ARRHYTHMIA DISCRIMINATION USING ECG

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Presentation Breakdown

Important Points to Discuss

- Problem Statement
- An Introduction
- ECG Analysis
- Algorithm
- Results and Observation
- Conclusions and limitations
- References

PROBLEM STATEMENT

Analysing Different types of Arrhythmia and comparing with normal ECG

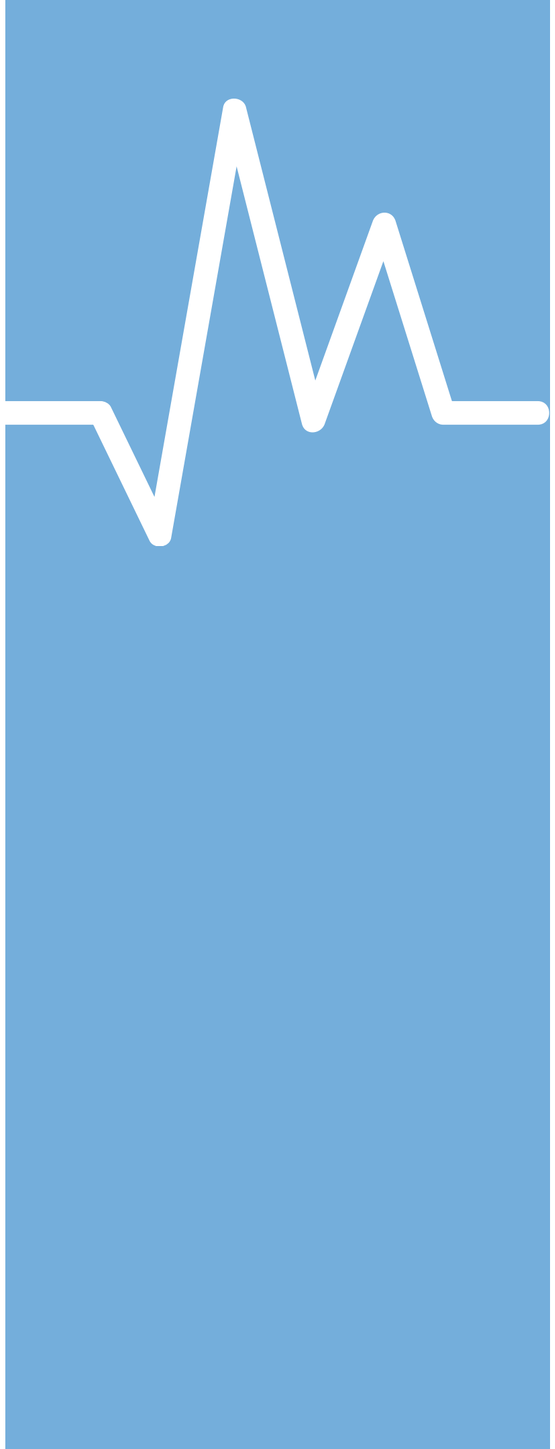
AN INTRODUCTION

WHAT IS AN ARRHYTHMIA?

Arrhythmia is defined as any sort of abnormality that takes place in the normal rhythm of the heart.

WHAT IS ECG ?

An ECG is a graph between potential developed due to polarization and depolarization during 1 heart beat vs time.



ECG ANALYSIS

DATASET

The whole dataset for this project has been taken from MIT-BIH arrhythmia database.

ANALYSING PROCESS

Various tools of signal processing have been used viz. band pass filter, in order to remove high frequency and low frequency noises, Fourier transform in order to analyze the frequency domain of the signal and correlation to compare two ECG signals that have been preprocessed.

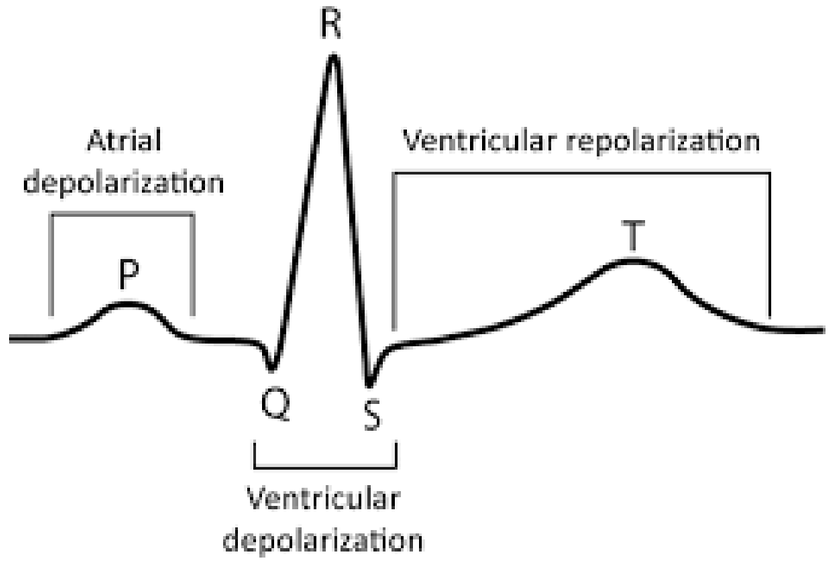


Figure 1: PQRST Complex in Normal ECG

ALGORITHM

What we have done

INPUT SIGNAL

- Normal ECG
- Supraventricular arrhythmia
- Malignant Ventricular Ectopy
- Artrial Fibrillation

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TRANSFORM

Converting Time domain to frequency domain using Fast Fourier Transform

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FILTERING

Using a band Pass filter
Normal ECG has frequency range between 1 Hz to 20 Hz

↓

INVERSE TRANSFORM

Converting frequency domain to time domain using Inverse Fast Fourier Transform

R PEAK DETECTION

Its a two cycle process including window analysis , peak storing , threshold filter

BPM CALCULATION

60 * Sampling Rate / (Average Distance between two peaks)
Average Distance = time / peaks
(Between 1st and last R peak)

CUTTING OF SIGNAL

Limiting a signal between index 1 and index 2
example k = val(x,y) label 1 to label 2

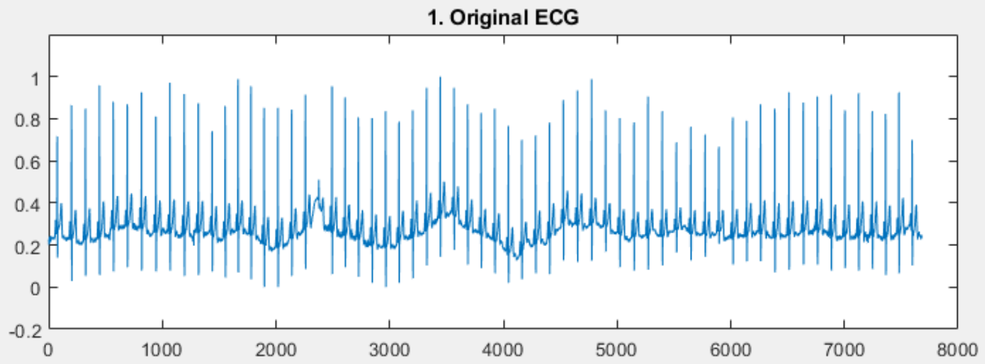
CORRELATION

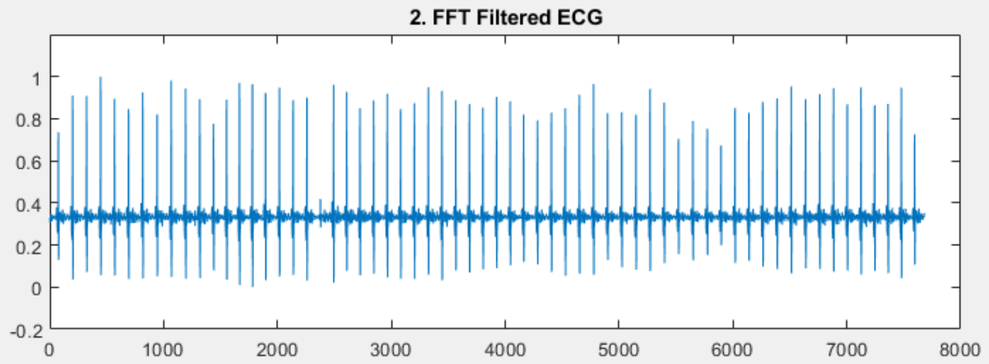
Finding correlation coefficient of two samples

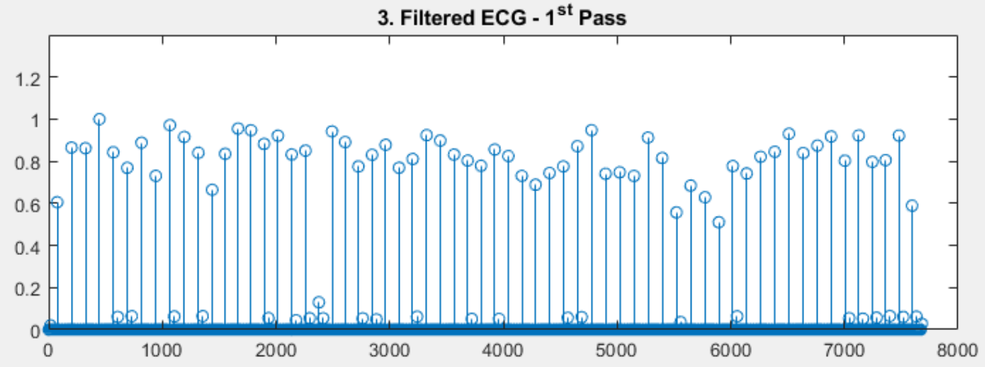
RESULTS AND CONCLUSION

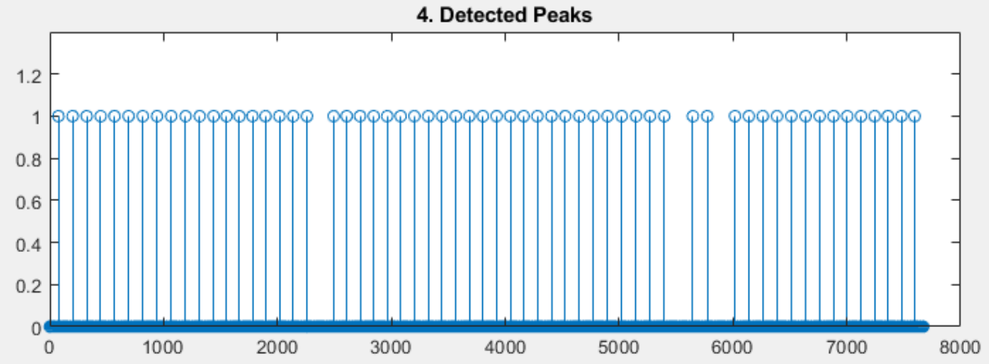
Using the above proposed algorithm we were able to get the data of one single PQRST complex of the patients and then compare it with a single PQRST complex of each type of arrhythmia signal present in the MIT-BIH database.

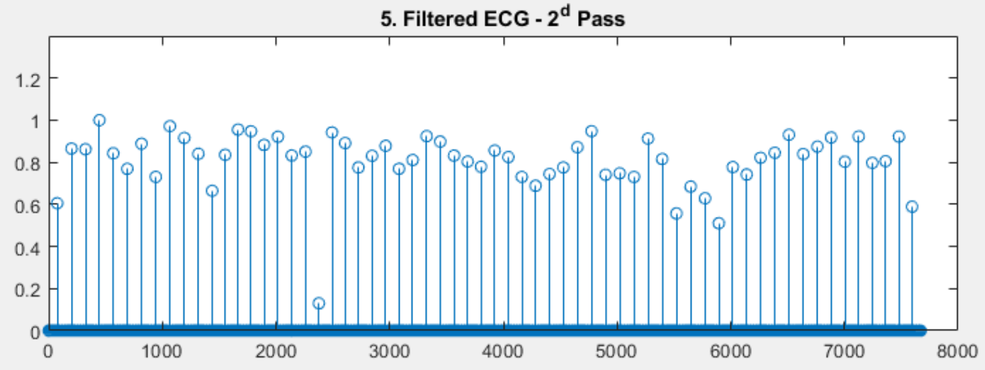
The correlation coefficient of these PQRST complexes is taken. The maximum correlation coefficient that is obtained from these comparisons is reported as the arrhythmia present. If maximum correlation coefficient is found with the normal healthy heart beat then the person is reported as healthy.

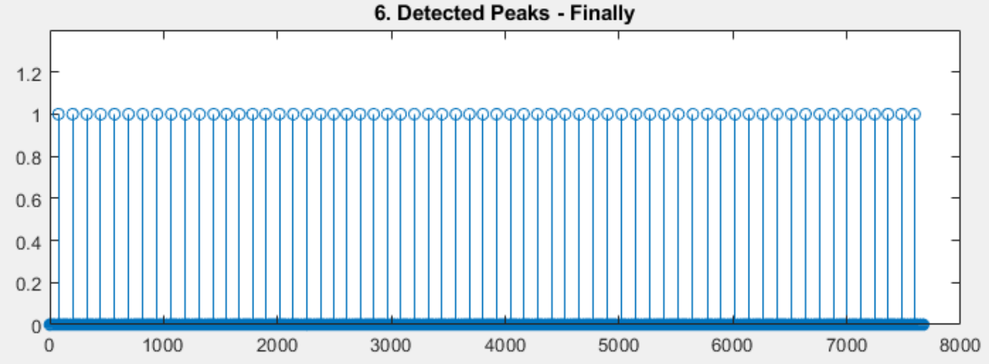

1. Original ECG
1
0.8
0.6
0.4
0.2
0
-0.2
0
1000
2000
3000
4000
5000
6000
7000
8000


2. FFT Filtered ECG
1
0.8
0.6
0.4
0.2
0
-0.2
0
1000
2000
3000
4000
5000
6000
7000
8000


3. Filtered ECG - 1st Pass
1.2
1
0.8
0.6
0.4
0.2
0
0
1000
2000
3000
4000
5000
6000
7000
8000


4. Detected Peaks
1.2
1
0.8
0.6
0.4
0.2
0
0
1000
2000
3000
4000
5000
6000
7000
8000


5. Filtered ECG - 2d Pass
1.2
1
0.8
0.6
0.4
0.2
0
0
1000
2000
3000
4000
5000
6000
7000
8000


6. Detected Peaks - Finally
1.2
1
0.8
0.6
0.4
0.2
0
0
1000
2000
3000
4000
5000
6000
7000
8000

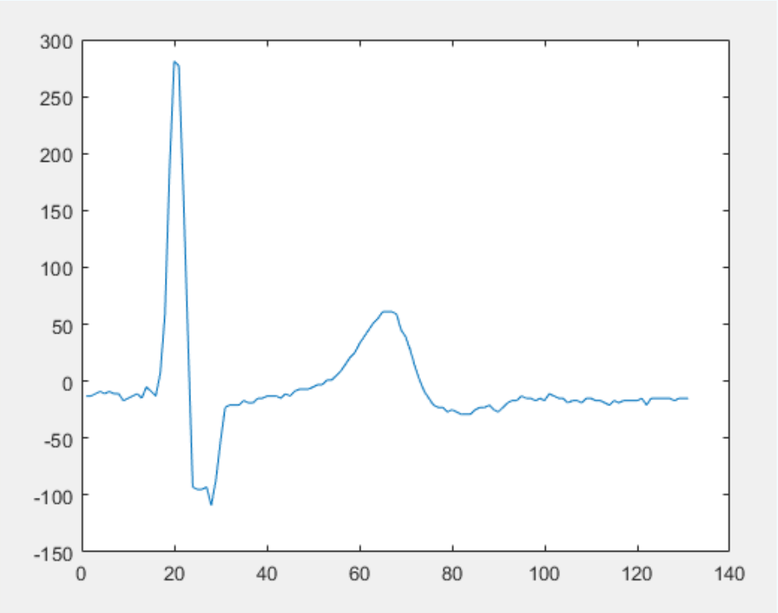


Figure 2: Supraventricular Arrhythmia

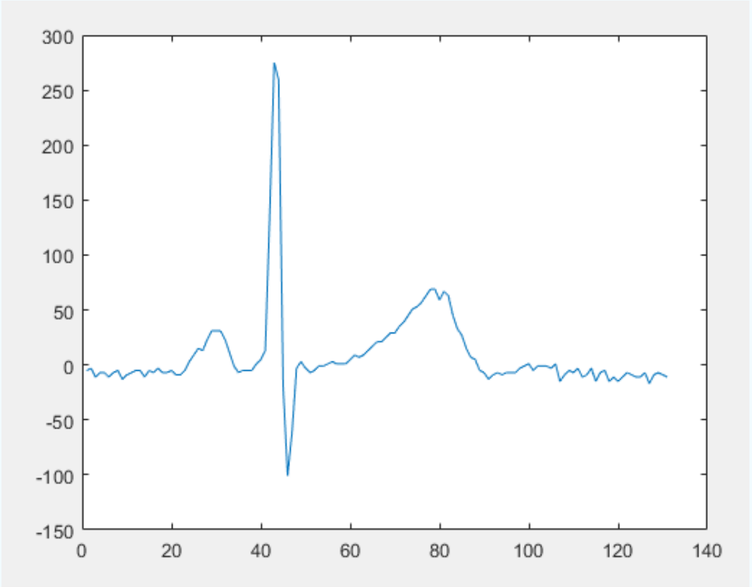


Figure 4: Normal ECG

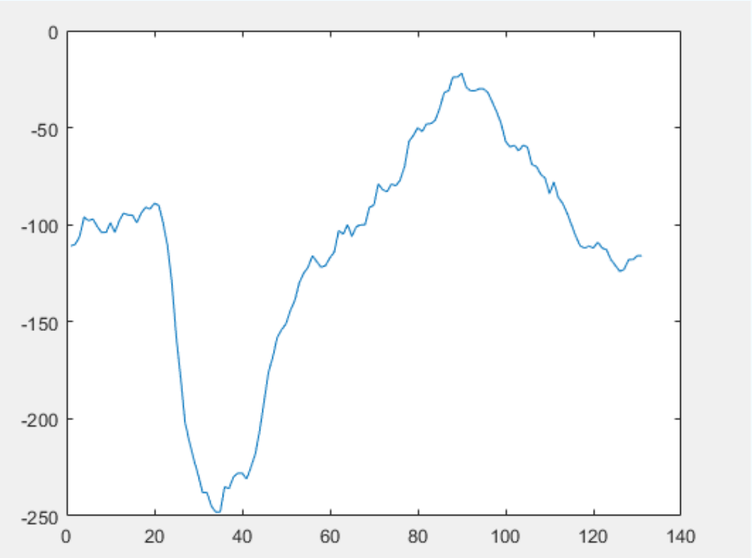


Figure 3: Malignant Ventricular Ectopy

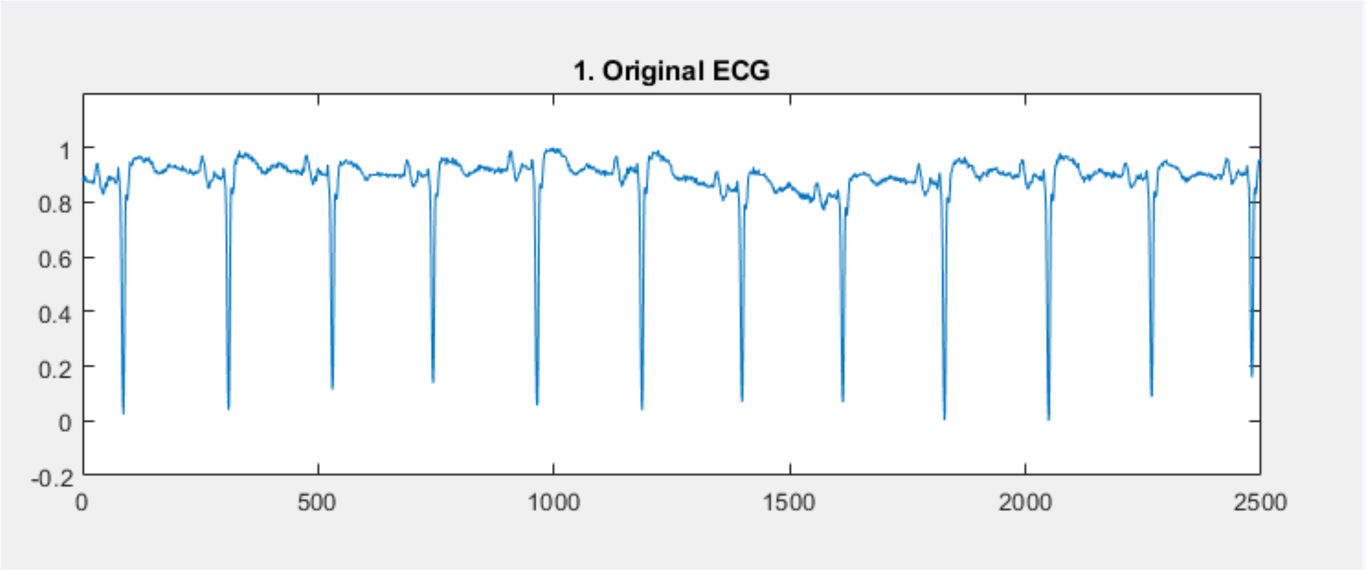
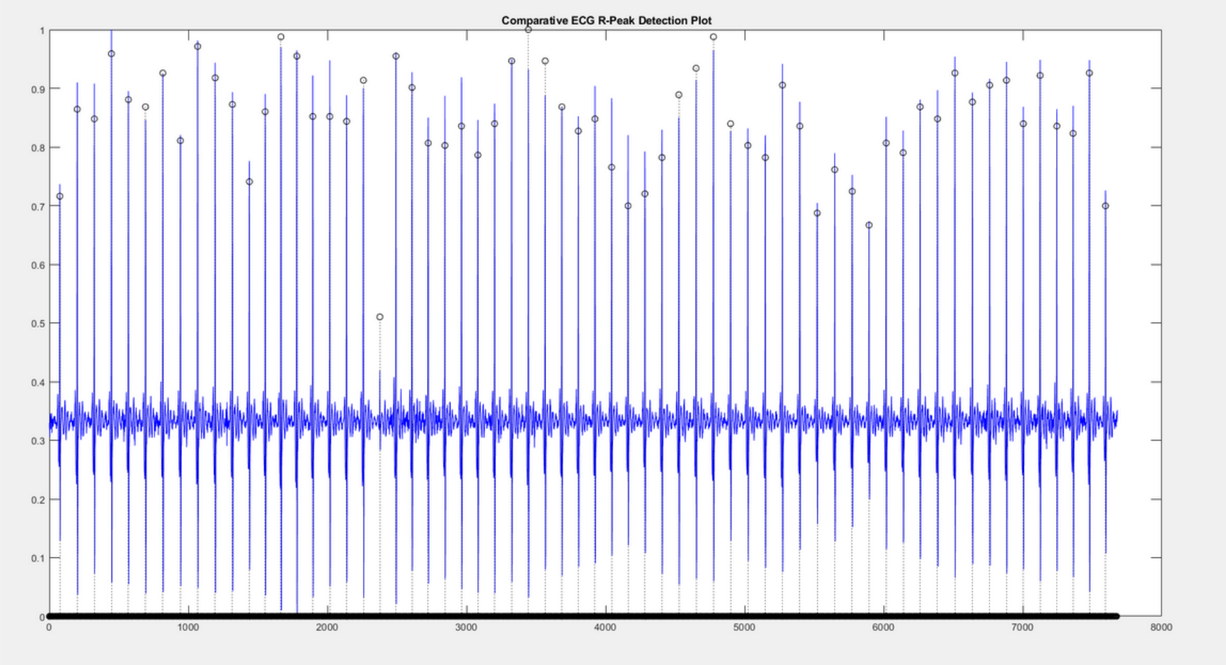


Figure 5: Atrial Fibrillation

Command Window

```
>> aFINAL_CODE
Inorder to compare the data of other Arrhythmias,
other signals will have to be loaded
in place of Ventrivular ECT.matfile
.....................................................................................
Test Variables
   73.0880

   300

   300

.....................................................................................
Average Heart Rate Normal =
   64.3490

Average Heart Rate Ventricular Ectopic =
   92.1413

Correlation Coefficient between sample and Ventricular Ectopic ECG =
   1.5355e-04

Correlation Coefficient between sample and Normal ECG =
    0.0011
```

Final Output



Detected Peaks

BPM

S.No.	Normal ECG	Ventricular Ectopy	Atrial Fibrillation	Supraventricular Arrhythmia
Patient 1	64	69	73	93
Patient 2	62	50	69	63
Patient 3	71	72	72	96
Patient 4	80	92	65	102
Ideal Range	60 to 100	< 100	100 to 175	> 100

CONCLUSIONS AND LIMITATIONS

We have developed a method for arrhythmia discrimination. This method is based on separating a single PQRST complex of the original arrhythmia signal and comparing it with all the complexes created from the patient’s data. In order to increase the accuracy we calculated BPM to compare them with the standard data available.

Our project is still under development and will require analysis of better databases to get the final accuracy of the algorithm. Difficulty in finding correlation coefficient with the algorithm used due to different resolution of the samples.

In the future, our goal is to integrate our project with larger databases and get the results live where input signal will be entered and the result will be given at the same time.

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