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Fall 2005

QT variability calculation using a template matching algorithm and power spectral analysis

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ABSTRACT

QT VARIABILITY CALCULATION USING A TEMPLATE MATCHING ALGORITHM AND POWER SPECTRAL ANALYSIS

by
Theodore Sami Rizkalla

ECG interval measurement and variability analysis has proven to be a useful tool in investigating autonomic nervous system function. Traditionally, the R to R interval has been the thrust of research conducted in this field. QT variability is another topic on which little research has been done.

This thesis uses an algorithm proposed by Dr. Berger, published in 2003. The algorithm stretches the template in the time domain, and composes a sum-squared error function, which is minimized to find the scaling factor for that beat. These scaling factors are compiled into an array, and an interpolated signal is generated of QT interval times. Using LabVIEW and MATLAB, the algorithm was put into place, and frequency spectral analysis conducted on patients with normal sinus rhythm and those with arrhythmias. This system has been tested statistically, showing a less than 10 percent deviation from a standardized database of QT interval lengths (Physionet MIT/BIH databases) in all cases and less than 5 percent in most. In addition, power spectral analysis was conducted on patients with normal sinus rhythms and those with arrhythmias. However, major differences between patient populations were not observed with the performed techniques.

QT VARIABILITY CALCULATION USING A TEMPLATE MATCHING ALGORITHM AND POWER SPECTRAL ANALYSIS

by
Theodore Sami Rizkalla

A Thesis
Submitted to the Faculty of
New Jersey Institute of Technology
in Partial Fulfillment of the Requirements for the Degree of
Master of Science in Biomedical Engineering

Department of Biomedical Engineering

August 2005

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QT VARIABILITY CALCULATION USING A TEMPLATE MATCHING ALGORITHM AND POWER SPECTRAL ANALYSIS

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ACKNOWLEDGEMENT

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CHAPTER 1

INTRODUCTION

1.1 Objective

The objective of this thesis is to present an algorithm for the calculation of the QT

interval variability and utilize its results for variability analysis. This paper will also

discuss the robustness of the algorithm through discussions of the validation methods, as

well as results of empirical analysis of ECG records. For the purpose of this thesis, we

have selected a template-matching algorithm developed by Dr. Ronald Berger of Johns-

Hopkins [1], initially to investigate sudden cardiac death.

1.2 Background Information

The following section will present a brief introduction to the cardiac system, the basic

concepts of interval measurement, and a review of previous work with the QT interval,

also referred to as the ventricular repolarization interval.

1.2.1 Physiology of the Heart

The heart is both an extremely important and unique organ in the human body. As such,

a short synopsis of its features and functions will help the reader understand the concepts

presented herein.

1.2.1.1 Physical Features. The heart is located centrally with the chest cavity, with its

apex pointing toward the left-hand side. It is a hollow muscle composed of special

1.2.1.1 Physical Features. The heart is located centrally with the chest cavity, with its apex pointing toward the left-hand side. It is a hollow muscle composed of special myocytes, different from both striated and smooth muscle, which are arranged in a mesh or grid layout to provide even, complete, and functionally simultaneous contraction of the muscle. The heart is composed of four chambers: the left and right atria and left and right ventricles. The sequential contraction of each of these chambers leads to a pumping effect, and as such, the heart moves blood throughout the body, both delivering chemicals to cells and removing waste [1].
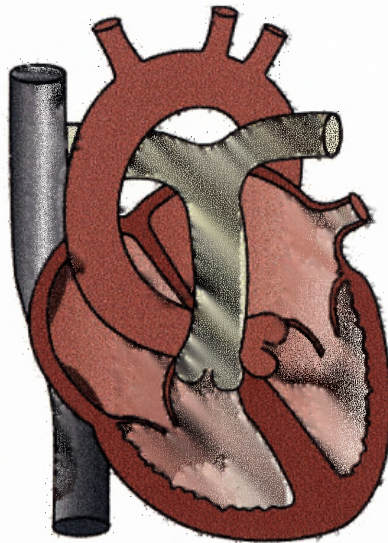
Figure 1.1 Cross-sectional view of the heart [1].

The cardiac cycle, as typically described, begins in the right atrium. The contraction of this atrium moves oxygen-deficient blood from the systemic circulation into the right ventricle, where the power contraction of the right heart is performed. The blood then continues through the pulmonary arteries into the lungs to oxygenate the hemoglobin in the red blood cell. From the lungs, the blood returns to the heart via the

pulmonary veins into the left atrium. The blood is pumped into the left ventricle during diastole, where the "final" contraction of the cardiac cycles takes place, and the blood reenters the systemic blood vessels for conduction around the body.

1.2.1.2 Cardiac Electrophysiology. The heart is unique in its mechanism for enervation. Throughout the heart there are no afferent nerves for the purpose of muscle contraction; instead, there is a complex system of excitable cells that are not quite neurons, and non-contractile, unlike the surrounding muscle cells. The existence of this system is a testament to the importance of sequential contraction and regulation of cardiac function.

The genesis of the contractile impulse begins at the sino-atrial (SA) node, located within the right atrium. The node is simply a connection of excitable cells that receives, under normal conditions, a regulatory signal to "fire", which is mediated by baroreceptors and other components of the autonomic nervous system (ANS). When this impulse is missing, the SA node has a natural resting frequency of 60-100 discharges per minute. The impulse spreads across the atrial septum to activate both left and right atria [2].

After a short delay to allow full atrial contraction, the atrio-ventricular (AV) node begins the process of enervating the ventricles. As opposed to the simplicity of atrial contraction, the ventricles require a more precise method of pumping. From the AV node, the signal travels down the Bundle of His, located centrally within the ventricular septum, down to the apex of the heart through the left and right bundles, and then back upwards through the cardiac muscle within enervating channels called Purkinje fibers. The resulting action is a contraction of the ventricles starting at the apex and moving up. This

creates a wrenching motion within the heart, which "wrings" the blood out of it like a wet towel, which is a surprisingly effective movement.

From this, one can see that the function of the heart as a muscle is very strongly connected to the pulsatile signals that it receives and the order and timing of those signals. In order to further understand how this relates to current medical practices, such as cardiac diagnostics and medical evaluations, a brief introduction to the electrocardiogram (ECG) and electrocardiography will be given.
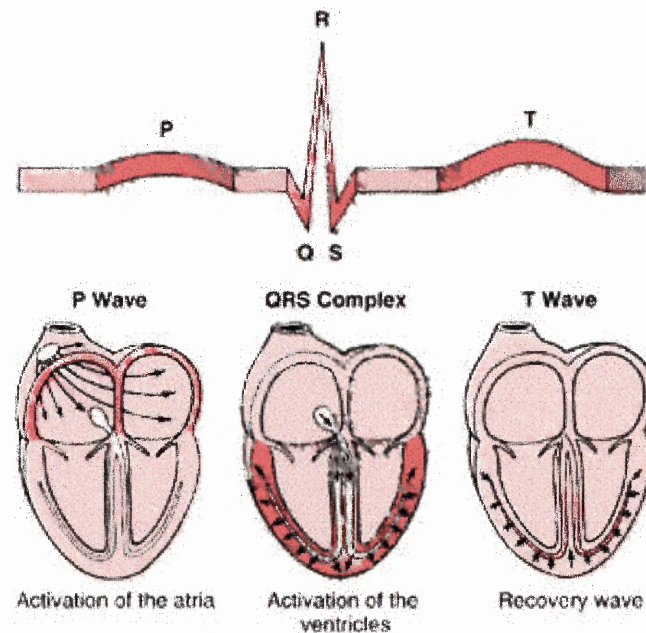
Figure 1.2 Sample ECG with corresponding functions [3].

The ECG is a time series of voltages recorded from electrodes placed on the chest, typically over multiple cardiac cycles. It is the primary tool used in the non-invasive diagnosis of many cardiac conditions such as congestive heart failure, various

arrhythmias, and valvular disease. Given its temporal nature, the ECG is also a useful tool for referencing specific cardiac events.

The ECG is composed of various subwaves, denoted by the letters P, Q, R, S and T (note: the U wave is sometimes included, however, its relation to cardiac contraction, and even its very existence, are contested, and as such, it is left out of this discussion), which are related to the major features of the typical ECG (see figure 1.2). The P wave, the first voltage noted on an ECG, is a relatively small (approximately 0.25 mV) voltage that signifies the depolarization of the atrial myocardium. The next major feature of an ECG recording is the QRS complex. This is the result of the repolarization of the atria and depolarization of the ventricles to create a large voltage peak, which is the R wave. The QRS is normally referred to as one feature rather than separate waves because the Q wave may not be present at all times, or the S and R have different shapes or do not stick to their typical amplitudes (for the R wave, this is around 1.6 mV). Following the QRS complex is the T wave, which is a result of the repolarization of the ventricles. Though it is beyond the scope of this paper, it is important to note that the shape and amplitude of these waves change with the position of the electrodes with reference to the heart. A typical clinical recording will use multiple leads to obtain many different perspectives of the electrical activity to obtain a better composite picture [4].

1.2.2 ECG Interval Variability

Other than simply looking at the ECG morphology and basing diagnoses on it, interval variability is an offshoot of traditional ECG signals, created by interpolating the interval values obtained from the ECG. These signals are taken by finding the time (typically in

milliseconds) of an interval on the ECG (R-wave to R-wave, P to T, etc.), then recreating a signal and performing analytical steps on that function to find more information not readily apparent on a conventional ECG recording. These signals and their creation process will be covered in detail in chapter 2. These intervals are closely related to many different cardiac phenomena; for example, the PQ interval is a measurement of the delay set by the AV node.

1.2.2.1 Heart Rate Variability. Heart rate variability (HRV) is a measurement of R-R variability. It was first realized as a clinically important quantity in the 1960s by Hon and Lee [5], and later further codified in 1977, when Wolf and colleagues [6] presented data pointing to reduced HRV as an indicator of post-MI mortality. Several years later, Akselrod et al [7] began the present day task of frequency power spectrum analysis as a measure of activity in the autonomic nervous system. There are many uses for the R-R interval as a diagnostic tool, the most simple of which is the heart rate of a patient.

Statistical time-domain measurements provide a picture of recorded ECG signals, giving quantities that can be used to compare general patient states such as paced breathing, sleep, activity or illness. Paced breathing is a process by which the breathing is set to a standard rhythm by use of a visual or aural metronome counting inhalations and exhalations. This is done to understand the effects of the respiratory rhythm on the heart rate by providing a known rhythm that the patient adheres to, thus reducing the unknowns for the researcher. Some sample quantities used in time-domain analysis are the standard deviation of normal-to-normal intervals (SDNN), the standard deviation of average NN intervals (SDANN), or the root mean squared difference of successive NN intervals

(RMSSD) [13]. These methods, while providing insight into the importance of HRV in cardiac diagnostics, do not provide detailed interpretations of variability, nor much information on the link between this variability and instantaneous changes in autonomic nervous system function, which regulates the electrical impulse of the heart.

From this aspect of R-R interval analysis, we shift directions to the frequency-domain. These methods do not use the ECG signal in the frequency domain, as it would not contain information about the beat-to-beat interval values. Instead, one popular method of frequency domain analysis is to create an inter-beat interval signal (IBI). This signal is a derived signal of the ECG, created by assigning each successive time point (T) in the interpolated signal a value equal to the R-R interval time in milliseconds between beat (N) and beat ($N+1$).
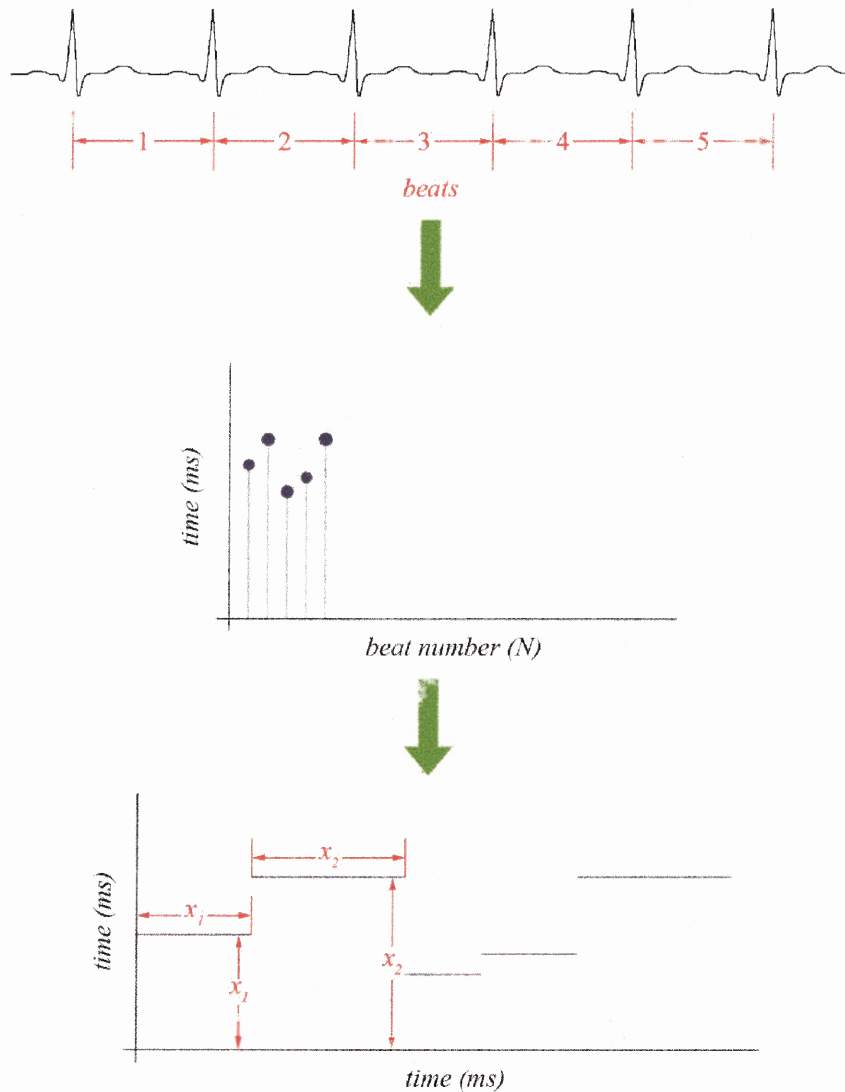
Figure 1.3 Steps from ECG signal to IIBI R-R interval signal.

As shown in figure 1.3, the IIBI signal, or interpolated inter-beat interval, is constructed by taking the value in the sequence of R-R interval values (the inter-beat-interval, or IBI), then repeating the value for the length of the value. For example, if the RR time for beat one is 350 ms, then the value 350 will be repeated for 350 ms, and if beat two is 338 ms, the value 338 will be repeated for 338 ms. This does not mean that the value will be repeated for 338 points; it is dependent upon signal sampling frequency.

If the sampling frequency is 1000 Hz, then the value will be repeated for those 338 points, but if the sampling frequency is 250 Hz, the value will be repeated for 84 points. This system gives more weight to larger values, and also provides for even sampling in the time domain, without which the frequency analysis will be incorrect. This signal can be manipulated further by subtracting the mean value from each point to center the signal around zero.

After the desired signal is created, the next step is frequency spectral analysis, where a Fourier transform is performed on the time domain signal, and a power spectrum for the signal is obtained. The spectral range of interest for HRV is between 0.05 Hz and 0.4 Hz. This range is chosen because it is the frequency band that shows autonomic nervous activity. Researchers then look for any outstanding differences in frequency content between two multiple types of records to try and generate information pertaining to the patient's health or current activity, such as varying states of sleep or comparing anxiety to calmness.

1.2.2.2 Implications for the Autonomic Nervous System. As stated earlier, the autonomic nervous system regulates the heart rate. The ANS is composed of two parts, the sympathetic and parasympathetic nervous systems (SNS and PNS respectively). The PNS is the dominant system during rest, as it slows down the heart rate, while the SNS is active in a "fight or flight" situation, as it speeds up the heart rate and activates other systems necessary for conditions of high activity or anxiety. Both these systems enervate the heart through separate means. PNS enervation is achieved through the vagus nerve, while the SNS uses a network of nerves termed the sympathetic plexus, as shown in

figure 1.4. During rest conditions, the PNS is the major force controlling heart rate, keeping it well below 100 beats per minute [1].
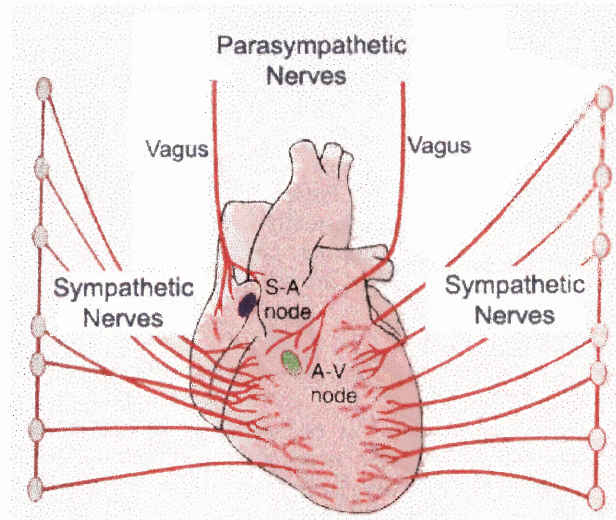
Figure 1.4 Sympathetic and parasympathetic enervation of the heart [9].

Since the heart rate is moderated by two opposing systems, and adjusted constantly, the heart rate has a degree of variability to it, as already discussed. The two main frequency bands, LF (0.05-0.15 Hz) and HF (0.15-0.4 Hz), each correlate to activity within the ANS. The summation area of HF activity over the band of interest relates closely to vagal nerve activity, while the summation of LF activity is a combination of both PNS and SNS enervation. Not only are these components monitored to achieve some understanding of ANS function and health in patients, but their ratio (LF/HF) is also an important quantity in determining which branch of the autonomic nervous system is dominant [8].

1.2.3 QT Interval Measurement

From the encouraging results obtained analyzing the R-R intervals using various methods, researchers have been branched into other types of interval measurements. QT interval measurement and variability have become a popular choice for seeking answers to complex problems like sudden cardiac death or the onset of mortal cardiac conditions. However, this field remains largely untouched in terms of power spectral analysis.

There has been a good deal of work conducted by researchers on the statistical analysis of QT variability as well as physiological investigations of the QT interval. Frljak et al [10] have shown that QT variability increases after cardiac surgery, suggesting that the cardiac conduction system has been disrupted as a result of the procedure. Another study conducted by researchers at Vanderbilt University [11] has shown that ANS blockade increases QT interval length, and patients with pre-existing autonomic failure, when residual ANS activity is suppressed, showed even longer QT intervals.

Work conducted on comparing QT variability to HRV has shown mixed results. In a subject with LQTS (long QT syndrome), Nakagawa [12] has shown differing relationships between QT interval length and LF/HF quantities depending on the position of the subject, while Malik [13] has shown that in healthy volunteers, the relationship between QT and RR intervals vary greatly between subjects, but remain fairly consistent for individual records from the same subject, which has also been noted by Batchvarov and colleagues [14].

Ventures into spectral analysis of QT interval lengths have shown potential as another indicator of ANS function. Yeragani, Berger, Pohl and Balon [15] have

demonstrated in a study that there are diurnal fluctuations of QT variability, and these fluctuations are quantifiable within the familiar frequency bands used in HRV analysis. From these previous studies, we can infer two things: QT variability is a viable method of judging ANS function, and it is more complex than HRV analysis, though this last observation may only be due to a poor understanding of the relation between ventricular repolarization lability and autonomic activity.

CHAPTER 2

TEMPLATE MATCHING ALGORITHM

2.1 Overview

Chapter 2 presents the reader with a description of Dr. Berger's template matching algorithm, which is currently used by the majority of published researchers in QT variability. In addition, it contains a detailed presentation of the methods employed to develop this algorithm for the purposes of this thesis, including equipment used, and program code.

2.1.1 Berger Method

The template matching algorithm used for this thesis was first developed in 2003 by Dr. Berger [1] for the investigation of sudden cardiac death. His subsequent statistical analysis methods are useful in gauging the method's efficacy, but not important to the purposes of this paper because two different aims are sought; that is, this thesis is searching for spectral analysis, and is also not interested in sudden cardiac death per se, but disease vs. health. This method was followed faithfully with the exception of a few minor differences due mainly to a shift in application purposes.

The method, as described by Dr. Berger, proceeds as follows:

1. The operator selects an ECG record, $x(n)$, to analyze. If multiple leads are present, the lead with the best signal quality (i.e. most prominent Q, R and T waves) is selected.

2. The time of each R-peak is identified using an automatic R-wave detection program (in this case developed by Dr. Ronald Rockland and Pierre Asselin [16], both of NJIT). These R beats are noted as T_i.
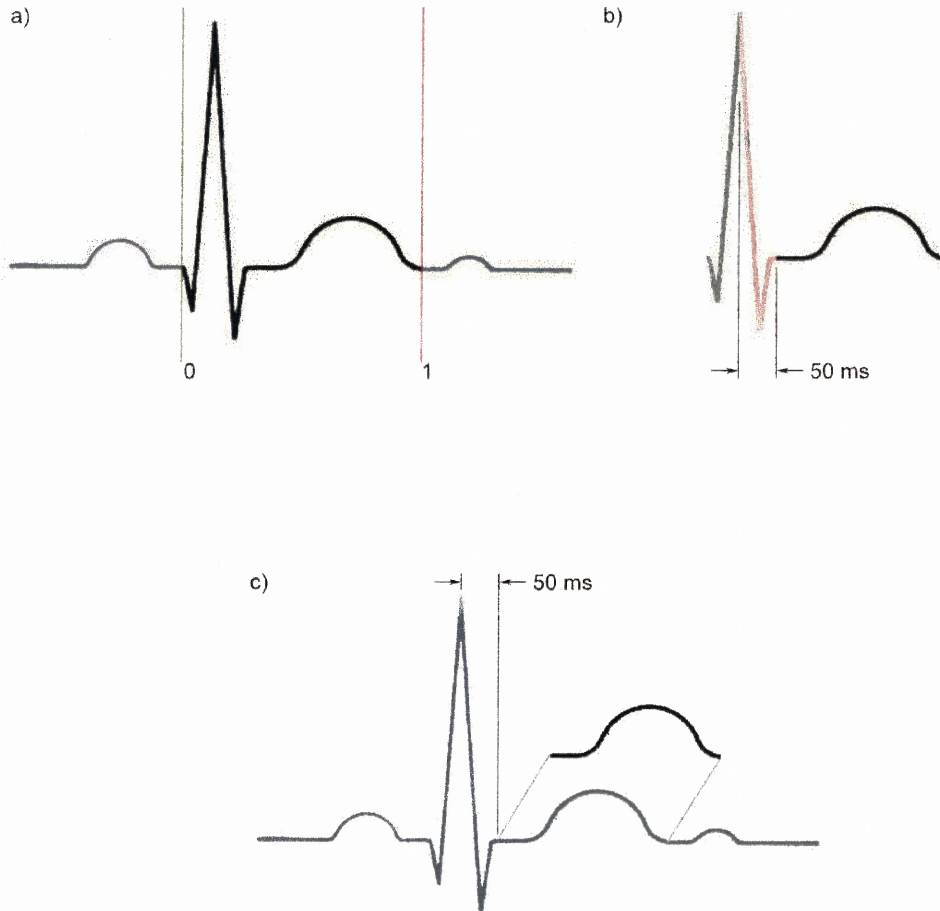
Figure 2.1 Graphical summary of Berger method. *a) Operator selects beginning and end points of QT interval (0 and 1). b) The R-peak is found within this template, and 50 ms beyond this point are removed. c) This new template (dark blue) is then fit on each successive beat starting 50 ms after the R peak.*

3. The operator selects the beginning and end of the QT interval template from one ECG cycle, denoted as beat k. This template becomes $\varphi(n)$, where n is the sample number. Thus,

$$\varphi(n) = x(n) \text{ from } n = n_0 \text{ to } n_1 \tag{2.1}$$

where n_0 and n_1 are the user-defined endpoints of the QT template. After the template is selected, the R peak within the template is detected, and a point 50 ms (n_∇) beyond the peak is found. This point becomes the new beginning of the QT template (it is important to note that the method ignores the actual QRS complex for simplicity and matches the ST segment of the wave).

4. For each successive heart beat, an error function $\varepsilon_i(\alpha)$ is defined.

$$\varepsilon_i(\alpha) = \sum_{j=n_\nabla}^{n_1 - T_k} [\varphi(T_k + j) - x(T_1 - \alpha j)]^2 \tag{2.2}$$

where α is a time stretching factor. $\varepsilon_i(\alpha)$ is a sum squared error function between the ECG signal, and the template scaled by α for beat i.

5. A search of alpha values between 0.9 and 1.1 is performed to minimize $\varepsilon_i(\alpha)$ and obtain $\underline{\alpha}_i$. A step size of 0.0001 is suggested.

6. The QT interval for the ith beat, QT_i, is given to be

$$QT_i = \underline{\alpha}_i N \Delta t \tag{2.3}$$

where $N \Delta t$ is the duration of the initial QT template [15]. The time sequence of subsequent QT_i is what is later used for the calculation of power spectral density.

2.1.2 Reasons for Using the Method

This method was selected for a few prominent reasons. First, the method itself is

extremely simple and straightforward. It is also programmatically less intensive than

other methods, such as identifying Q and T wave separately using decomposition

techniques or differentiation, and provides relatively quick computation times.

2.2 Algorithm – A detailed explanation

This section will show, in detail, how the algorithm was put into use, and the methods

used to accomplish it. For the purposes of this paper, all computations were performed on

an HP pavilion ze4430 running Microsoft Windows XP. "LabVIEW" refers to Texas

Instruments' LabVIEW 7 Express, and MatLab refers to MathWorks Inc.'s MatLab 7.0.

2.2.1 R-wave Detection

R-wave detection for use in this thesis was conducted using a utility developed previously, as mentioned above, and was written in LabVIEW [16]. It uses multiple methods to recognize R peaks and minimize missed beats and false positives.

Initially, a single lead ECG recording is provided to the program, where it is passed through a band pass filter (0.5 Hz – 40 Hz) and generates an array of points above a threshold (40% of maximal value). This array, with the initial ECG and a "start" group (defined as the next group of points above 40% whose index is greater than 150ms after the current index), is passed through a second level of detection based on the first derivative of the ECG and comparison with the first group of points. This information is then compared, validation checks are performed, and the process is iterated for 30 second blocks of data for the signal. After this is completed, duplicate R peak indexes (due to program looping) are removed from the array of R peak indexes (Note: this process is modified slightly. The original R peak detector provided an array of RR interval values. It was subsequently modified to present the index points of the R peaks).

This R wave detector is a fairly robust program, able to cope with noisy ECG recordings, significant baseline wander, changes in R peak height, and negative R peaks.

2.2.2 Template Selection
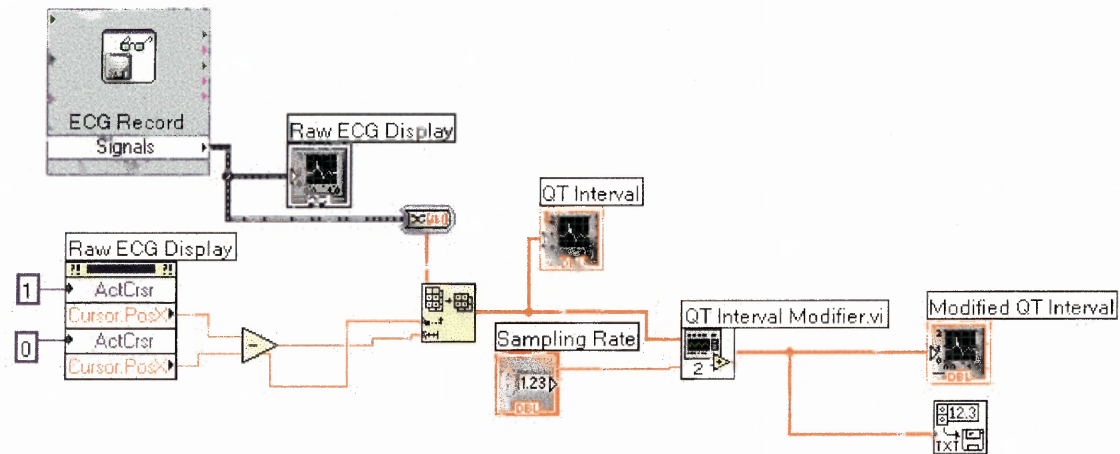
Figure 2.2 Block diagram of template selection VI.

The template matching portion of the algorithm implementation was written in

LabVIEW. The program accepts the same single-lead ECG as the R wave detector. It

displays to the user the ECG, and asks the user to denote the beginning and end of the

template interval with two cursors (0 and 1, respectively). From here, an array is

composed of the points on the ECG record between cursor position 0 and cursor position

1. This is displayed as the QT interval to the user. After this, the data, along with the

sampling rate, is passed into the QT interval modifier, as shown below. During the course

of this thesis, the beginning of the Q wave was defined as the final isoelectric point

before the QRS complex, while the end of the T wave was defined as the first isoelectric

point after the T wave.

Figure 2.3 Block diagram of QT interval modifier.

The QT interval modifier takes the array of the base QT template as its input. First, it finds the R peak within the template. Finding that position, it then creates an RT interval by finding the next peak in the signal. The sampling rate is used to determine how many points 50 ms would be equivalent to, and then the RT interval is shortened by removing that many points from the beginning. The removal of these 50 ms of data is performed so that the entire QRS complex will be removed from the template. This step reduces the error that will be calculated later during template scaling due to the QRS complex. If the QRS is not identical each time in both voltage and temporal position, the error calculated will be large, and as such, its inclusion in the QT template is a detriment rather than a benefit in calculating the error during template scaling. The final result of this is the modified QT interval, which is then redisplayed to the user (figure 2.1). Since array manipulation in LabVIEW are complex and time consuming, as can be seen in figure 2.2, only portions of the algorithm that require user input were coded using LabVIEW, which in this case is only template selection.

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2.2.3 Template Scaling

Template scaling is handled through a MatLab function script (`compare.m`). This script performs the calculation of the error function $\varepsilon_i(\alpha)$. This function takes as its inputs the ECG file, an array of R peak positions (generated from the R wave detector), the modified QT template, and the sampling frequency. From there, a `for` loop is used incrementing `alpha` from 1.35 to 0.65 using a step size of -0.0001. Berger [1] suggests that a range of 0.8 to 1.2 should be sufficient, but to test this method, the range was increased in order to see if accurate alpha values are being calculated outside of this arbitrary range. The new array length (`c_len`) is then calculated by multiplying the original template length (`o_len`) by `alpha` (if this quantity is not an integer, the value is floored). Next, a null array is created of length `c_len`, and the corresponding values from the template are inserted into their scaled position in the array.

After this new, scaled array (`QT_scaled`) is composed, it is then compared with an array of identical length taken from the current beat on the ECG, starting 50 ms after the respective R peak. A typical summed squared error value (`total_e2`) is calculated, and this number is placed in an array indexed by `alpha`. This process is repeated for all values of `alpha` in the range. The resulting array of alpha vs. error numbers is then searched sequentially to find the lowest value of `total_e2`. This alpha value is said to be the scaling factor α_i as described by Berger [1]. The results of this calculation (a graph of error vs. alpha) are displayed to the user for visual verification. For the source of `compare.m`, reference Appendix A, section 1.

2.2.4 Interpolated Signal

The interpolated signal is generated by another MatLab script, `ias.m`. This script is the main application script, as it calls the function `compare` from `compare.m`. This step is of importance to this thesis because it will later be used in the calculation of the power spectrum, however, it is not necessary if frequency analysis is not to be performed. The first role of this script is to repeat the alpha generating function for each successive beat in the ECG record and compile an array of alpha values by beat number. Next, the script calculates the length of the QT intervals in the following manner: for each value in the alpha array, the base time of the template (QT_i)is multiplied by the alpha value. Next, 50 ms is added to account for the missing QRS complex. This value is written to an array of strictly QT interval times, and also written to an array to create the interpolated signal. This gives an interpolated signal to provide variance with respect to the initial ECG recording, which is the focus of the investigation.

After this array is created, the mean is taken, and then subtracted from each value in the array to center the signal around zero for easier frequency analysis. From here, the signal can be manipulated in any manner necessary, which will be covered in greater depth later. The interpolated signal, as well as beat by beat QT interval values, is displayed for visual verification by the user. For the source code of this script, reference Appendix A, section 2.

2.2.5 Outliers

One issue that it is important to note is the occurrence of outliers in the interpolated signal. When the algorithm has finished matching the QT intervals to the template, there

are invariably some outliers in the data. These outliers are very easy to spot visually, as they are much lower than the lowest true interval value. When the template matching algorithm fails to match an interval, for reasons such as a noisy signal or a change in T-wave morphology, it returns the lowest error computed. This will always be the lowest value of alpha available; since the error function will be summing the error over the shortest interval, it will have the least error.

As stated earlier, the range of alpha was increased to outside what was proposed by Dr Berger. The claim that alpha will vary by no more than ±20 percent proved to be correct. Therefore, the alpha values that fall outside of the Berger range (between 0.65 and 0.8 and between 1.2 and 1.35) were determined to be outliers. If the QT template selected was actually too large or too small in comparison to the average value of QT intervals for that record, it can be said that anything beyond 20 percent above or below the mean QT value is an outlier.

It is important to note that this is a non-standard definition of outlier identification. More traditional methods of outlier identification would utilize a threshold of standard deviations away from the mean as a cutoff point, but given how frequently the outliers occur, and their patently obvious appearance, this method was not used. A simple visual review of the IIBI signal, in addition to the criteria here described, clearly shows these outliers and they can then be manually removed.

Once the outliers have been identified, the next step is to remove them from the interpolated signal. Two techniques were tried in relation to outlier removal – removing the outlier and condensing the signal, and removing the outlier and replacing its empty

space with the average of the neighboring intervals. These two techniques will be

explained in more detail in section 3.2.1.

CHAPTER 3

RESULTS

3.1 QT Interval Validation

Validation of the implementation of the template-matching algorithm must be performed.

This validation was completed by using statistical testing between two groups of QT

intervals, one generated using the algorithm described in this thesis, and one obtained

from the QT interval database found at Physionet, an online resource for physiological

signal research.

3.1.1 Selection of Samples

All data used for validation was obtained from Physionet. Within Physionet, there are

many databases containing different types of physiological signals. With respect to ECG

data, there are many options, from patients with ST depressions to atrial fibrillation. One

such database contains pre-annotated ECG records containing markers for the

beginnings, peaks, and ends of the P, QRS, and T wave. This database was used for

testing against because it is a verfiable source of QT interval values.

Four records were chosen from this database for three reasons – clarity of signal,

visibly identifiable T-waves, and stability of R wave height. These are important

considerations because if the signal is noisy, the template-matching algorithm will not

work to its optimal performance, or may not work at all. The T-waves must be

pronounced. This is due to the nature of the template-matching algorithm. If the T-waves

do not have significant peaks, or are not visible on the lead with the clearest QRS

complexes, the template-matching algorithm will not be able to calculate the QT intervals. One can see these criteria are important to the function of the algorithm by remembering that the process involves creating an error function as the template is scaled. If the T-wave is small, or exists where there is ambiguity in the QRS complex, then the template will have similar error values over the range of scaled templates, or will have skewed error readings because the position of the R wave or Q notch are not easily detected. Stability of R-wave height is a minor concern, but aids in the R-wave detection portion of the algorithm, as varying R-wave height creates missed beats and requires more operator input.

The four records chosen are: sel231, sel16273, sel16420, and sel16483. The first record, sel231, was taken from a 73 year-old male experiencing ventricular tachycardia. This record is also available, minus annotations, in the MIT-BIH arrhythmia database, also found on Physionet. The other records, sel16273, sel16420, and sel16483, are annotated copies of records available in the MIT normal sinus rhythm database on Physionet. All records were either initially recorded at 250 Hz (sel231), or resampled to 250 Hz using applications available through Physionet's waveform database (WFDB) toolkit.

3.1.2 Processes

This section presents the methods used and steps taken to validate the template-matching algorithm. The steps, which will be explained in detail, are as follows:

1) Access records using WAVE, a graphical program written specifically to manipulate files found in the MIT ECG databases at Physionet.

2) Obtain intervals from annotated files

3) Run records through template-matching algorithm to obtain interval values

4) Compare overall interval values using Student's T-test for statistical significance.

5) Compare individual interval values using statistical tests for significant difference.

In the first step, a program called WAVE is used to view and export the annotations from the records. WAVE is a program native to Unix-type operating systems, as are all programs in the WFDB toolkit. However, they can be run under Microsoft operating systems using a third-party Unix emulator such as Cygwin. Once the record is read in, it can be manipulated, data analysis can be performed (only if the analysis routines are tailored for working within WAVE), and annotations can be added and edited.

A QT-annotated record contains 12 files, many of which contain annotation information which are compiled into a large annotation file. Detailed information on the format of an annotated record can be found in Table 3.1.

File Type	Purpose
.DAT	Contains the digitized signal values
.HEA	Header file containing information such as patient age, sampling frequency, and any other notes the recording operator deemed pertinent to the record
.MAN	File related to commentary of record
.ATR	Attribute file. This contains non-marker annotations, or annotations not related to temporal position in the file
.PU	The main annotation file. Contains markers for P, QRS, T, and U waves for leads one and two
.PU0	Similar to .pu, but only for lead one
.PU1	Similar to .pu. but only for lead two
.Q1C	Contains data for QRS complexes of lead one
.Q2C	Contains data for QRS complexes of lead two
.QT1	Contains data for T waves of lead one
.QT2	Contains data for T waves of lead two
.XWS	WaveScript file. This allows for graphical display of information in the .dat file.

Table 3.1 Details of a Physionet QT interval record.

When WAVE is called, it accesses the `record.dat` and `record.pu` files.

After this, the intervals annotated in the `.pu` file are exported to a text file. In actuality,

this process is quite involved due to the availability of specific marker exports in WAVE.

Though programs can be written to export only the QT interval from a record read into

WAVE, there are currently none in existence. To get around this problem, the entire

record of annotations is sampled (in this case to at least 30 seconds or 30 R-R intervals,

whichever is longer). Then this annotation record, which contains time of incident, data

point of incident, the marker type (as displayed on the WAVE screen), and which lead it is on, is copied to a text file. Once this record is attained in an easy to use ASCII text format, the file is parsed for occurrences of the QRS marker, and the end-of-T marker. Time values of these points are subtracted for successive beats, and the QT interval array is obtained.

These intervals are technically RT intervals. The reason for this is due to the way the template-matching algorithm works. Since it works by finding the R beat, and moving 50 ms forward to compare the template, the fiduciary point which is referenced after the interval time is calculated is the R peak, not the Q wave. To simplify validation purposes, the MIT QT database was modified to display RT intervals instead of QT intervals. This is not as large of a concern as may seem, since the Q wave may be non-present, and the QRS complex itself is of such a short interval that the loss of the QR portion of the larger QT interval is insignificant. Initially, template-matched QT interval arrays were to be compensated for by replacing the missing QR interval with an average QR interval length; however, there has been little research into QR interval lengths, due to the varying morphologies of QRS complexes, and the small size of the QR interval. To rectify this, one can simply utilize the unmodified QT template from section 2.2.2 instead of its modified counterpart. This unmodified template (before removal of the 50 ms blanking period) is the true QT template, however, this point was not well conveyed in [1]. An alternative method is to utilize the modified template obtained at the end of 2.2.2, include the 50 ms period removed, and then utilize an average QR interval obtained from the record itself, however, this is much more tedious and almost unnecessary in light of the fact that a true QT interval length is available in the process of template generation. There

is one benefit of using the RT interval over the QT interval; that is, the R peak is a much easier point to identify than the Q wave as it is a peak, and the Q-wave is a change from an isoelectric component to a minimum.

After the interval values are obtained from the test records using WAVE and the pre-annotated QT files, the same records, across the same time period, are run through the template-matching algorithm, which is described in chapter 2. Before the statistical analysis is performed, outliers are removed from the array, though not as described in section 2.2.5. These outliers are removed manually from the array of QT interval values (no manipulation is made to the interpolated signal, as it is not used in this portion). This is accomplished by visually inspecting the array for the lowest value available. This value, when graphed, is typically repeated multiple times, and is not within proximity of the surrounding values, and corresponds to sixty-five percent of the original QT template length. The corresponding value from the annotated QT array is removed to preserve the pairing of data.

These two sets of QT interval values are then compared using Student's T-test, which is a statistical test for finding the probability that two samples of numbers are from the same parent population, given as

$$t_0 = \frac{\overline{y}_1 - \overline{y}_2}{S_p \sqrt{\dfrac{1}{n_1} + \dfrac{1}{n_2}}} \tag{3.1}$$

where

$$S_p^2 = \frac{(n_1 - 1)S_1^2 + (n_2 - 1)S_2^2}{n_1 + n_2 - 2}. \tag{3.2}$$

This test is relevant to this work because the end purpose of generating the QT intervals is to calculate a power spectrum of the variability of the QT intervals, and as such, the variance and means of the template-matched and annotated QT intervals should be statistically similar. This test assumes that the variances of the sample populations are equal, as they should be, since they are of the same physical record. For all tests, the null hypothesis is the two samples are from the same parent population, and the alternative hypothesis is that the two samples are from different parent populations, which shows that the QT template matching algorithm lacks the ability to find the correct length of the QT interval.

To test individual QT intervals, a percent difference between the Berger and Physionet intervals was taken, and then a z-test was performed. Z-tests are a statistical tool used to compare a sample set of data to a given mean. In this case, the sample averages were tested at three threshold levels to see if the mean percent difference was less than a given percent difference; here, these three levels are three, five and ten percent. The equation for a z-test is given below.

$$Z_0 = \frac{\bar{y} - \mu_0}{\sigma / \sqrt{n}},$$ (3.3)

where μ_0 is the threshold value for comparison, in this case, the mean percent difference between Physionet and algorithm-generated interval lengths, $\bar{y}$ is the mean percent difference, and sigma and n are the standard deviation and number of data points, respectively. From this z-score, one can calculate the probability that the mean $\bar{y}$ is less than μ_0 by using a lookup table.

3.1.3 Conclusion

The results of the validation test will be presented in this section. First, the data and probabilities will be presented, and afterwards, commentary and explanation of the results will be given. For analysis purposes, when a probability is given, it means that the means are equal for any significance level less than a given probability P. T-test scores, Z-test scores, and beat-to-beat data are available in Appendix B.

The first record, sel231, started out as a set of 42 QT intervals, but after outlier removal, 19 intervals were left to perform statistical analysis on, giving 18 degrees of freedom. The Physionet data had an average of 0.454, and a standard deviation of 0.0122, while the template-matched QT intervals had an average of 0.445, and a standard deviation of 0.189. T-tests for this record give a t-value of 1.809, which supports the null hypothesis for a significance level of 0.05. For individual interval testing, the z-test yielded the following results: for $\mu_0 = 0.03$, a z-score of 1.809 was obtained, correlating to a probability of 0.0352 that the mean percent difference is less than three percent. For $\mu_0 = 0.05$, a z-score of -1.303 was obtained, correlating to a probability of 0.9037 that the mean percent difference is less than five percent. For $\mu_0 = 0.10$, a z-score of -9.084 was obtained, correlating to a probability of 1.0 that the mean percent difference is less than ten percent. A probability of 1.0 is reached when the z-score is significantly more negative than -4, which correlates to a probability of 0.99997.

The next record, sel16273, started out as a set of 38 QT intervals, and after outlier removal, 32 intervals were left, giving 31 degrees of freedom. The Physionet data had an average of 0.323, and a standard deviation of 0.0042, while the template-matched QT intervals had an average of 0.298, and a standard deviation of 0.0162. T-tests for this

record give a t-value of 8.6501, upon which the null hypothesis is rejected for all significance levels. For individual interval testing, the z-test yielded the following results: for $\mu_0 = 0.03$, a z-score of 6.34 was obtained, correlating to a probability of 0.0000000001 that the mean percent difference is less than three percent. For $\mu_0 = 0.05$, a z-score of 3.912 was obtained, correlating to a probability of 0.00004 that the mean percent difference is less than five percent. For $\mu_0 = 0.10$, a z-score of -2.157 was obtained, correlating to a probability of 0.9844 that the mean percent difference is less than ten percent.

The next record, sel16420, started out as a set of 36 QT intervals, with no intervals requiring removal, giving 35 degrees of freedom. The Physionet data had an average of 0.371, and a standard deviation of 0.03402, while the template-matched QT intervals had an average of 0.366, and a standard deviation of 0.0103. T-tests for this record give a t-value of 0.4802, which supports the null hypothesis for a significance level of 0.05 or greater. For individual interval testing, the z-test yielded the following results: for $\mu_0 = 0.03$, a z-score of -6.603 was obtained, correlating to a probability of 1.0 that the mean percent difference is less than three percent. For $\mu_0 = 0.05$, a z-score of - 11.051 was obtained, correlating to a probability of 1.0 that the mean percent difference is less than five percent. For $\mu_0 = 0.10$, a z-score of -22.0103 was obtained, correlating to a probability of 1.0 that the mean percent difference is less than ten percent.

The last record, sel16483, started out as a set of 40 QT intervals, but after outlier removal, 36 intervals were left to perform statistical analysis on, giving 35 degrees of freedom. The Physionet data had an average of 0.339, and a standard deviation of 0.00252, while the template-matched QT intervals had an average of 0.349, and a

standard deviation of 0.00375. T-tests for this record give a t-value of 13.386, upon which the null hypothesis is rejected for all significance levels. For individual interval testing, the z-test yielded the following results: for $\mu_0 = 0.03$, a z-score of 0.07998 was obtained, correlating to a probability of 0.5301 that the mean percent difference is less than three percent. For $\mu_0 = 0.05$, a z-score of -9.611 was obtained, correlating to a probability of 1.0 that the mean percent difference is less than five percent. For $\mu_0 = 0.10$, a z-score of -33.839 was obtained, correlating to a probability of 1.0 that the mean percent difference is less than ten percent.

One benefit of the beat-to-beat analysis is the ability to check the most erroneous beats (the beats with the largest percent difference from the Physionet values). For example, beat 31 of record sel16273 (Appendix B) shows a 21.875% difference from the Physionet data. This is 80 ms shorter than the accepted value. Graphical review of that beat in the ECG data shows that 250 ms (the Berger-generated value) is, in fact, off from the true length of the QT interval.

The results of the statistical validation show disconcerting and conflicting results. Percent difference of individual QT interval values showed that for all records, the mean percent difference of interval values is less than ten percent, and for three of those records, the mean percent difference is less than five percent at the 0.10 significance level. Even more so, one record, sel16420, showed at the 0.20 significance level a mean percent difference of less than three percent. This shows that over all, there is little difference between the QT intervals calculated by the Berger template matching method and the intervals obtained from the Physionet file annotations.

However, the t-tests conducted to judge the statistical probability of two data sets being from the same parent set had less positive results. Two of the records, sel231 and sel16420, are shown, at the 0.05 significance level or higher, to have similar means, while the other two records, sel16273 and sel16483, are significantly different. What does this mean to the validity of the template matching algorithm? At first glance, it shows that fifty percent of the tested records return statistically similar results, which is not encouraging, and may lead one to believe that the template matching algorithm fails to accurately represent the variance of the QT intervals in a given ECG record. However, there are numerous reasons to explain these results.

Record *sel231*			N = 19
Threshold	P	Z-score	Number above threshold
0.0300	0.0352	1.8094	12
0.0500	0.9037	-1.3031	5
0.1000	1.0000	-9.0845	1
Record *sel16273*			N = 32
Threshold	P	Z-score	Number above threshold
0.0300	0.0000	6.3401	29
0.0500	0.0000	3.9124	27
0.1000	0.9845	-2.1569	9
Record *sel16420*			N = 35
Threshold	P	Z-score	Number above threshold
0.0300	0.8034	-6.6031	8
0.0500	1.0000	-11.0051	2
0.1000	1.0000	-22.0103	1
Record *sel16483*			N = 35
Threshold	P	Z-score	Number above threshold
0.0300	0.5302	0.0800	10
0.0500	1.0000	-9.6112	3
0.1000	1.0000	-33.8390	0

Table 3.2 Summary of mean percent difference (MPD) statistical validation

First is the inherent difference of interval calculation. The Physionet data obtained their QT intervals using traditional decomposition techniques, filtering the signal to find the QRS complexes and T waves, and using further processes such as first-derivative analysis to find the beginning and end of the wave. This method provides undeniable identification of the T and Q waves, and exact locations for their beginning and end. The template matching algorithm is dependent upon the least error given by comparing the template against a sampled section of the ECG record. This method is much more susceptible to error due to signal noise and changes in T wave morphology.

Both methods are dependent upon operator interaction, but in different ways. The calculated QT intervals from Physionet are automated detections of component waves, but the operator had the final option to move the points for annotation should the automatic detection fail in any way. Even though the primary means of determining the wave locations is through automatic detection, the end result is still a manually annotated record, though by a trained operator. In contrast, the template-matching algorithm is dependent upon operator interaction only initially, and afterwards, it is a fully automatic calculation. The operator, as explained in chapter 2, selected the template QT interval to be matched against all other QT intervals. If the operator selects a smaller QT interval, all subsequent matches will be shortened. This leads to skewed data. While the interval times encountered may be different, the matching algorithm still works to match the template. This presents one interesting feature about the template matching algorithm – the absolute QT intervals may or may not match up with the accepted length of the QT intervals, but their variations will be the same, because the shortened or lengthened QT template will return proportionally shorter or longer QT intervals.

Another reason for these results is the normality of the QT interval distribution. If the QT interval values are not normally distributed, the t-test will not operate properly, and will return incorrect results as to the matching of the data sets. This will become apparent in situations where the ECG interval observed spans periods of paced to non-paced breathing, episodes of arrhythmia to normal rhythm, or other state changes. Data for these tests can be found in Appendix B.

These conclusions must be qualified with a not about the data. The records chosen were manually selected from a large population of records available at Physionet, and were heavily edited beyond their initial condition due to outlier removal. As such, the data is the result of a selective process involving the selection of high-quality records (prominent R and T features) and removal of inconsistent and detrimental data points. As such, the data used and conclusions drawn are only applicable to the data used here and may not be able to be extrapolated to the population at large.

After receiving these results, it became necessary to compare them to the results obtained by Dr. Berger in his validation of the method, but he did not perform any comparable statistical analyses comparing his QT interval values to an accepted method of calculating the QT interval. In his paper [1], he reports only on the reproducibility of his results, and their comparison to heart rate variability, which does not address the issue of whether or not the intervals being reported by the method are accurate. It reports the coefficient of variation, given by the standard deviation over the mean, as 0.22 for the QT interval in 30 patients. From this thesis' results, an average QT coefficient of variation is shown as 0.034, however, this sample population was much smaller (four records), and his sample population contained patients with no organic heart disease, patients with

coronary artery disease, and nonischemic dilated cardiomyopathy, so as such, the patient populations are different and are not suitable to be compared to each other.

3.2 Comparative Analysis

Section 3.2 presents the steps taken to perform the power spectral analysis using the template-matching method. 3.2.1 discusses the sample selection criteria, 3.2.2 discusses the processes involved in analyzing the data, and 3.2.3 discusses the results and notes any observations made about the data analysis.

Data analysis was performed to investigate the power spectra of the interpolated QT interval signal. Investigations were carried out with respect to two main concerns – self-similarity and health vs. illness.

3.2.1 Sample Selection

Samples for the data analysis portion were selected using slightly different criteria than for validation. A total of 21 records were initially selected from the Physionet databases – 9 from the normal sinus rhythm database (NSR), 6 from the congestive heart failure database (CHF), and 6 from the arrhythmia database (ARR). Out of these records, 10 were rejected for various reasons. Two records were rejected because there was significant intermittent signal noise, probably created by a nearby machine being turned off and on. This created difficulties in the error function tabulating a reliable measurement for many of the beats in the signal, and reduced the initially 500 beat records down to a small number of useable QT intervals (10 and 13 respectively). Five were rejected due to latent 60 Hz noise that was of such a high voltage that it dwarfed the

T wave morphology, and made template matching impossible. Three were removed due to significant events of either arrhythmia or other ventricular incidents such as temporary fibrillation. This created difficulties of the template-matching algorithm to pick an appropriate QT interval length, and since the incidents happened frequently, the manipulations necessary to create a useable signal were very involved, and would represent a severely manipulated version of the interpolated signal, with the majority of the intervals being created by processes other than the template matching method. After these ten files were removed, twelve records remained – three ARR records, four CHF records, and four NSR records.

The ARR records were recorded from patients experiencing continues or sporadic arrhythmias. The records used were 100, 102, and 103. The CHF records were taken from patients with severe congestive heart failure. Patients exhibited changes in QRS complex morphology, but the morphologies were consistent throughout the record, and as such, their records were used to test the method's ability to compute the QT interval length on non-standard morphologies. The records used were 01, 02, 05, and 06 as found online at www.physionet.org. The normal records were taken from patients with natural normal sinus rhythm. They ranged from youthful patients with no history of heart disease to patients on medications affecting cardiac health, but still considered healthy by physicians. The records used for analysis were 16265, 16273, 16483, and 16539.

After these records were selected, they were run through the template-matching algorithm to generate the interpolated signal to later be analyzed. Unfortunately, the CHF records provided a problem. Since the ECG morphology was so drastically different than the standard ECG morphology witnessed in healthy patients, the template-matching

process failed. The general shape of the ECG was an inverted R wave, normal ST

interval, and a small T-wave following. The key reason for this failure was the lack of a

defined T-wave. This meant that the algorithm was comparing only the rise from the R

trough to the T wave, which was so small in some cases it was invisible. The matching

procedure returned outliers for almost all beats in the CHF records. For this reason, all

CHF records were excluded from the data analysis. This does not mean that CHF patients

with drastically non-standard morphologies cannot use this type of method for calculating

QT variability, but that the records that were selected were unable to be used because no

single lead contained the necessary information for the calculation process.

This meant that there could be no evaluation of the method for non-standard

morphologies, and only comparisons can be made between patients with arrhythmias and

normal sinus rhythms to see if frequency content is the same. The analysis process is

explained in detail below.

3.2.2 Processes

This section consists of three main parts – analysis performed on the signals before

outliers are removed, analysis with removal and no replacement, and analysis with outlier

removal and average replacement.

First, the interpolated QT signal with outliers intact was analyzed utilizing a

MATLAB script called `analysis.m`. The first step of the analysis program is to rectify

the signal to a number of points equivalent to 2^n. This maximizes the efficiency of the

Fast Fourier Transform (FFT), which is the method of obtaining the power spectrum used

in this thesis. If the signal is longer than 65536 points, it truncates the signal to that

length. If it is shorter, the signal gets zero-padded up until that number of points. This is to ensure there is sufficient resolution, due to the fact that the areas of import to this work are of a very low frequency (0.05-0.4 Hz). Without zero-padding, there are only a few points within that range, and as such, one can only tell the greatest of differences in the records. With the zero-padding, the time of the interpolated signal is increased, and the signal therefore has more data points between 0.05 and 0.4 Hz. This is due to a property of Fourier transforms that states

$$\frac{\text{Hz}}{\text{point}} = \frac{1}{\text{length of signal (sec)}}.$$
(3.4)

Next, the program obtains the FFT of the signal, and begins to compute the summed power bands of the signal. Two different groups of sums are calculated. The first group sums the power spectrum from 0.05 to 0.15 Hz and from 0.15 to 0.4 Hz. These are the traditional two bands used for heart rate variability analysis. Since this thesis partially aims to compare QT variability to heart rate variability, these numbers will be useful. The second group of summations is a seven band decomposition of the power spectrum. Bands are summed at intervals of 0.05 Hz. In addition, the power spectrum is graphed for visual inspection.

For the records where outliers are simply removed, the process is as follows. The interpolated signal is taken from the file ias.m, outliers are identified, and then those intervals containing outliers are removed from the signal. The blank spaces where the outliers were are removed, and the signal is effectively shortened. The new interpolated signal is now put through the same process as above.

In the case where the outliers are replaced with an averaged value, the process is slightly different. This process is automated, as opposed to the manual removal of

outliers previously discussed. The procedure is carried out in a MATLAB script

`rectify.m.` This program first finds the outliers. This is done by a simple check for the

minimum value of the signal. The operator, however, must check if the record needs

rectification, or else valid intervals will be removed simply because they are the lowest

interval value encountered. After this value is set aside for exclusion, the program finds

all occurrences of this value, and stores their position in an array. Next, this array is

parsed to compile an array, `position`, of interval start points and end points. This is

achieved by checking if the next point in `position` is one plus the current value in

`position`. If it is, the function continues. If not, it then marks the current point as the

end of the interval, and the next point as the start of an interval.

After these interval boundaries are identified, the surrounding values are found,

and an average of them is taken. Next, the script replaces the values in between the two

boundary points with this average. This is performed for all intervals containing the

exclusion value. After this rectification process is performed, data analysis steps as

discussed above are performed to obtain the summed power spectra. The code of

`rectify.m` is available in Appendix A.

These analyses were conducted with two aims in mind. The first is to compare the

normal sinus rhythm records to the arrhythmia records to see if there is any quantifiable

difference in power spectra. The idea for this comparison is seated deep within cardiac

interval measurement. In heart rate variability, comparisons are routinely made between

healthy individuals and sick individuals, or individuals at rest in comparison to rest,

sleep, meditation, or other different states [8]. In addition, it has been shown that QT

interval variability changes after surgery, indicating that autonomic nervous system

function plays an important role in QT interval regulation [9, 17]. Researchers [1, 11, 12, and 18] have also shown that QT variability differs with different disease states in comparison to healthy subjects.

The second purpose of analysis was to judge statements made by some researchers [13, 14] that QT interval predictability is high within subjects, but low between subjects. More specifically, they assert that the QT-RR relationship is stable between records of a single patient, but quite variable between subjects. This method was tested in a round about way – breaking a single six-minute record into four 150 second parts and viewing the power spectra for similar patterns.

3.2.3 Conclusion

The data analysis conducted yielded some expected and some unexpected results. Patterns were observed in both two-band and seven-band power spectra summations, which will be discussed presently.

As seen in figures 3.1 and 3.2, the arrhythmia data shows evidence of a general pattern to QT interval power spectra. In the two-band summation, it appears that the high frequency (HF) region tends to be higher than the low frequency (LF) region. Using Student's T-test, the mean value of the HF region is significantly larger than the LF at the 0.05 significance level. In addition, when one looks at the seven-band summation, there is a general shape of high power in the lower frequencies, sloping to the lowest power in the higher end of the frequency range.

ARR Power
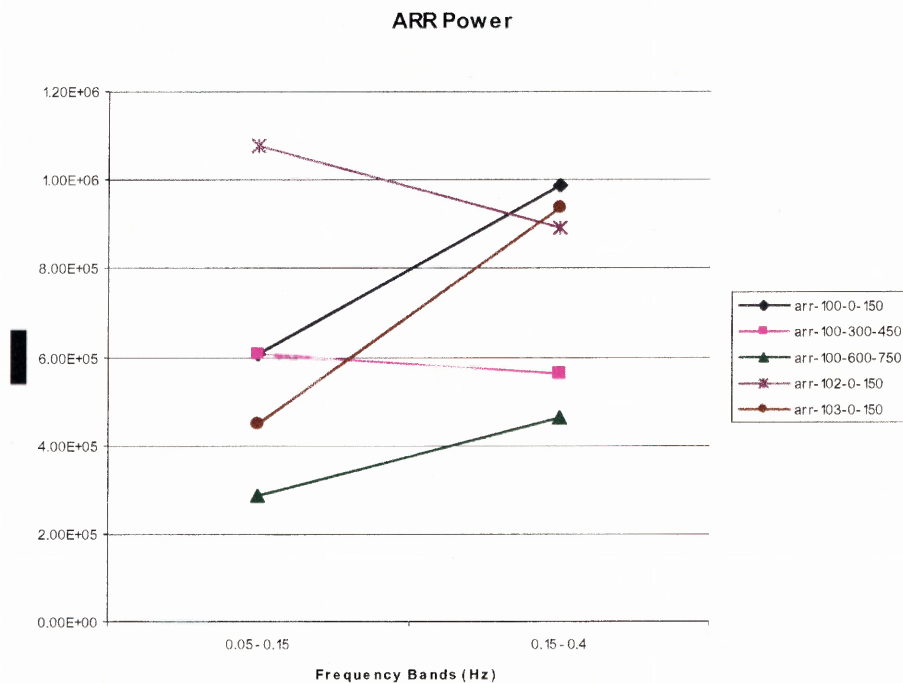
Figure 3.1 Uncorrected Arrhythmia Power (Two-Band).

ARR Power
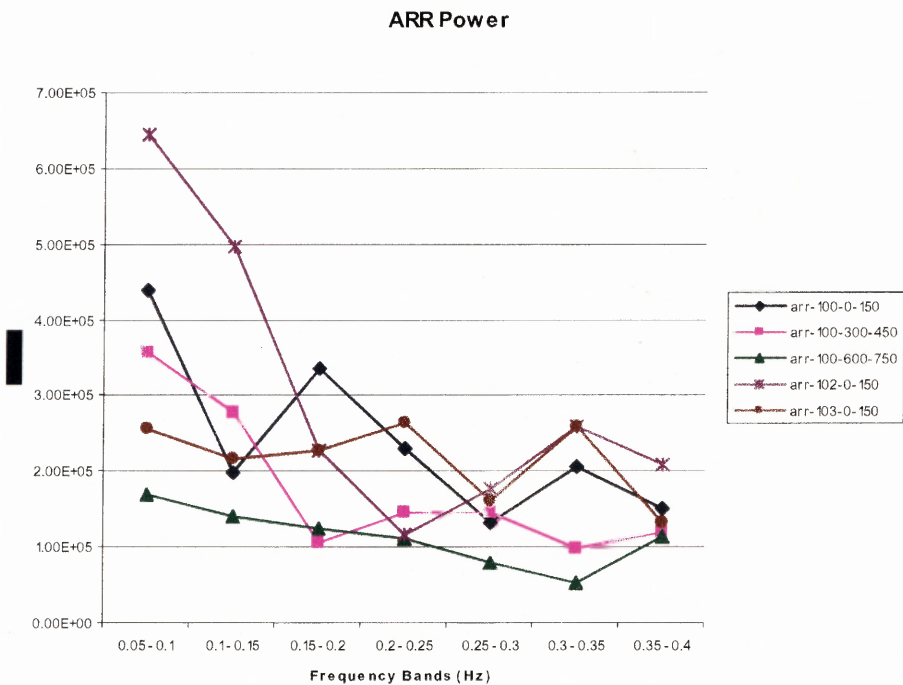
Figure 3.2 Uncorrected Arrhythmia Power (Seven-Band).

When the outlier corrected power spectra (figures 3.3-3.6) are viewed, the results are slightly more encouraging than uncorrected. Specifically, figure 3.4 shows the corrected power spectra for arrhythmia patients without replacing the outlying interval with an average. It can be seen that each individual record has a distinct shape, though the reasons for these differences of similar records is unknown at this time. Replacement corrects this occurrence, and returns the shape of the power spectrum to that obtained in the records without outlier removal. One interesting note that the record arr-102 is quite different from the others in both corrected graphs (figures 3.4 and 3.6) as it shows a very high power level in the upper regions of the frequency range (0.25-0.4). As can be seen in the figures 3.2, 3.4, and 3.6, arr-102 shows different behavior, giving some weight to the argument that QT interval variability differs greatly between subjects.
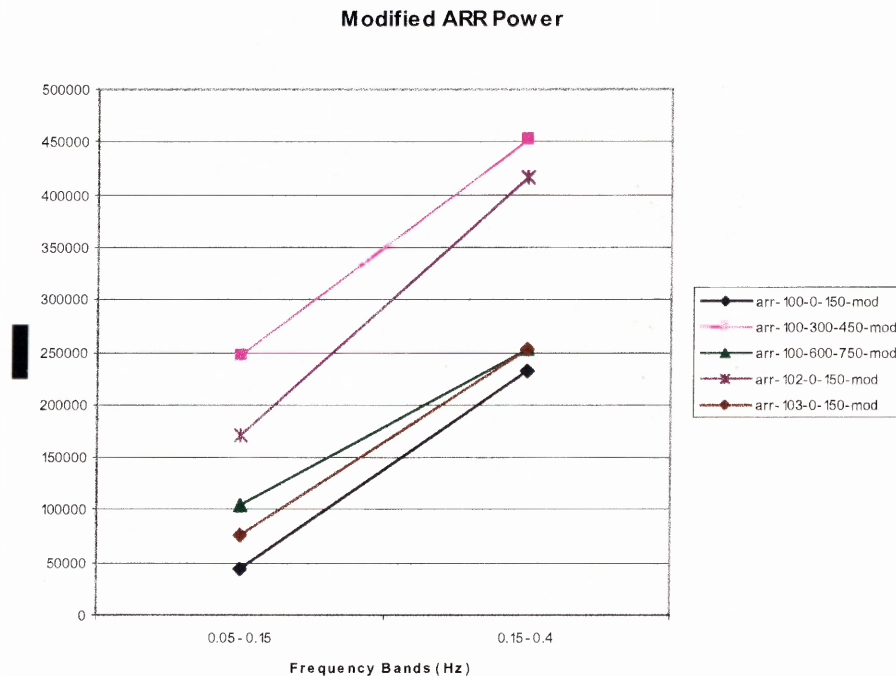
Modified ARR Power

Figure 3.3 Corrected ARR Power - no replacement, two-band.
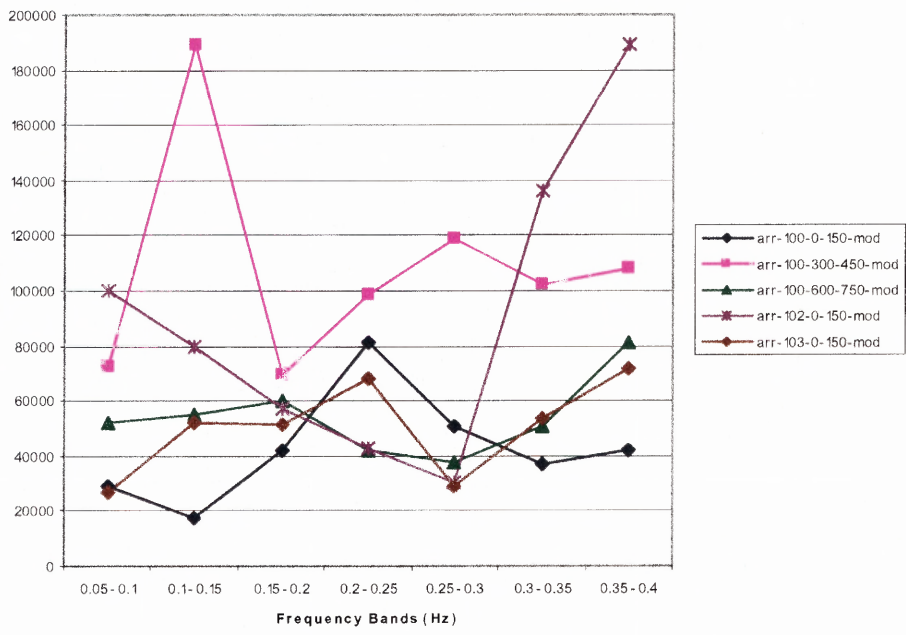
Modified ARR Power

Figure 3.4 Corrected ARR Power - no replacement, seven-band.

Modified ARR Power
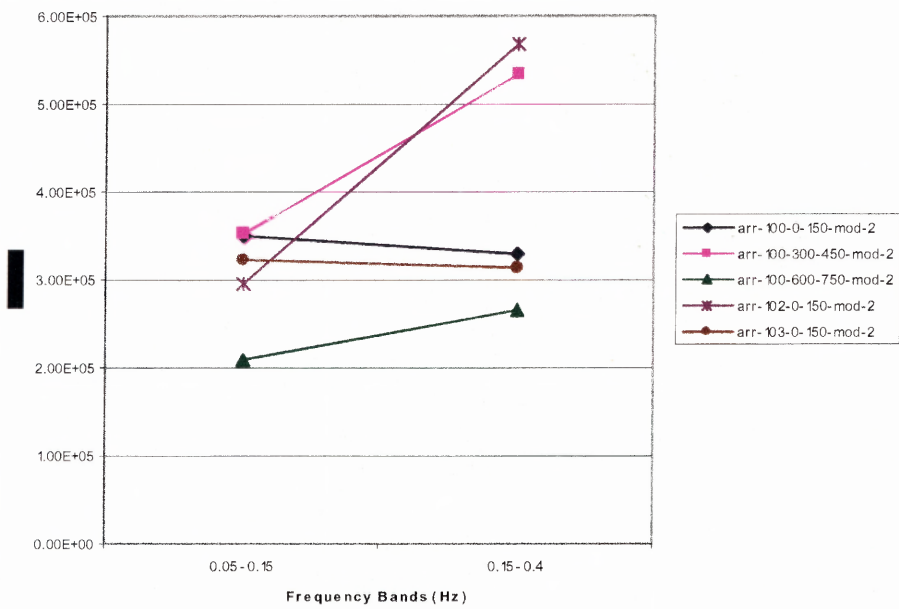
Figure 3.5 Corrected ARR Power - replacement, two-band.

Modified ARR Power
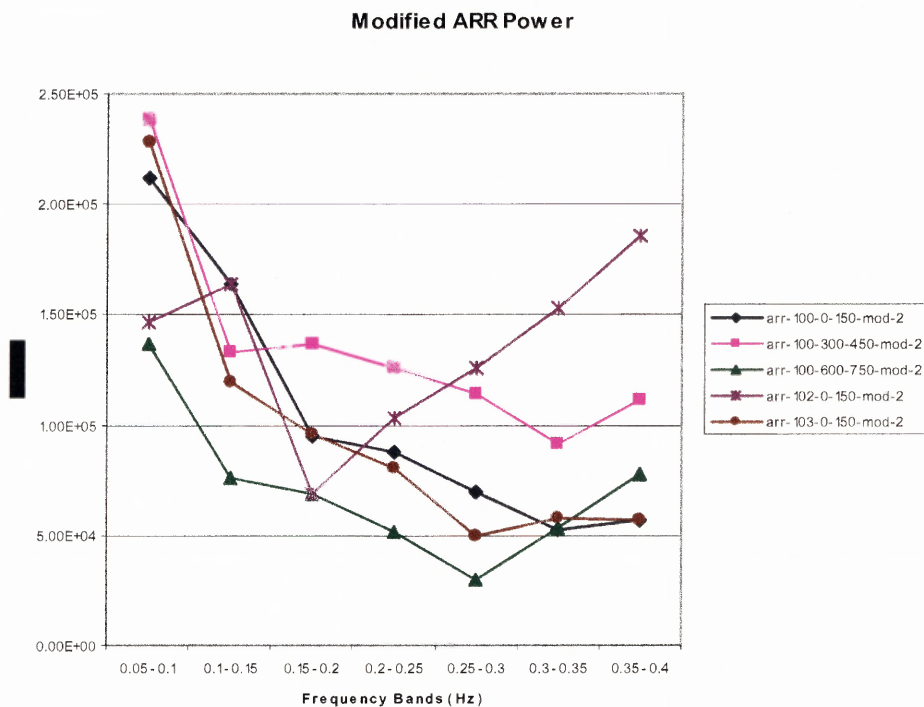
Figure 3.6 Correct ARR Power - replacement, seven-band.

Normal sinus rhythm records yielded similar results with data analysis, as shown in figures 3.7-3.12.
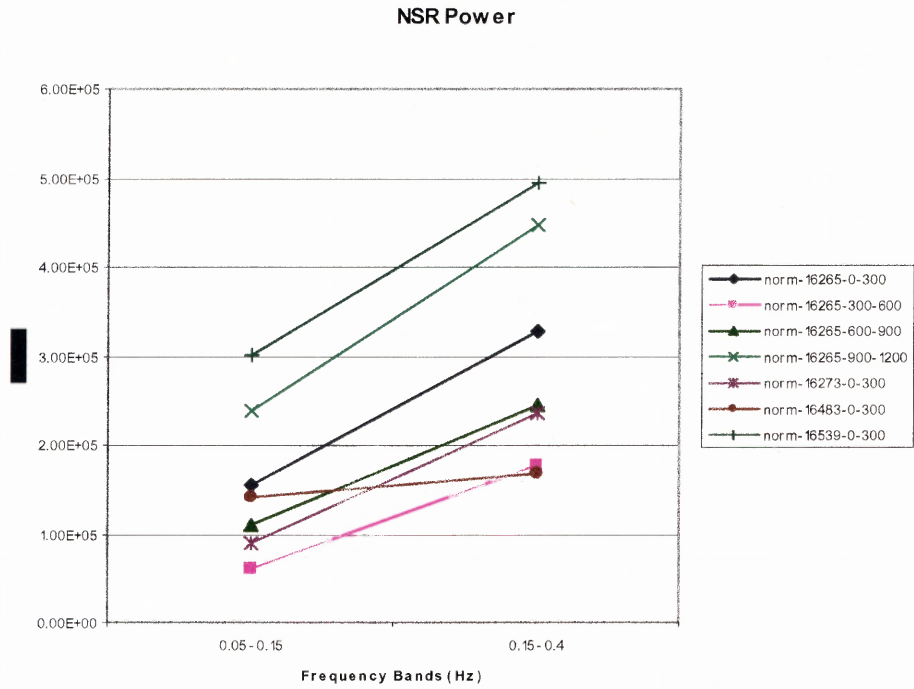
NSR Power

Figure 3.7 Uncorrected Normal Sinus Rhythm Power – two-band.
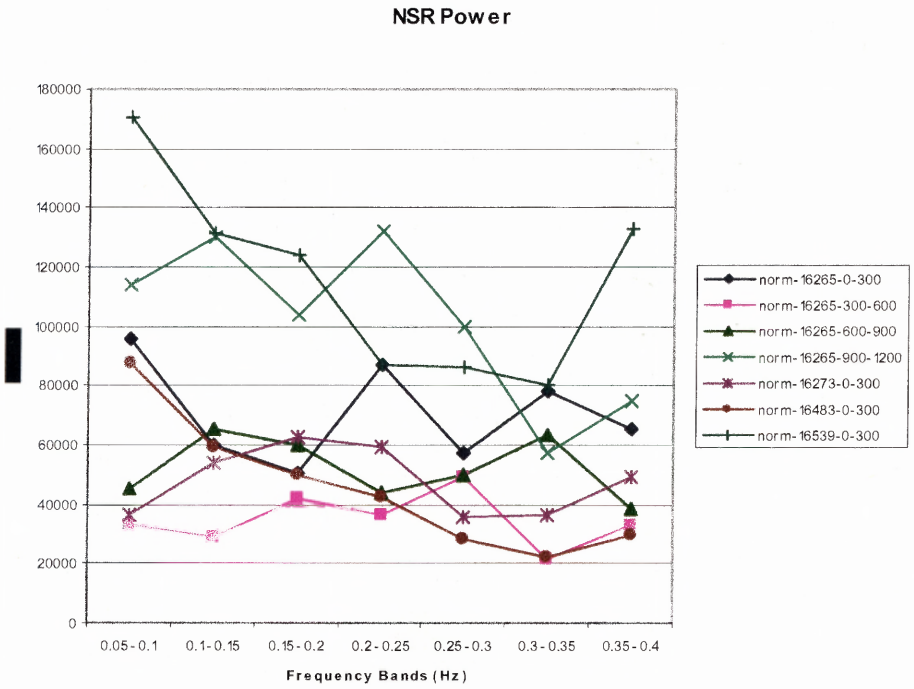
NSR Power

Figure 3.8 Uncorrected NSR Power - seven-band.

Modified NSR Power
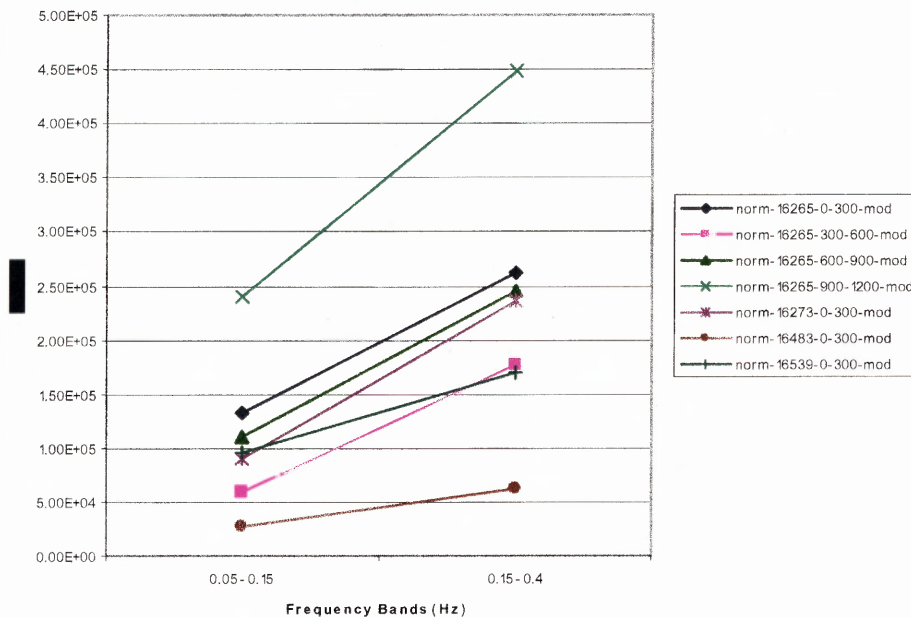
Figure 3.9 Corrected NSR Power - no replacement, two-band.
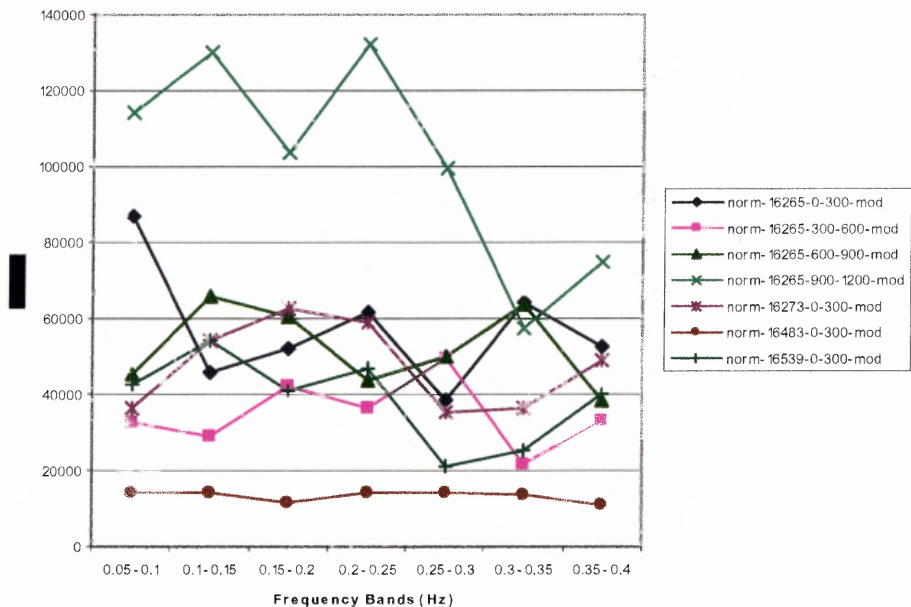
Modified NSR Power

Figure 3.10 Corrected NSR Power - no replacement, seven-band.
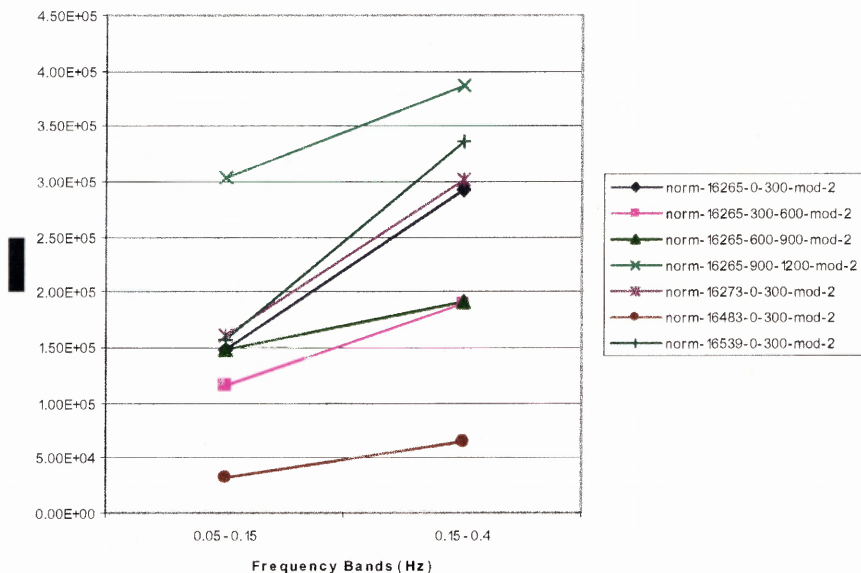
Modified NSR Power

Figure 3.11 Corrected NSR Power - replacement, two-band.

Modified NSR Power
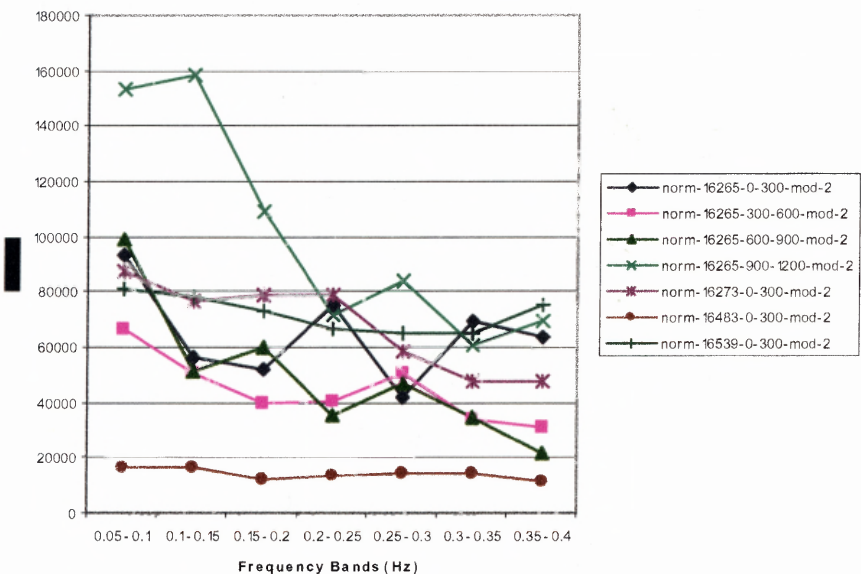
Figure 3.12 Corrected NSR Power - Replacement, seven-band.

Figures 3.13 and 3.14 show averaged values for the seven-band summation of the power spectra. Here, the patterns of both patients with arrhythmia and with normal sinus rhythms can be seen, as well as the effects of correction. It is interesting to note that when outliers are removed, but no averaged value is replaced, the power spectra become very equally distributed.

Average Power Spectra of Patients with Arrhythmia
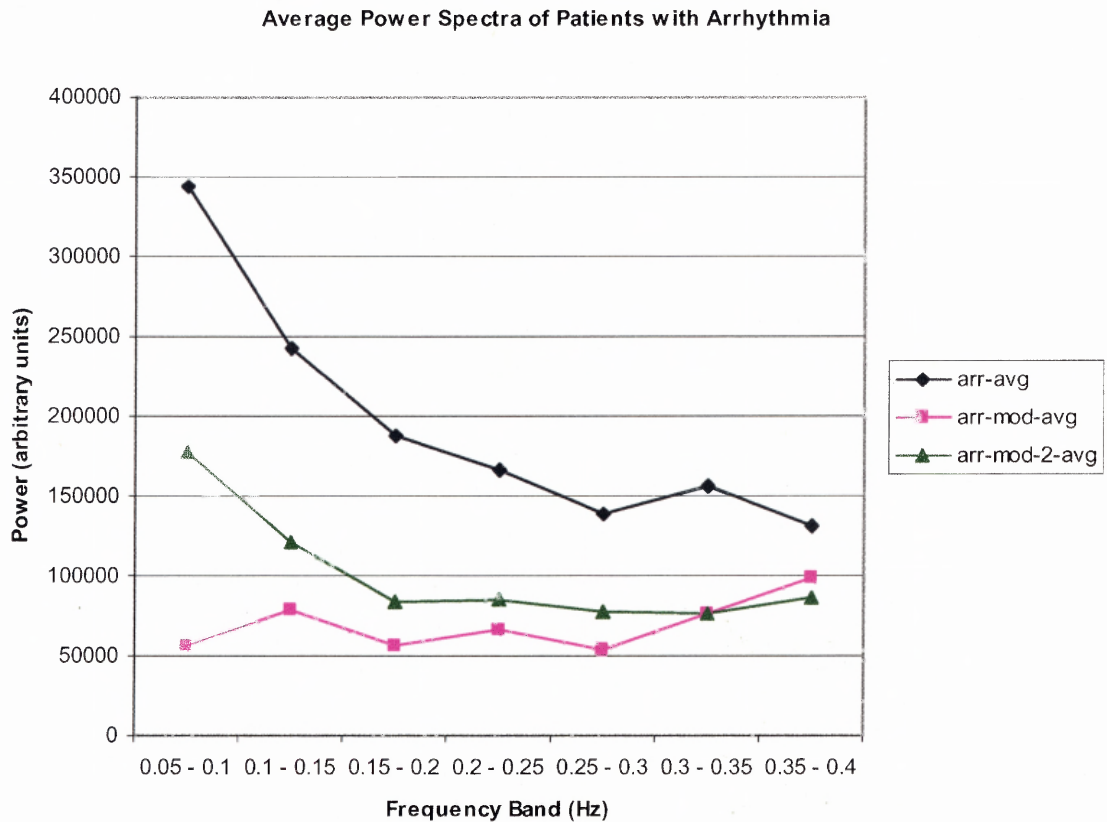
Figure 3.13 Average ARR Power Spectra.

Average Power Spectra of Patients with Normal Sinus Rhythm
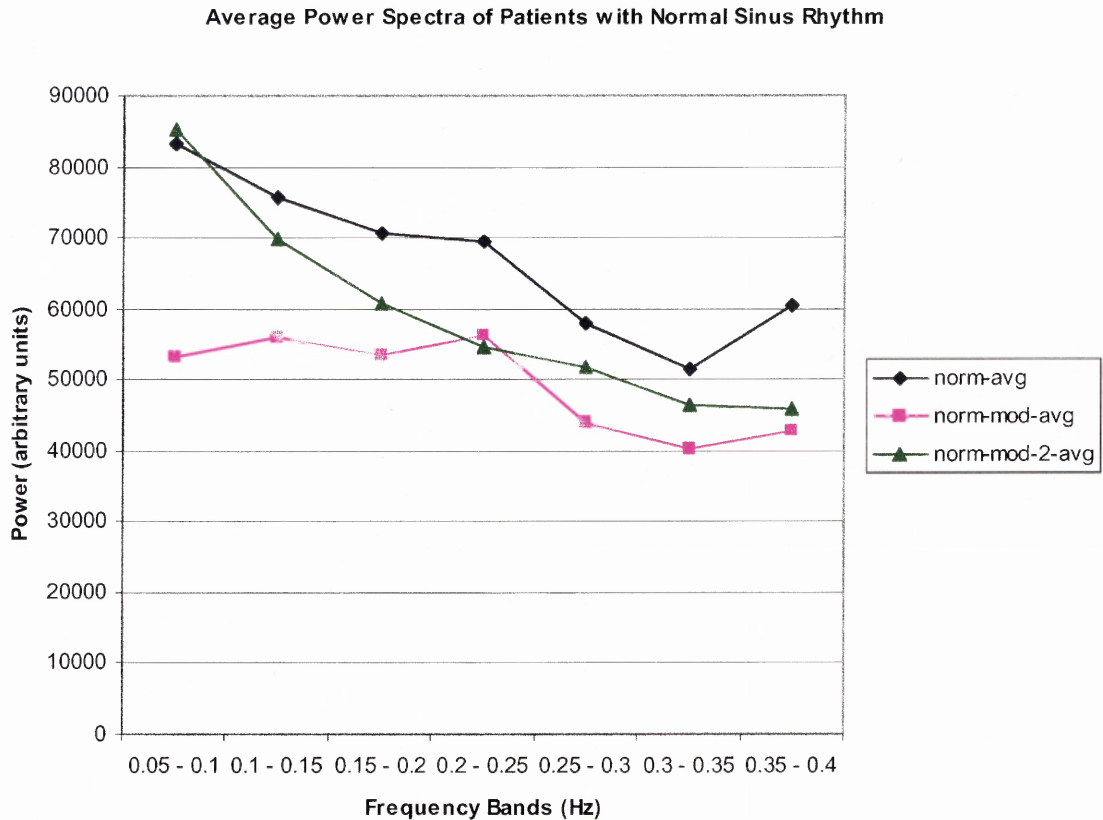
Figure 3.14 Averaged NSR Power Spectra.

From these figures, and the data presented in Appendix B, it can be seen that the power

spectral analysis did not yield obviously different spectra between patients with

arrhythmias and those with a normal sinus rhythm with respect to shape; that said, the

power spectral analysis did show some patterning with the QT power spectrum. (A

detailed method for analyzing these data for differences is presented in section 3.3.) After

replacement of the outlying intervals with an average, the arrhythmia patients show high

power content between 0.05-0.15 Hz, and then an evening out of the curve between 0.15-

0.4 Hz, while the normal sinus rhythm patients show a steady decrease in power from

0.05-0.4 Hz. In addition, arrhythmia records exhibited higher frequency power than

normal sinus rhythm records (on the order of four times higher). This is especially interesting considering that the NSR records were twice as long as the arrhythmia records (300 seconds vs. 150 seconds).

However, these results are not entirely encouraging. The individual records show little similarity to these averaged curves, and the steps taken to correct the outlying intervals have not indicated whether they had brought the power spectra closer to their actual values or not. There are two possible reasons for this. One simple option is to declare the template-matching algorithm non-functional. However, this method ignores the fact that many researchers [10, 15, 18, 19] have used this template-matching algorithm effectively in their respective research. The second possible cause for the failure of the data analysis could be the files themselves. Some of the records experienced state changes in the middle of the record; however, these points were not properly identified, such as changes to paced breathing, drug delivery, or cardiac episodes such as mild tachycardia. These influence the records to be a combination of QT interval variability during multiple states, in which case the records themselves do not accurately reflect the categories they are a part of. Once again, these conclusions are made with respect to the fact that the data used is highly selective and accordingly, the conclusions presented herein are only useful for the purposes explicitly stated.

3.3 Discussion of Future Work

It is clear that much work needs to be done on QT variability. The author proposes many suggestions for further work on this subject. First is modifications to the template-matching algorithm. One example could be resampling the ECG data to a standardized,

high frequency version (for example, taking the 360 Hz MIT records and resampling them at 1000 Hz). This may prevent resolution issues with matching the QT interval. When the template matching algorithm works, it picks the best alpha value, and then judges how many points it would take to replicate the interval value in the interpolated signal. When the sampling frequency is low, the algorithm must choose the number of points closest to the calculated value. A higher sampling frequency will allow more freedom for the algorithm to properly identify the QT interval.

Another aspect of algorithm modification would be to add a second step to the scaling. In addition to stretching the template along the time axis, the template can also be scaled across the voltage axis. Though this step may be trivial, and may not add much to the ability of the algorithm to find the QT interval, it may be able to cope with changes in T-wave morphology within the record more easily. This method would run through each prescribed stretch-interval as the algorithm does now, but for each iteration, it would also scale the wave larger or smaller along the y-axis, which will pinpoint the exact dimension of the QT interval in relation to the template. This may also lead to some correlation between vertical variability and health, though this is only speculations.

Additionally, there are some questions about the algorithm's details. For example, Dr. Berger chose 50 ms to remove from the signal beyond the R-peak to eliminate the QRS complex, however, this process has shown to be ineffective. When the 50 ms are removed, typically, portions of the R peak were left, and in almost all cases, the S wave was remaining in the signal. From the S minima onward until the T-wave is a useful interval, however, the inclusion of parts of the R-peak only adds to the difficulty in calculating a reliable error number. A larger period, such as 100 or 120 milliseconds is

most likely a more appropriate number if the intent is to remove the QRS complex. This does however reduce this method to less of a measure of QT variability, and more a measure of T-wave variability.

The second suggestion for further work involves the samples chosen for analysis. The pre-recorded signals available at Physionet were used solely because of their quick availability. As stated earlier, patients with normal sinus rhythm were not all healthy, just possessing a normal contraction sequence and no obvious arrhythmias. This presents a problem because the control group of this small data study really was a conglomeration of various types of patients and records, which makes comparative analysis much more difficult. In addition, the disease population, patients with arrhythmias, may not be the best group to contrast against a healthy patient. Perhaps patients with long-QT syndrome or post-MI subjects may provide larger differences in QT interval times. Also, a younger subject population might be better, because in general, young people are healthier, and when there is one health problem, there is a higher chance that it is not compounded by other health factors, either known or unknown.

One step left untouched by this thesis is the quantification of differences between patients with arrhythmias and those with normal sinus rhythms. A method for determining these differences is presented below. First, all data collected on patients with arrhythmias and patients with normal sinus rhythms is broken into three groups – uncorrected, corrected without replacement, and corrected with replacement. Next, these are grouped into 2-band summations and 7-band summations. From this, three tests can be performed. First, using the first records in each set (nsr16273 and arr100), t-tests can be utilized to judge how self similar the signals are (as these records already contain four

different sections of data from the same patient and same record). After that, the averaged signals of the arrhythmia and NSR data can be normalized and subtracted to create an error function. This error function can then be squared to provide the maximization of difference, and then statistically analyzed to tell how different these two sets of numbers are from each other. This will allow future researchers to learn where within the frequency spectrum the greatest differences between sick and healthy patients lie. A final step would be to take all the data in one set (arrhythmia or normal sinus rhythm) and compare the records to each other statistically to determine any trending information.

Another step that can be taken in this direction is the spectral analysis of IIBI signals generated from the Physionet data directly, and then a comparison against the data taken from the Berger method. If the two sets of spectral data are similar, then it will lend some insight into the power content of QT variability, however if they differ considerably, this may show that the Berger method is an ineffective process for accurately calculating the QT interval.

On a final note, this new field of research shows much promise of giving insight into autonomic nervous function in tandem with and apart from heart rate variability. Whether or not the template matching techniques presented here will be of importance is not known to the author; however, this method deserves more attention in the future, as it is a quick and simple method for calculating QT variability.

APPENDIX A

PROGRAM MATERIALS

A.1 – Compare.m MATLAB Code

```
function [alpha_match] = compare(ECG,RPOS,QT_template,f_s)

o_len = length(QT_template); % length of 'QT_template'
e_a = []; % NULL error array
a_a = []; % NULL alpha array
c = 1; % counter
SCALE_A = [];

for alpha = 1.35:-0.0001:0.65
    c_len = o_len * alpha; % new length of scaled array

    % create scaled array
    if isinteger(c_len)
        c_len = c_len;
        true_alpha = alpha;
    else
        c_len = floor(c_len);
        true_alpha = c_len / o_len;
    end

    QT_scaled = [];
    for i = 1:1:c_len
        j = i / alpha;
        j = floor(j) + 1;
        if j <= o_len
            QT_scaled(i) = QT_template(j);
        else
            QT_scaled(i) = QT_template(o_len);
        end
    end
    % plot(QT_scaled)
    % hold all

    % compare template to ECG
    point = RPOS; %RPOS(6); % R BEAT NUMBER --- SET TO SIX AS EXAMPLE
    delay = int16(floor(((f_s / 1000) * 50)));
    begin = point + delay;
    take = int16(begin) + int16(c_len);
    comp_a = ECG(begin:take); % select ECG data; length of scaled
template
%       plot(comp_a)
%       hold all
    total_e2 = 0;
    if (c_len > length(comp_a))
        int_len = length(comp_a);
    else
```

```
            int_len = c_len;
        end
        for i = 1:1:int_len
            error = comp_a(i) - QT_scaled(i);
            e2 = error^2;
            total_e2 = total_e2 + e2;
        end
        a_a(c) = true_alpha;
        e_a(c) = total_e2;
        c = c + 1;
end


% error vs. alpha array creation
e_a = rot90(e_a);
a_a = rot90(a_a);
% figure('Name','QT Error Function (All)')
% plot(a_a, e_a)
% hold all


mini = min(e_a); % find lowest error
position = strmatch(mini, e_a); % find position in array of 'min'
h = size(position);
if h(1) ~= 1
    position = position(1);
end
alpha_match = a_a(position) % find corresponding alpha value
```

A.2 – IAS.m MATLAB Code

```
% File I/O
QT_file = 'C:\val\qt\sel16483.txt';
QT_template = load(QT_file); %4open data file into 'QT_template' array
ECG_file = 'C:\val\sel16483-mod.txt';
ECG = load(ECG_file);
RPOS_file = 'C:\val\rbi\sel16483.txt';
RPOS = load(RPOS_file);
f_s = 250;


ar = [];
for a = 1:1:(length(RPOS)-1)
    alpha_out = compare(ECG,RPOS(a),QT_template,f_s);
    ar(a) = alpha_out;
end


IQTS = []; % interpolated alpha signal
VA = []; % DIAGNOSTIC PURPOSES
p = 1; % position
base_time = (length(QT_template) * f_s);
fms_offset = 0.050 * f_s;
base_time = length(QT_template);
for a = 1:1:length(ar)
    value = ar(a);
    value = base_time * value;
    value = value + fms_offset;
```

```
        VA(a) = value / 250;
        for b = 1:1:value
            IQTS(p) = value;
            p = p + 1;
        end
end

avg = mean(IQTS);
for a = 1:1:length(IQTS)
    IQTS(a) = IQTS(a) - avg;
end

dlmwrite('C:\iqts.txt',IQTS, 'delimiter', '\n');

figure('Name','Interpolated QT Signal')
plot(IQTS) % recentered interpolated signal

figure('Name','RT interval lengths')
plot(VA)
```

A.3 – Rectify.m MATLAB Code

```
% file array
f_array = struct('filename','N','f_s','F');

%Contents of file array

for count = 1:1:13
    IQTS_file = strcat('c:\rec\iqts_mod2\', f_array(count).filename,
'.txt'); % Interpolated QT signal
    IQTS = load(IQTS_file);
    f_s = f_array(count).f_s; % sampling frequency

    points = length(IQTS); % length of signal file

    new_array = [];
    if points < 65536
        new_array = IQTS;
        for a = 1:1:(65536-points)
            new_array(points+a) = 0;
        end
    end
    IQTS = new_array;
    points = length(IQTS);

    time = points / f_s; % time of signal file in seconds
    hz_pt = 1 / time; % Hertz per point
    lb = floor(0.05 / hz_pt); % index for 0.05 Hz
    mb = round(0.15 / hz_pt);% index for 0.15 Hz
    ub = ceil(0.40 / hz_pt); % index for 0.40 Hz

    fft_iqts = fft(IQTS); % fast fourier transform of IQTS
    mod_fft = fft_iqts(lb:ub); % fft between 0.05-0.40 Hz
```

```
    mod_fft = abs(mod_fft);

    % adjust boundaries to new fft array
    mb = floor(mb - lb);
    ub = floor(ub - lb);
    ab = floor(round(0.10 /hz_pt) - lb);
    cb = floor(round(0.20 / hz_pt)- lb);
    db = floor(round(0.25 / hz_pt) - lb);
    eb = floor(round(0.30 / hz_pt) - lb);
    fb = floor(round(0.35 / hz_pt) - lb);

    figure('Name','FFT between 0.05 and 0.4 Hz')
    plot(mod_fft)

    % 2-band sum
    l_sum = sum(mod_fft(1:mb));
    u_sum = sum(mod_fft(mb:ub));

    % 7-band sum
    a_sum = sum(mod_fft(1:ab));
    b_sum = sum(mod_fft(ab:mb));
    c_sum = sum(mod_fft(mb:cb));
    d_sum = sum(mod_fft(cb:db));
    e_sum = sum(mod_fft(db:eb));
    f_sum = sum(mod_fft(eb:fb));
    g_sum = sum(mod_fft(fb:ub));

    % output array
    out = [l_sum u_sum a_sum b_sum c_sum d_sum e_sum f_sum g_sum]
    file_out = strcat('C:\out\mod2\out_', f_array(count).filename,
'.txt');
    dlmwrite(file_out, out, 'delimiter', '\t');
end
```

A.4 – Analysis.m MATLAB Code

```
% file array
f_array = struct('filename','N','f_s','F');

% Contents of File Array

for a = 1:1:13
    file_string = strcat('c:\rec\iqts\', f_array(a).filename, '.txt');
    file = load(file_string);

    exclude = min(file); % value of outlier
    position = strmatch(exclude, file); % find location of outlier

    % this section blocks out groups of outliers for replacment
    count = 1;
    beg_array = []; % array to find blocks of outliers
    end_array = [];
```

```
    beg_array(1) = position(1); % assign first instance of outlier to
first value in array
    for b = 1:1:length(position)
        if b+1 <= length(position)
            if (position(b) + 1) == position(b + 1)
                b;
            else
                end_array(count) = position(b);
                count = count + 1;
                beg_array(count) = position(b + 1);
            end
        end
    end
    end_array(count) = position(length(position));


    % this section replaces outliers with the average of neighboring
values
    for c = 1:1:length(beg_array)
        pos1 = beg_array(c) - 1;
        pos2 = end_array(c) + 1;
        if pos1 > 1
            val1 = file(pos1);
        else
            val1 = val2;
        end
        if pos2 < length(file)
            val2 = file(pos2);
        else
            val2 = val1;
        end
        average = (val1 + val2)/2;
        for d = beg_array(c):1:end_array(c)
            file(d) = average;
        end
    end


    % truncate erroneous tail of file
    for e = 1:1:length(file)
        f = length(file)-e;
        g = f - 1;
        if file(f) ~= file(g)
            file2 = file(1:g);
            break
        end
    end


    % write to new file
    file_out = strcat('C:\rec\iqts_mod2\', f_array(a).filename,
'.txt');
    dlmwrite(file_out, file, 'delimiter', '\n');
end
```

APPENDIX B

DATA

B.1 – Statistical Validation Data

This section gives the QT intervals in seconds obtained from the template-matching algorithm (BERG), and the annotated Physionet records (PHYS). Absolute differences and percent differences are given, in addition to T- and Z- test scores.

Record – sel231

BEAT	BERG	PHYS	ABS DIFF	% DIFF
1	0.430	0.460	0.030	6.522%
2	0.438	0.460	0.022	4.783%
3	0.470	0.460	0.010	2.174%
4	0.430	0.464	0.034	7.328%
5	0.470	0.456	0.014	3.070%
6	0.438	0.456	0.018	3.947%
7	0.478	0.480	0.002	0.417%
8	0.438	0.456	0.018	3.947%
9	0.438	0.452	0.014	3.097%
10	0.466	0.460	0.006	1.304%
11	0.434	0.444	0.010	2.252%
12	0.430	0.468	0.038	8.120%
13	0.462	0.452	0.010	2.212%
14	0.422	0.432	0.010	2.315%
15	0.430	0.456	0.026	5.702%
16	0.434	0.440	0.006	1.364%
17	0.430	0.456	0.026	5.702%
18	0.478	0.428	0.050	11.682%
19	0.430	0.444	0.014	3.153%
AVG	0.445	0.454	0.019	4.163%
STDEV	0.019	0.012	0.012	2.801%

T-test   -1.80918

Threshold	P	Z-score
0.03	0.0352	1.8094
0.05	0.9037	-1.3031
0.1	1.0000	-9.0845

Record – sel16273

BEAT	BERG	PHYS	DIFF	% DIFF
1	0.322	0.316	0.006	1.899%
2	0.330	0.320	0.010	3.125%
3	0.318	0.320	0.002	0.625%
4	0.306	0.328	0.022	6.707%
5	0.270	0.324	0.054	16.667%
6	0.306	0.324	0.018	5.556%
7	0.278	0.320	0.042	13.125%
8	0.294	0.328	0.034	10.366%
9	0.294	0.316	0.022	6.962%
10	0.298	0.324	0.026	8.025%
11	0.294	0.324	0.030	9.259%
12	0.310	0.328	0.018	5.488%
13	0.306	0.312	0.006	1.923%
14	0.294	0.320	0.026	8.125%
15	0.306	0.328	0.022	6.707%
16	0.310	0.328	0.018	5.488%
17	0.298	0.324	0.026	8.025%
18	0.306	0.324	0.018	5.556%
19	0.302	0.324	0.022	6.790%
20	0.282	0.328	0.046	14.024%
21	0.294	0.328	0.034	10.366%
22	0.306	0.324	0.018	5.556%
23	0.306	0.324	0.018	5.556%
24	0.294	0.324	0.030	9.259%
25	0.298	0.320	0.022	6.875%
26	0.306	0.332	0.026	7.831%
27	0.282	0.324	0.042	12.963%
28	0.270	0.324	0.054	16.667%
29	0.282	0.320	0.038	11.875%
30	0.310	0.324	0.014	4.321%
31	0.250	0.320	0.070	21.875%
32	0.306	0.324	0.018	5.556%
AVG	0.298	0.323	0.027	8.223%
STDEV	0.016	0.004	0.015	4.660%

T-test   -8.65013

Threshold	P	Z-score
0.03	0.0000	6.3401
0.05	0.0000	3.9124
0.1	0.9845	-2.1569

Record – sel16420

BEAT	BERG	PHYS	DIFF	% DIFF
1	0.378	0.368	0.010	2.717%
2	0.366	0.364	0.002	0.549%
3	0.346	0.360	0.014	3.889%
4	0.370	0.360	0.010	2.778%
5	0.370	0.360	0.010	2.778%
6	0.362	0.372	0.010	2.688%
7	0.342	0.376	0.034	9.043%
8	0.362	0.360	0.002	0.556%
9	0.370	0.364	0.006	1.648%
10	0.354	0.396	0.042	10.606%
11	0.378	0.364	0.014	3.846%
12	0.378	0.364	0.014	3.846%
13	0.366	0.360	0.006	1.667%
14	0.354	0.364	0.010	2.747%
15	0.370	0.364	0.006	1.648%
16	0.374	0.372	0.002	0.538%
17	0.362	0.368	0.006	1.630%
18	0.342	0.352	0.010	2.841%
19	0.366	0.356	0.010	2.809%
20	0.366	0.352	0.014	3.977%
21	0.378	0.368	0.010	2.717%
22	0.366	0.364	0.002	0.549%
23	0.366	0.352	0.014	3.977%
24	0.374	0.364	0.010	2.747%
25	0.362	0.360	0.002	0.556%
26	0.354	0.360	0.006	1.667%
27	0.370	0.368	0.002	0.543%
28	0.370	0.368	0.002	0.543%
29	0.374	0.384	0.010	2.604%
30	0.378	0.368	0.010	2.717%
31	0.378	0.360	0.018	5.000%
32	0.382	0.372	0.010	2.688%
33	0.362	0.364	0.002	0.549%
34	0.366	0.360	0.006	1.667%
35	0.354	0.364	0.010	2.747%
AVG	0.366	0.365	0.010	2.688%
STDEV	0.010	0.009	0.008	2.162%

T-test   0.4802

Threshold	P	Z-score
0.03	0.8034	-6.6031
0.05	1.0000	-11.0051
0.1	1.0000	-22.0103

Record – sel16483

BEAT	BERG	PHYS	DIFF	% DIFF
1	0.354	0.340	0.014	4.118%
2	0.350	0.344	0.006	1.744%
3	0.346	0.340	0.006	1.765%
4	0.350	0.340	0.010	2.941%
5	0.350	0.340	0.010	2.941%
6	0.350	0.340	0.010	2.941%
7	0.350	0.340	0.010	2.941%
8	0.350	0.340	0.010	2.941%
9	0.346	0.336	0.010	2.976%
10	0.350	0.340	0.010	2.941%
11	0.350	0.340	0.010	2.941%
12	0.346	0.344	0.002	0.581%
13	0.354	0.340	0.014	4.118%
14	0.350	0.336	0.014	4.167%
15	0.350	0.336	0.014	4.167%
16	0.350	0.332	0.018	5.422%
17	0.342	0.336	0.006	1.786%
18	0.346	0.336	0.010	2.976%
19	0.354	0.344	0.010	2.907%
20	0.354	0.340	0.014	4.118%
21	0.350	0.340	0.010	2.941%
22	0.350	0.340	0.010	2.941%
23	0.350	0.344	0.006	1.744%
24	0.342	0.340	0.002	0.588%
25	0.350	0.340	0.010	2.941%
26	0.342	0.340	0.002	0.588%
27	0.350	0.340	0.010	2.941%
28	0.358	0.340	0.018	5.294%
29	0.358	0.340	0.018	5.294%
30	0.350	0.336	0.014	4.167%
31	0.346	0.340	0.006	1.765%
32	0.350	0.340	0.010	2.941%
33	0.350	0.340	0.010	2.941%
34	0.354	0.340	0.014	4.118%
35	0.350	0.340	0.010	2.941%
AVG	0.3497	0.3395	0.0102	3.017%
STDEV	0.0037	0.0025	0.0041	1.221%

T-test   13.3857

Threshold	P	Z-score
0.03	0.5302	0.0800
0.05	1.0000	-9.6112
0.1	1.0000	-33.8390

B.2 – Power Spectral Summation Data

This section presents the summation data from the data analysis. Corrected data with no replacement is denoted by *-mod. Corrected data with replacement is denoted by *-mod-2.

RECORD	0.05 - 0.15	0.15 - 0.4	0.05 - 0.1	0.1 - 0.15	0.15 - 0.2	0.2 - 0.25	0.25 - 0.3	0.3 - 0.35	0.35 - 0.4
arr-100-0-150	6.06E+05	9.89E+05	4.39E+05	1.98E+05	3.36E+05	2.29E+05	1.32E+05	2.06E+05	1.50E+05
arr-100-300-450	6.07E+05	5.60E+05	3.57E+05	2.78E+05	1.06E+05	1.45E+05	1.45E+05	97147	1.19E+05
arr-100-600-750	2.84E+05	4.60E+05	1.69E+05	1.39E+05	1.23E+05	1.11E+05	80408	53021	1.14E+05
arr-100-900-1050	3.01E+05	4.53E+05	1.95E+05	1.24E+05	1.08E+05	1.27E+05	1.36E+05	63909	63143
arr-102-0-150	1.08E+06	8.91E+05	6.46E+05	4.97E+05	2.27E+05	1.17E+05	1.77E+05	2.59E+05	2.09E+05
arr-103-0-150	4.47E+05	9.36E+05	2.55E+05	2.17E+05	2.26E+05	2.65E+05	1.61E+05	2.60E+05	1.31E+05
norm-16265-0-300	1.54E+05	3.28E+05	95781	60221	50738	86647	57608	77947	65717
norm-16265-300-600	59607	1.78E+05	32697	28768	42095	36467	49396	21810	32942
norm-16265-600-900	1.10E+05	2.45E+05	45399	65533	60329	43511	49827	63567	38347
norm-16265-900-1200	2.39E+05	4.48E+05	1.14E+05	1.30E+05	1.04E+05	1.32E+05	99615	57468	74993
norm-16273-0-300	89906	2.36E+05	36389	54046	62490	59149	35499	36431	48881
norm-16483-0-300	1.42E+05	1.68E+05	87574	59508	49997	42207	27981	22416	29628
norm-16539-0-300	3.00E+05	4.95E+05	1.71E+05	1.32E+05	1.24E+05	86941	86432	80243	1.33E+05
arr-100-0-150-mod	43394	2.32E+05	28832	17439	42254	81364	50993	36980	42207
arr-100-300-450-mod	2.47E+05	4.52E+05	72528	1.89E+05	69509	98728	1.19E+05	1.02E+05	1.08E+05
arr-100-600-750-mod	1.04E+05	2.53E+05	52432	55406	60152	41723	37491	50970	81506
arr-100-900-1050-mod									
arr-102-0-150-mod	1.71E+05	4.16E+05	1.00E+05	79353	57550	42870	30706	1.36E+05	1.89E+05
arr-103-0-150-mod	75554	2.54E+05	26664	52298	51340	68449	28737	53354	71816
norm-16265-0-300-mod	1.32E+05	2.62E+05	86647	45679	52313	61495	38317	64375	52640
norm-16265-300-600-mod	59607	1.78E+05	32697	28768	42095	36467	49396	21810	32942
norm-16265-600-900-mod	1.10E+05	2.45E+05	45399	65533	60329	43511	49827	63567	38347
norm-16265-900-1200-mod	2.39E+05	4.48E+05	1.14E+05	1.30E+05	1.04E+05	1.32E+05	99615	57468	74993
norm-16273-0-300-mod	89906	2.36E+05	36389	54046	62490	59149	35499	36431	48881
norm-16483-0-300-mod	27969	63440	14146	14338	11369	14133	14324	13495	11128
norm-16539-0-300-mod	95754	1.70E+05	42632	54214	41086	46691	20797	25261	40229

RECORD	0.05 - 0.15	0.15 - 0.4	0.05 - 0.1	0.1 - 0.15	0.15 - 0.2	0.2 - 0.25	0.25 - 0.3	0.3 - 0.35	0.35 - 0.4
arr-100-0-150-mod-2	3.50E+05	3.29E+05	2.12E+05	1.64E+05	95224	87507	70027	52441	56836
arr-100-300-450-mod-2	3.53E+05	5.34E+05	2.38E+05	1.33E+05	1.37E+05	1.26E+05	1.14E+05	91417	1.11E+05
arr-100-600-750-mod-2	2.08E+05	2.67E+05	1.37E+05	76116	69047	51371	29651	53864	78225
arr-100-900-1050-mod-2	1.58E+05	2.35E+05	1.03E+05	68842	37036	58569	77995	46180	30301
arr-102-0-150-mod-2	2.96E+05	5.69E+05	1.47E+05	1.64E+05	68475	1.03E+05	1.26E+05	1.53E+05	1.86E+05
arr-103-0-150-mod-2	3.23E+05	3.14E+05	2.28E+05	1.20E+05	96109	80419	49755	57939	56929
norm-16265-0-300-mod-2	1.48E+05	2.93E+05	93404	56515	51729	75238	42096	69252	63401
norm-16265-300-600-mod-2	1.15E+05	1.90E+05	66633	50832	40001	40802	50534	33656	31401
norm-16265-600-900-mod-2	1.48E+05	1.92E+05	99385	51068	60336	35107	47028	34727	21573
norm-16265-900-1200-mod-2	3.04E+05	3.86E+05	1.53E+05	1.58E+05	1.09E+05	71792	84136	60762	69708
norm-16273-0-300-mod-2	1.60E+05	3.02E+05	87481	76603	78869	78485	58901	47896	47495
norm-16483-0-300-mod-2	32756	64988	16331	16969	12469	14049	14428	14266	11290
norm-16539-0-300-mod-2	1.57E+05	3.37E+05	81011	77829	72900	66319	64950	64770	75458

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