:ndirs
        phi = (k-1)*pi/ndirs;
        [indmin,indmax] = extr(real(exp(i*phi)*r));
        ner(k) = length(indmin) + length(indmax);
    end
    stop = any(ner < 3);
else
    [indmin,indmax] = extr(r);
    ner = length(indmin) + length(indmax);
    stop = ner < 3;
end
end
%-----
% computes the mean of the envelopes and the mode amplitude estimate
function [envmoy,nem,nzm,amp] =
mean_and_amplitude(m,t,INTERP,MODE_COMPLEX,ndirs)
NBSYM = 2;
if MODE_COMPLEX
    switch MODE_COMPLEX
    case 1
        for k = 1:ndirs
            phi = (k-1)*pi/ndirs;
            y = real(exp(-i*phi)*m);
            [indmin,indmax,indzer] = extr(y);
            nem(k) = length(indmin)+length(indmax);
            nzm(k) = length(indzer);
            [tmin,tmax,zmin,zmax] = boundary_conditions(indmin,indmax,t,y,m,NBSYM);
            envmin(k,:) = interp1(tmin,zmin,t,INTERP);
            envmax(k,:) = interp1(tmax,zmax,t,INTERP);
        end
        envmoy = mean((envmin+envmax)/2,1);
        if nargout > 3
            amp = mean(abs(envmax-envmin),1)/2;
        end
    case 2

```

```

for k = 1:ndirs
    phi = (k-1)*pi/ndirs;
    y = real(exp(-i*phi)*m);
    [indmin,indmax,indzer] = extr(y);
    nem(k) = length(indmin)+length(indmax);
    nzm(k) = length(indzer);
    [tmin,tmax,zmin,zmax] = boundary_conditions(indmin,indmax,t,y,y,NBSYM);
    envmin(k,:) = exp(i*phi)*interp1(tmin,zmin,t,INTERP);
    envmax(k,:) = exp(i*phi)*interp1(tmax,zmax,t,INTERP);
end
envmoy = mean((envmin+envmax),1);
if nargout > 3
    amp = mean(abs(envmax-envmin),1)/2;
end
end
else
    [indmin,indmax,indzer] = extr(m);
    nem = length(indmin)+length(indmax);
    nzm = length(indzer);
    [tmin,tmax,mmin,mmax] = boundary_conditions(indmin,indmax,t,m,m,NBSYM);
    envmin = interp1(tmin,mmin,t,INTERP);
    envmax = interp1(tmax,mmax,t,INTERP);
    envmoy = (envmin+envmax)/2;
    if nargout > 3
        amp = mean(abs(envmax-envmin),1)/2;
    end
end
end
%-----
% default stopping criterion
function [stop,envmoy,s] = stop_sifting(m,t,sd,sd2,tol,INTERP,MODE_COMPLEX,ndirs)
try
    [envmoy,nem,nzm,amp] =
mean_and_amplitude(m,t,INTERP,MODE_COMPLEX,ndirs);
    sx = abs(envmoy)./amp;
    s = mean(sx);
    stop = ~((mean(sx > sd) > tol | any(sx > sd2)) & (all(nem > 2)));
    if ~MODE_COMPLEX
        stop = stop && ~(abs(nzm-nem)>1);
    end
catch
    stop = 1;
    envmoy = zeros(1,length(m));
    s = NaN;

```

```

end
end
%-----
% stopping criterion corresponding to option FIX
function [stop,moyenne]= stop_sifting_fixe(t,m,INTERP,MODE_COMPLEX,ndirs)
try
    moyenne = mean_and_amplitude(m,t,INTERP,MODE_COMPLEX,ndirs);
    stop = 0;
catch
    moyenne = zeros(1,length(m));
    stop = 1;
end
end
%-----
% stopping criterion corresponding to option FIX_H
function [stop,moyenne,stop_count]= stop_sifting_fixe_h(t,m,INTERP,stop_count,FIXE_H,MODE_COMPLEX,ndirs)
try
    [moyenne,nem,nzm] = mean_and_amplitude(m,t,INTERP,MODE_COMPLEX,ndirs);
    if (all(abs(nzm-nem)>1))
        stop = 0;
        stop_count = 0;
    else
        stop_count = stop_count+1;
        stop = (stop_count == FIXE_H);
    end
catch
    moyenne = zeros(1,length(m));
    stop = 1;
end
end
%-----
% displays the progression of the decomposition with the default stopping criterion
function display_emd(t,m,mp,r,envmin,envmax,envmoy,s,sb,sx,sdt,sd2t,nbit,k,display_sifting,stop_sift)
subplot(4,1,1)
plot(t,mp);hold on;
plot(t,envmax,'--k');plot(t,envmin,'--k');plot(t,envmoy,'r');
title(['IMF ',int2str(k),' iteration ',int2str(nbit),' before sifting']);
set(gca,'XTick',[])
hold off
subplot(4,1,2)
plot(t,sx)
hold on

```

```

plot(t,sdt,'--r')
plot(t,sd2t,':k')
title('stop parameter')
set(gca,'XTick',[])
hold off
subplot(4,1,3)
plot(t,m)
title(['IMF ',int2str(k),'; iteration ',int2str(nbit),' after sifting']);
set(gca,'XTick',[])
subplot(4,1,4);
plot(t,r-m)
title('residue');
disp(['stop parameter mean value : ',num2str(sb),' before sifting and ',num2str(s),' after'])
if stop_sift
    disp('last iteration for this mode')
end
if display_sifting == 2
    pause(0.01)
else
    pause
end
end
%-----
% displays the progression of the decomposition with the FIX and FIX_H stopping
criteria
function display_emd_fixe(t,m,mp,r,envmin,envmax,envmoy,nbit,k,display_sifting)
subplot(3,1,1)
plot(t,mp);hold on;
plot(t,envmax,'--k');plot(t,envmin,'--k');plot(t,envmoy,'r');
title(['IMF ',int2str(k),'; iteration ',int2str(nbit),' before sifting']);
set(gca,'XTick',[])
hold off
subplot(3,1,2)
plot(t,m)
title(['IMF ',int2str(k),'; iteration ',int2str(nbit),' after sifting']);
set(gca,'XTick',[])
subplot(3,1,3);
plot(t,r-m)
title('residue');
if display_sifting == 2
    pause(0.01)
else
    pause
end
end
end

```

```

%-----
% defines new extrema points to extend the interpolations at the edges of the
% signal (mainly mirror symmetry)
function [tmin,tmax,zmin,zmax] = boundary_conditions(indmin,indmax,t,x,z,nbsym)
    lx = length(x);
    if (length(indmin) + length(indmax) < 3)
        error('not enough extrema')
    end
    % boundary conditions for interpolations :
    if indmax(1) < indmin(1)
        if x(1) > x(indmin(1))
            lmax = fliplr(indmax(2:min(end,nbsym+1)));
            lmin = fliplr(indmin(1:min(end,nbsym)));
            lsym = indmax(1);
        else
            lmax = fliplr(indmax(1:min(end,nbsym)));
            lmin = [fliplr(indmin(1:min(end,nbsym-1))),1];
            lsym = 1;
        end
    else
        if x(1) < x(indmax(1))
            lmax = fliplr(indmax(1:min(end,nbsym)));
            lmin = fliplr(indmin(2:min(end,nbsym+1)));
            lsym = indmin(1);
        else
            lmax = [fliplr(indmax(1:min(end,nbsym-1))),1];
            lmin = fliplr(indmin(1:min(end,nbsym)));
            lsym = 1;
        end
    end
    if indmax(end) < indmin(end)
        if x(end) < x(indmax(end))
            rmax = fliplr(indmax(max(end-nbsym+1,1):end));
            rmin = fliplr(indmin(max(end-nbsym,1):end-1));
            rsym = indmin(end);
        else
            rmax = [lx,fliplr(indmax(max(end-nbsym+2,1):end))];
            rmin = fliplr(indmin(max(end-nbsym+1,1):end));
            rsym = lx;
        end
    else
        if x(end) > x(indmin(end))
            rmax = fliplr(indmax(max(end-nbsym,1):end-1));
            rmin = fliplr(indmin(max(end-nbsym+1,1):end));
            rsym = indmax(end);
        end
    end
end

```

```

else
    rmax = fliplr(indmax(max(end-nbsym+1,1):end));
    rmin = [lx,fliplr(indmin(max(end-nbsym+2,1):end))];
    rsym = lx;
end
end
tlmin = 2*t(lsym)-t(lmin);
tlmax = 2*t(lsym)-t(lmax);
trmin = 2*t(rsym)-t(rmin);
trmax = 2*t(rsym)-t(rmax);

% in case symmetrized parts do not extend enough
if tlmin(1) > t(1) || tlmax(1) > t(1)
    if lsym == indmax(1)
        lmax = fliplr(indmax(1:min(end,nbsym)));
    else
        lmin = fliplr(indmin(1:min(end,nbsym)));
    end
    if lsym == 1
        error('bug')
    end
    lsym = 1;
    tlmin = 2*t(lsym)-t(lmin);
    tlmax = 2*t(lsym)-t(lmax);
end
if trmin(end) < t(lx) || trmax(end) < t(lx)
    if rsym == indmax(end)
        rmax = fliplr(indmax(max(end-nbsym+1,1):end));
    else
        rmin = fliplr(indmin(max(end-nbsym+1,1):end));
    end
    if rsym == lx
        error('bug')
    end
    rsym = lx;
    trmin = 2*t(rsym)-t(rmin);
    trmax = 2*t(rsym)-t(rmax);
end
zlmax = z(lmax);
zlmin = z(lmin);
zrmax = z(rmax);
zrmin = z(rmin);
tmin = [tlmin t(indmin) trmin];
tmax = [tlmax t(indmax) trmax];
zmin = [zlmin z(indmin) zrmin];

```

```

    zmax = [zlmax z(indmax) zrmax];
end
%-----
%extracts the indices of extrema
function [indmin, indmax, indzer] = extr(x,t)
if(nargin==1)
    t=1:length(x);
end
m = length(x);
if nargout > 2
    x1=x(1:m-1);
    x2=x(2:m);
    indzer = find(x1.*x2<0);
    if any(x == 0)
        iz = find( x==0 );
        indz = [];
        if any(diff(iz)==1)
            zer = x == 0;
            dz = diff([0 zer 0]);
            debz = find(dz == 1);
            finz = find(dz == -1)-1;
            indz = round((debz+finz)/2);
        else
            indz = iz;
        end
        indzer = sort([indzer indz]);
    end
end
d = diff(x);
n = length(d);
d1 = d(1:n-1);
d2 = d(2:n);
indmin = find(d1.*d2<0 & d1<0)+1;
indmax = find(d1.*d2<0 & d1>0)+1;
% when two or more successive points have the same value we consider only one
% extremum in the middle of the constant area
% (only works if the signal is uniformly sampled)
if any(d==0)
    imax = [];
    imin = [];
    bad = (d==0);
    dd = diff([0 bad 0]);
    debs = find(dd == 1);
    fins = find(dd == -1);
    if debs(1) == 1

```

```

    if length(debs) > 1
        debs = debs(2:end);
        fins = fins(2:end);
    else
        debs = [];
        fins = [];
    end
end
if length(debs) > 0
    if fins(end) == m
        if length(debs) > 1
            debs = debs(1:(end-1));
            fins = fins(1:(end-1));
        else
            debs = [];
            fins = [];
        end
    end
end
lc = length(debs);
if lc > 0
    for k = 1:lc
        if d(debs(k)-1) > 0
            if d(fins(k)) < 0
                imax = [imax round((fins(k)+debs(k))/2)];
            end
        else
            if d(fins(k)) > 0
                imin = [imin round((fins(k)+debs(k))/2)];
            end
        end
    end
end
if length(imax) > 0
    indmax = sort([indmax imax]);
end
if length(imin) > 0
    indmin = sort([indmin imin]);
end
end
end
%-----
function ort = io(x,imf)
% ort = IO(x,imf) computes the index of orthogonality
%
```

```

% inputs : - x : analyzed signal
%          - imf : empirical mode decomposition
n = size(imf,1);
s = 0;
for i = 1:n
    for j = 1:n
        if i~=j
            s = s + abs(sum(imf(i,:).*conj(imf(j,:)))/sum(x.^2));
        end
    end
end
ort = 0.5*s;
end
%-----

function
[x,t,sd,sd2,tol,MODE_COMPLEX,ndirs,display_sifting,sdt,sd2t,r,imf,k,nbit,NbIt,MAXI
TERATIONS,FIXE,FIXE_H,MAXMODES,INTERP,mask] = init(varargin)
x = varargin{1};
if nargin == 2
    if isstruct(varargin{2})
        inopts = varargin{2};
    else
        error('when using 2 arguments the first one is the analyzed signal X and the second one
is a struct object describing the options')
    end
elseif nargin > 2
    try
        inopts = struct(varargin{2:end});
    catch
        error('bad argument syntax')
    end
end

% default for stopping
defstop = [0.05,0.5,0.05];
opt_fields =
{'t','stop','display','maxiterations','fix','maxmodes','interp','fix_h','mask','ndirs','complex_ve
rsion'};
defopts.stop = defstop;
defopts.display = 0;
defopts.t = 1:max(size(x));
defopts.maxiterations = 2000;
defopts.fix = 0;
defopts.maxmodes = 0;

```

```

defopts.interp = 'spline';
defopts.fix_h = 0;
defopts.mask = 0;
defopts.ndirs = 4;
defopts.complex_version = 2;
opts = defopts;
if(nargin==1)
    inopts = defopts;
elseif nargin == 0
    error('not enough arguments')
end
names = fieldnames(inopts);
for nom = names'
    if ~any(strcmpi(char(nom), opt_fields))
        error(['bad option field name: ',char(nom)])
    end
    if ~isempty(eval(['inopts.',char(nom)])) % empty values are discarded
        eval(['opts.',lower(char(nom)), ' = inopts.',char(nom),';'])
    end
end
t = opts.t;
stop = opts.stop;
display_sifting = opts.display;
MAXITERATIONS = opts.maxiterations;
FIXE = opts.fix;
MAXMODES = opts.maxmodes;
INTERP = opts.interp;
FIXE_H = opts.fix_h;
mask = opts.mask;
ndirs = opts.ndirs;
complex_version = opts.complex_version;
if ~isvector(x)
    error('X must have only one row or one column')
end
if size(x,1) > 1
    x = x.';
end
if ~isvector(t)
    error('option field T must have only one row or one column')
end
if ~isreal(t)
    error('time instants T must be a real vector')
end
if size(t,1) > 1
    t = t';
end

```

```

end
if (length(t)~=length(x))
    error('X and option field T must have the same length')
end
if ~isvector(stop) || length(stop) > 3
    error('option field STOP must have only one row or one column of max three elements')
end
if ~all(isfinite(x))
    error('data elements must be finite')
end
if size(stop,1) > 1
    stop = stop';
end
L = length(stop);
if L < 3
    stop(3)=defstop(3);
end

if L < 2
    stop(2)=defstop(2);
end
if ~ischar(INTERP) || ~any(strcmpi(INTERP,{'linear','cubic','spline'}))
    error('INTERP field must be "linear", "cubic", "pchip" or "spline"')
end
%special procedure when a masking signal is specified
if any(mask)
    if ~isvector(mask) || length(mask) ~= length(x)
        error('masking signal must have the same dimension as the analyzed signal X')
    end
    if size(mask,1) > 1
        mask = mask.';
    end
    opts.mask = 0;
    imf1 = emd(x+mask,opts);
    imf2 = emd(x-mask,opts);
    if size(imf1,1) ~= size(imf2,1)
        warning('emd:warning',['the two sets of IMFs have different sizes:
',int2str(size(imf1,1)),' and ',int2str(size(imf2,1)),' IMFs.'])
    end
    S1 = size(imf1,1);
    S2 = size(imf2,1);
    if S1 ~= S2
        if S1 < S2
            tmp = imf1;
            imf1 = imf2;

```

```

        imf2 = tmp;
    end
    imf2(max(S1,S2),1) = 0;
end
    imf = (imf1+imf2)/2;
end
    sd = stop(1);
    sd2 = stop(2);
    tol = stop(3);
    lx = length(x);

    sdt = sd*ones(1,lx);
    sd2t = sd2*ones(1,lx);
    if FIXE
        MAXITERATIONS = FIXE;
        if FIXE_H
            error('cannot use both "FIX" and "FIX_H" modes')
        end
    end
    MODE_COMPLEX = ~isreal(x)*complex_version;
    if MODE_COMPLEX && complex_version ~= 1 && complex_version ~= 2
        error('COMPLEX_VERSION parameter must equal 1 or 2')
    end
    % number of extrema and zero-crossings in residual
    ner = lx;
    nzs = lx;
    r = x;
    if ~any(mask) % if a masking signal is specified "imf" already exists at this stage
        imf = [];
    end
    k = 1;
    % iterations counter for extraction of 1 mode
    nbit=0;
    % total iterations counter
    NbIt=0;
end

%% *****

% Apply EMD

%% *****

%% Doing the EMD of the noise removed signal

```

```

x=Y_nfree;
L=length(x);
x_emd=emd(x);

%% *****

% Find R peak
%% *****

%% Calculations for R-peak detection
f2c3=sum(x_emd(1:3,:));
a1=abs(f2c3);
T=0.3*max(a1);
a2=a1.*(a1>=T); % e2 = e1 after thresholding
step=SAMPLES2READ*.2; % interval to search R peak
i=1; j=1;
while i<=L-1
if a2(i)~=0
[Rpoint(j),Rindex(j)]=...
max(a1(i:(i+step)*((i+step)<=(L-1))+(L-1)*((i+step)>(L-1)))));
Rindex(j)=Rindex(j)+i-1;
j=j+1; i=i+step;
end
i=i+1;
end
Rpoint=x(Rindex); % [Rpoint, Rindex] = value and position of R peak
LR=length(Rindex);
% Plot a1 and a2
figure(2)
subplot(211),plot(a1)
subplot(212),plot(a2)
% Plot ECG signal with R peaks marked
figure(3)
plot(x), hold on, plot(Rindex,Rpoint,'ro'), hold off

```

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