CHAPTER - 6

RECOGNITION AND EXTRACTION OF ECG-FEATURES - A SYNTACTIC APPROACH

It has already mentioned in chapter 1 that the interpretation of ECGs is done by two stages. At the first stage some characterstic features (waveforms and line segments) are recognised and their parameters (amplitudes and durations) are measured and at the second stage, the ECG is interpreted on the basis of these measured parameters and some diagnostic criteria. This chapter proposes methodology for identification and extraction of ECG features (a set of characteristic measurements) from the digitized 12 lead ECG data using syntactic algorithms. The syntactic approach provides a capability for describing a complex pattern in terms of a composition of simplest subpatterns, called pattern primitives, and of grammatical rules. As discussed eariler, the terminal primitives of any language directly affect the length of the terminal string and the complexity of the generating grammars and consequently, the efficiency of the parsing algorithm.

The method proposed here consists of a number of stages. The first stage is, being optional, may include the data acquisition system, the analog or digital filtering and digitization of the ECG pattern, as well as base line selection. The second stage transforms the patterns into the string like representation with the help of a finite set of preselected

pattern primitives. To make the processing in the latter stages of the system more efficient, some sort of data compression is applied after this stage. The subsequent stages detect and measure different ECG waves and parameters. These measurements are essential for classification of cardiac diseases.

6.1 Feature selection

Once the forms of the ECG wave have been recognised, the numerical values of amplitudes and durations, their on and offsets, and the time intervals are to be measured in order to classify the ECG signal to one of the classes under consideration.

This approach lends itself as a formal front-end methodology for identifying those features that are relevent to the subsequent classifications of ECGs. Thus extraction of structural and qualitative information from the compressed digitized ECG data is necessary.

In this work, the analysis is based on the features taken into account by physicians and also from different medical literature. They are,

- the amplitude and duration of the P wave which reflects the atrial depolarization.
- the amplitude and duration of the QRS complex which reflects the ventricular depolarization.
- the RR rates (heart rate).
- the PR, QT and ST intervals.
- the ventricular activation time (VAT) and ST-onset.
- the electrical axis.

The algorithms for detection and of fixing the on and

offsets of the P and T waves and the QRS complexes are presented in this chapter.

6.2 Baseline detection

Baseline wandering, powerline interference, and various artifacts affect the performance of ECG wave detectors. Since the amplitude of a wave is measured with respect to its baseline or zero line, it is necessary to measure the baseline accurately as far as possible. In practice, a very low amplitude value will generally correspond to the ideal zero baseline. In most practical situations, the input waveform is contaminated with noise from a variety of sources and can appear within the waveform in different nature. Of these, noise due to powerline interference is very much important. In general low frequencey noise shifts the baseline, causing the signal to rise and fall and high frequency noise appears as small spikes, often randomly distributed throughout the original signal. It is almost impossible to eleminate these types of noise patterns completely from the ECG signal, however, some analog or digital filtering techniques are able to minimize errors due to noise. It was already mentioned in chapter 2 that preprocessing of digitized ECG signal with moving average technique can be of great help to improve the signal-to-noise ratio of the ECG signal. The main argument against averaging sample values has always been that it causes smooting errors [69].

It has also been seen that a noise level below 50 μv is clinically meaningless [29]. In view of the above fact a baseline tolerance (BASETOL) of the order of 50 μv is used, i.e., BASETOL $\leq$ 0.5 mv. So the sample points lying within this range are treated

as zero values and all other sample points are normalized accordingly.

6.3 Selection of pattern primitives†

As discussed earlier, the first step in formulating a syntactic model for pattern description is the determination of a set of primitives in terms of which the patterns of interest may be described. This determination will be largely influenced by the nature of the data, the specific application in question, and the technology available for implementing the system. There is no general solution for the primitive selection problem at this time. Primitives should provide a compact yet, adequate description of the data in terms of the specified structural relation (e.g., concatenation relation).

The pattern primitives are described here in terms of the first differences (slope) between consecutive ECG samples and are expressed by the formula

$$\triangle y_i = y_{i+1} - y_i$$

where y_{i+1} and y_i represent the voltage of the (i+1)-th and i-th ECG samples respectively. The digital waveform is thus segmented into primitives by piecewise approximatiion.

Let an ECG waveform be represented by a discrete set of points (t_1, y_1), (t_2, y_2),..., (t_i, y_i),..., (t_n, y_n) representing the analog function $y = f(t)$ with $t_i < t_{i+1}$ for all $i = 1,2,...,n$.

The following definitions of pattern primitives are selected for the analysis of the ECG waveforms.

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† This section is based on the author's pubilished paper no. 5.

Definition 1 :

Any first difference greater than zero is called 'positive first difference' and is represented by the primitive 'a'. Mathematically it is defined as follows :

$$\left[\forall_i \mid \Delta y_i > 0 \right]$$

Definition 2 :

Any first difference less than zero is called 'negative first difference' and is represented by the primitive 'b'. Mathematically it is defined as follows :

$$\left[\forall_i \mid \Delta y_i < 0 \right]$$

Definition 3 :

Any first difference equal to zero is called 'zero first difference' and is symbolically expressed by the primitive 'c'. Mathematically it is defined as follows :

$$\left[\forall_i \mid \Delta y_i = 0 \right]$$

Definition 4 :

Any first difference followed by the zero first difference is expressed by the primitive 'd'. Mathematically it is defined as follows :

$$\left[\exists_i \mid \left[\Delta y_i = 0 \right] \cap \left[\Delta y_{i+1} > 0 \right] \right]$$

Definition 5 :

A zero first difference followed by a negative first difference is represented by the primitive 'e'. Mathematically it

is defined as follows :

$$\left[\exists_i \mid \left[\Delta y_i < 0 \right] \cap \left[\Delta y_{i+1} = 0 \right] \right]$$

Definition 6 :

A negative first difference followed by the zero first difference is represented by primitive 'f'. Mathematically it is defined as follows :

$$\left[\exists_i \mid \left[\Delta y_i = 0 \right] \cap \left[\Delta y_{i+1} < 0 \right] \right]$$

Definition 7 :

A zero first difference followed by the positive first difference is represented by the primitive 'g'. Mathematically it is defined as follows :

$$\left[\exists_i \mid \left[\Delta y_i > 0 \right] \cap \left[\Delta y_{i+1} = 0 \right] \right]$$

Definition 8 :

'Zero crossing point' is defined as the point at which positive or negative first differences cross the zero line (base line). It is represented by the primitive 'h'. Mathematically it is defined as follows :

$$\left[\exists_i \mid \left[y_{i-1} < 0 \cap y_i > 0 \right] \cup \left[y_{i-1} > 0 \cap y_i < 0 \right] \cup \left[y_{i-1} < 0 \cap y_i = 0 \cap y_{i+1} > 0 \right] \cup \left[y_{i-1} > 0 \cap y_i = 0 \cap y_{i+1} < 0 \right] \right]$$

The reasons for this selection are

1) Efficient algorithms can be written for approximating ECG waveforms.

2) Primitives can be encoded into symbols.

3) These symbols can be used as terminals of the grammar used for describing different ECG complexes.

6.4 String generation†

After the proper selection of the pattern primitives, the next task is to convert the digitized data into a string composed of those primitives. While conversion of the digitized ECG data, the choice of start and end point is a vital problem. The problem arises due to the fact that an un-ending continious waveform is generated on the electrocardiographic-paper as soon as the ECG leads are attached on the respective positions of the body. In most cases the cardiologist considers only 4 to 5 cardiac cycles for the classification of cardiac diseases. For ease of clasification, they take 4 to 5 cardiac cycles preceded and followed by two isoelectric lines. In the present approach the analog ECG signal is first sampled uniformly at the rate of 250 samples/sec. for a duration of 4 secs. Then the first and last occurances of atleast three consecutive zeros are searched in the entire sampled data. The first and last sample values thus obtained (indicated by at least three consecutive zeros) point to the start and end point of the data stream for ECG analysis.

This procedure is based on the assumption that a single zero or a group of two consecutive zeros in the data stream may be the part of any ECG complex. i.e. they are not the begining or ending points of the ECG complexes.

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† This section is based on the author's pubilished paper no. 5.

A simple algorithm to generate the string from these truncated digitized data is now presented.

Algorithm STRINGEN

Input : Y- array contains sample values.

Output : STRIN- array contains a string composed of ECG pattern primitives corresponding to the digitized ECG data.

Step 1 : Initialize array STRIN with zero. Set I = 2.

Step 2 : If Y(I-1) is zero then continue, otherwise go to step 9.

Step 3 : If (Y(I)-Y(I-1) is zero, then set STRIN(I-1) = primitive 'c' and go to step 15, otherwise continue.

Step 4 : If Y(I-2) is zero continue, otherwise go to step 7.

Step 5 : If (Y(I)-Y(I-1)) is positive, then set STRIN(I-1) = primitive 'd' and go to step 15, otherwise continue.

Step 6 : If (Y(I)-Y(I-1)) is negative, then set STRIN(I-1) = primitive 'f' and go to step 15, otherwise continue.

Step 7 : If (Y(I)-Y(I-1)) is negative, then set STRING(I-1) = primitive 'b' and go to step 15, otherwise continue.

Step 8 : Set STRIN(I-1) = primitive 'a' and go to step 15.

Step 9 : If Y(I) is zero, then continue, otherwise go to step 14.

Step 10 : If Y(I+1) is zero, then continue, otherwise go to step 13.

Step 11 : If (Y(I)-Y(I-1)) is positive, then set STRIN(I-1) = primitive 'g' and go to step 15, otherwise continue.

Step 12 : Set STRIN(I-1) = primitive 'e' and go to step 15.

Step 13 : If (Y(I-1)*Y(I+1)) is negative, then set STRIN(I-1) = primitive 'h' and go to step 15, otherwise go to step 7.

Step 14 : If (Y(I)*Y(I-1) is negative, then set STRIN(I-1) = primitive 'h' and continue, otherwise go to step 7.

Step 15 : If I > number of sample values in Y-array, then exit, otherwise set I = I + 1 and go to step 2.

Example 6.1

Let us consider the ECG waveform containing P,QRS, and T waves shown in Fig. 6.1. To understand the primitive description from the digitized ECG data, the A-B partion is considered for ease of understanding. This approach can be extended to the whole ECG waveform. It is assumed here that time interval between A and B is 0.04 sec. and the number of sample values, at the sampling rate of 250 samples/sec., is 10 samples. The sample values and the corresponding first differences are given in Table 6.1.

Table 6.1

Amplitude of the samples and corresponding first differences (A-B) portion of the ECG waveform

Sl. No.	Amplitude of the sample values (y_i)	First differences ($\triangle y_i = y_{i+1} - y_i$)	String
1	0.0	0.0	c
2	0.0	0.0	c
3	0.0	1.0	d
4	1.0	1.0	a
5	2.0	-1.0	b
6	1.0	-0.6	b
7	0.4	-0.4	e
8	0.0	0.0	c
9	0.0	0.0	c
10	0.0		

It is obvious that if there are n-number of samples, then the number of first difference is n-1.

Based on the string generation algorithm STRINGEN, the A-B portion of the ECG waveform is represented by the string 'ccdabbecc' of length 9.

It appears from the example that some redundant pattern primitives are always formed during string formation. For example, the string 'cdabec' of length 6 can also represent the nature of the truncated waveform. Thus there is an ample scope to compress the string.

6.5 String compression†

In this section, approach to ECG data compression based on the compression of the generated string is presented. It may be noted that there is every possibility that one or more pattern primitives may occur more than once successively. So, those primitives, which occur successively more than once, can be merged into one primitive retainig the structural information of the input wave. For example, a string representing a positive P-wave can be expressed as 'cccdaaabbbecc' in terms of five different primitives. The length of the string is thirteen. So thirteen memory locations are required to store it. This positive P-wave can also be represented by the string 'cdabec' of length six without any loss of information. In this case, only six memory locations are required, thus obtaining a reduction of about 46% storage requirement even in this simple case. While applying the

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† This section is based on the author's pubilished paper no. 5.

idea of string compression, another important point should also be considered. In wave recognition problems, it is necessary not only to recognise the wave but also to retain the information regarding amplitude and duration of several waves. So, whenever a string containig the same primitives is successfully compressed, the time and amplitude information of primitives should be updated accordingly. The string compression algorithm is now presented.

Algorithm STRNCOMP

Input : Y-array contains sample values.
T1-array contains time information for the corresponding sample values.
STRIN-array contains a string composed of ECG pattern primitives corresponding to the digitized data.

Output : STRN-array is used to store compressed string. The Y1-array will contain the updated sample values. The time information of the compressed string will be stored in the T2-array.

Step 1 : Initialise STRN-array, T2-array and Y1-array with zero. set I = 1 and J = 1.

Step 2 : If STRIN (I+1) - STRIN(I), then go to step 18.

Step 3 : If STRIN (I) = 'a', then go to step 11.

Step 4 : If STRIN (I) = 'b', then go to step 11.

Step 5 : If STRIN (I) = 'c', then go to step 11.

Step 6 : If STRIN (I) = 'd', then go to step 11.

Step 7 : If STRIN (I) = 'e', then go to step 12.

Step 8 : If STRIN (I) = 'f', then go to step 11.

Step 9 : If STRIN (I) = 'g', then go to step 12.

Step 10 : If STRIN (I) = 'h', then go to step 13.

Step 11 : Set STRN(J) = STRIN(I),

T2(J) = T1(I+1),

Y1(J) = Y(I+1) and go to step 17.

Step 12 : Set STRN(J) = STRIN(I),

T2(J) = T1(I),

Y1(J) = Y(I) and go to step 17.

Step 13 : Set STRN(J) = STRIN(I) and Y1(J) = 0.

Step 14 : If Y(I+1) = 0, then go to step 16.

Step 15 : Set T2(J) = (T1(I)+T1(I+1))/2 and go to step 17.

Step 16 : Set T2(J) =(T1(I)+T1(I+2))/2.

Step 17 : Set J = J+1.

Step 18 : Set I = I+1.

Step 19 : If I < number of sample values in Y-array, then continue, *otherwise go to step 2.*

Step 20 : Set STRN(J) = STRN(I-1),

Y1(J) = 0 and

T2(J) = T1(I-1).

Step 21 : Exit.

Example 6.2

Let us consider the following digitized sample values (Table 6.2) along with their time of occurrances for the positive P-wave part(the A-B portion) of the ECG wave as shown in Fig. 6.2. After utilizing the string generation algorithm STRINGEN, the string obtained is 'ccdaaabecc'. The Table 6.2 shows the generated string with other information.

Table 6.2

Sample values, their time of occurrences and the generated string.

Sample No.	Amplitude of samples	Time of occurrences	String
1	0.00	0.0	c
2	0.00	0.1	c
3	0.00	0.2	d
4	0.08	0.3	a
5	1.00	0.4	a
6	1.04	0.5	a
7	1.06	0.6	b
8	1.01	0.7	e
9	0.00	0.8	c
10	0.00	0.9	c
11	0.00	1.0	

Here five primitives i.e., c,d,a,b, and e, are required to represent the postive P-wave part. The length of the string is ten. In this representation, primitive 'c' occurs successively twice at the start and end side of the string. The primitives 'd', 'b' and 'e' occur once in the string and the primitive 'a' occurs thrice in the string successively. So these three 'a' s can be merged into one 'a'. Whenever same primitive appears successively

in the string, only the last primitive of the successively primitives in the compressed string list is retained. In otherwords, if the same primitive occur n times consecutively, then the n-th primitive is only stored in the compressed string list. This is true for any primitive. The time and amplitude information for the primitives are updated accordingly. Table 6.3 shows the compressed string along with their amplitude and time information obtained by applying algorithm STRNCOMP.

Table 6.3

Compressed string with their amplitude and time information.

Amplitude of sample	Time of occurence	Compressed string
0.00	0.2	c
0.08	0.3	d
1.06	0.6	a
1.01	0.7	b
1.01	0.7	e
0.00	0.8	c

It may be noted here that the time information of the last primitive 'c' is the begining of that primitive and this is valid while compressing any string of interest.

6.6 QRS detection†

Good performance of computerized ECG processing systems relies heavily upon accurate and reliable detection of QRS complexes. A QRS complex is a recording of the electrical activity caused by the ventricular depolarization of the human heart. Once the positions of QRS complexes are known, a more detailed examination of the ECG signal can be carried out in order to study the complete cardiac period.

A few syntactic algorithm for ECG waveform processing have been reported in the literature, particularly on the problem of QRS detection [23,27,50,54,86,159].

This section presents an approach for recognizing QRS complexes.

QRS patterns are distinguished from the other electrocardiographic patterns (P patterns and T patterns) by their steep slopes. The algorithm for the detection of QRS patterns, which is formulated below, is based upon this 'a priori' knowledge. More specifically, above a certain threshold, one expects to find a large proportion of strings with steep slopes and of sufficient length only in the QRS patterns. This is only true, however, when no noise is superimposed on the ECG signal. The effect of noise on the ECG signal is manifested as extraneous peaks and as a shift of its base line. Small extraneous peaks (small spikes) superimposed on the QRS result in shortening the length of the strings of steep slopes, and may result in failure to detect the QRS pattern. Large extraneous peaks (high spikes)

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† This section is based on the author's pubilished paper no. 6.

with steep slopes, on the other hand, can incorrectly be identified as QRS patterns. Finally, a steep abrupt change in the baseline (a jump) creates also a string of large slopes which may erroneously be detected as a QRS pattern. Thus it is evident that the accurate detection of QRS is possible only when the contaminate noise level is much much small. In otherwords, a good performance of the preprocessor and baseline detector contributes to the QRS detection accuracy.

The amplitude of QRS complexes is usually higher than in any other parts of the tracing. Computer recognition of QRS complexes can be done by noting the first differences of the sampled values. If the first difference exceeds a certain threshold, a QRS complex is identified. It is seen that when the ECG is digitized at a sampling rate of 250 samples per sec. and with an eight bit accuracy, the first difference whose absolute values are smaller than or equal to 1 conversion unit are found within the base-line, P waves, T waves and occassionally at the onset or end of QRS complexes [103]. Consequently, a string of the first differences exceeding the threshold set at 1 conversion unit is regarded as a 'Locum' for the QRS complex.

The above idea has been utilized here for detecting the QRS complex. An amplitude threshold is used to identify the begining of QRS complex. After string compression, a string of pattern primitives has been obtained earlier. The presence of waves can be calculated from the total number of primitive 'c'. If the total number of primitive 'c' is n, then n-1 waves are present there. Next the maximum absolute value of first differences between the consecutive primitive 'c' is computed and is stored in

L1-array. Next, every element of L1-array will be compared with the fixed threshold value. Those elements of L1-array, which exceed the fixed threshold, indicate the presence of QRS waves in the corresponding zone.

Once the begining of every QRS complex has been located, an attempt is made to determine its onset and end. The finding of QRS-onset and QRS-end is very simple. The primitive following the start primitive 'c' of a QRS complex indicates the QRS-onset point where as the primitive before the end primitive 'c' indicates the QRS-end point.

Now the algorithm for the QRS detection is presented.

Algorithm QRSDETCT

Input : STRN-array contains compressed string of length J.
Y1-array contains updated sample values.
FTHSD-fixed threshold value.

Output : T3-array contains the location of different ventricular complexes. T4-array contains the locations of the primitive 'c'.

Step 1 : Set I1 = 0, I = 1 and initialise T4-array with zero.

Step 2 : If STRN(I) = 'c' then continue, otherwise go to step 4.

Step 3 : Set I1 = I1 + 1 and T4(I1) = I.

Step 4 : If I > J then continue, otherwise set I=I+1 and go to step 2.

Step 5 : Set I = 1 and K1 = 1.

Step 6 : Set F1 = T4(I), F2 = T4(I+1), I5 = F1+1 and I6 = F2

Step 7 : Find the maximum absolute value of first differences

by searching the elements Y1(I5) through Y1(I6), and store the maximum value in the element L1(K1).

Step 8 : If I = I1-1 the continue otherwise set I = I + 1, K1 =K1 + 1 and go to step 6.

Step 9 : Set I2 = 1, I4 = 1 and initialize T3 array with zero.

Step 10 : If L1(I2) > FTHSD then continue, otherwise go to step 12.

Step 11 : Set T3(I4) = I2 and I4 = I4 + 1.

Step 12 : If I2 = K1 - 1 then continue, otherwise set I2 = I2 + 1 and go to step 10.

Step 13 : Exit.

6.7 P and T-wave detection†

It was already mentioned that the ECG signal consists of the P wave, QRS complex, and T wave. Out of them only the QRS complex is necessarily present and readily detectable. The P and T waves may be extremely small or may not be present at all in some cases, thereby creating identification problems.

Identification of P-waves remains among the more complex problems in automated processing of electrocardiograms. The problem arises from atleast four sources :

1) The low amplitude of P-waves and their consequent low signal to noise ratio.
2) The wide range of morphologies associated with the onset and offset of P-waves.

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† This section is based on the author's pubilished paper no. 3.

3) The presence of other signals and artifacts in the some region.

4) The variability of human observers in accessing the location of P-waves in individual cases.

Throughout the history of efforts to improve P-wave detection, the parameter of choice has been spatial velocity, wheather alone or in combination. It shows dramatic changes at P-wave boundaries [151], and attains values in excess of 5mv/sec. only inside P-waves [112], QRS complexes and T-wave [48]. The second most preferred parameter for P-wave detection is amplitude, also called 'baseline distance' to reflect corrections made to eliminate the effect of baseline fluctuations.

Similarly, locating ECG waveform fiducial points (e.g., R-wave maximum, T-wave ending, etc.) is a critical step in automated ECG analysis since these fiducial points become the basis for all subsequent amplitude and interval measurements. This critical step is most difficult where a single ECG lead is recorded, since the absence of other ECG lead precludes mathematical waveform enhancement. With this in mind, the R-wave is relatively easy to locate because of its prominence and its generally consistent morphology. Conversly, fiducial points within the T-wave are difficult to locate because the T-wave itself varies widely in amplitude and morphology. Hence, one approach is to locate the T-wave and its fiducial points in relation to some preceding event within the ECG waveform.

A simple algorithm for detection of P-waves and T-waves will now be presented.

Algorithm PTDETECT

Input : The T3-array contains the locations of different ventricular complexes. The T4-array contains the locations of the primitive 'c'. The STRN-array contains compressed string. The variable CNUMBER gives the number of primitive 'c' between the two elements of T3-array.

Output : The L1-array will contain strings for P-wave. The strings representing T-waves will be stored in L2-array.

Step 1 : Set INITIAL = 1 and FINAL = INITIAL +1.

Step 2 : CNUMBER = T3(FINAL)-T3(INITIAL).

Step 3 : If CNUMBER = 3 then go to step 6.

Step 4 : If CNUMBER = 2 then go to step 7.

Step 5 : P-wave and T-wave are not present, go to step 8.

Step 6 : Set I = T4(T3(INITIAL)+1),

J = T4(T3(INITIAL) + 2),

and K = T4(T3(FINAL)).

Store STRN(1) to STRN(J) in L2-array and STRN(J) to STRN(K) in L1-array and go to step 8.

Step 7 : Set I = T4(T3(INITIAL) + 1) and K = T4(T3(FINAL)).

Store STRN(I) to STRN(K) in L2-array.

Step 8 : If FINAL is equal to end of T3-array then continue, otherwise set INITIAL = FINAL, FINAL = INITIAL +1.

Go to step 2.

Step 9 : Exit.

Besides the above algorithm another procedure has been tried and identical results are obtained. The method is as follows :

The QRS off-set is precisely determined by conducting a backward search for primitive 'c' from the R-wave peak. The QRS off-set is also found similarly. From the QRS off-set, a search is performed over a 50ms. window for the peak of the T-wave. Once the peak is found, the T-wave end is searched over a 70ms. window. If no T-wave is detected, a flag is set. The P-wave is detected by setting a slope threshold of 5mv/sec. Once a P-wave is found, a backward search is conducted over a 20ms. window for the P-wave begining . Then, a forward search is made from the threshold point for the P-wave end.

6.8 Identification of wave types†

Once the QRS complex has been located and its onset and end determined, an attempt is made to establish the QRS configuration. It was mentioned in the section 2.6 that QRS configuration consists exclusively of i) a R wave or a QRS wave or ii) a QR wave or a RS wave or iii) a QS wave or iv) a RSR'S' wave.

Here, an attempt is made to explore the usefulness of syntactic methods in recognition to the QRS configuration problems. The method proposed here uses the structural differences among the different QRS complex configurations and generates distinctively different description in terms of the chosen set of primitives for recognition purposes (section 6.3). The string for

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† This section is based on the author's pubilished paper no. 6.

some possible different QRS complexes are shown in Table 6.4.

The next step in the formulation of a syntactic model for pattern recognition is syntax analysis. Context free grammar in Chomsky normal form has been used for identification of different QRS complexes. The non-terminals chosen in the grammar represent sub-patterns (e.g., Q,R,S etc.) in an ECG complex. The names used for such nonterminals are the same as those used in conventional ECG nomenclature so that the sub-patterns they represent can be easily understood.

Table 6.4

Diff. QRS complexes with

string representations.

Sl. No.	QRS complex	String
1	QR	cfbahabec
2	RS	cdabhbagc
3	QRS	cfbahabhbagc
4	R	cdabec
5	QRS	cfbagc
6	RSR'S'	cdabhbahabhbagc

The only exception is the case of R' and S' waves. They are denoted here by the symbol 'X'. The grammar has been designed in such a fashion that inspection of first column of C-Y-K parsing

table will reveal the presence of sub-patterns along with other nonterminals and starting symbol.

The above procedure is repeated to other QRS complexes present in the entire ECG wave for a particular lead.

The same procedure is also followed for the QRS waveforms obtained from different leads and also for P-wave and T-wave identification. The grammars developed for describing different wave patterns for the QRS, P and T waves will now be presented in the following two sections.

6.0 Development of a QRS wave-grammar†

In Table 6.4 possible wave sequences for the QRS complex have been given with the aid of representations stated in section 6.3, it is possible to construct a context-free grammar in Chomsky normal form that recognizes the different waveforms.

Let $G_1 = (V_{N_1}, V_{T_1}, P_1, S)$ be a context-free grammar where V_{N_1} is the set of nonterminals, V_{T_1} is the set of production rules and S is the start symbol $\in V_{N_1}$. The grammar derived for the problem under consideration is presented below :

$$L_{QRS} = L(G_1)$$

$$G_1 = (V_{N_1}, V_{T_1}, P_1, K)$$

$$V_{N_1} = \{ A,B,C,D,E,F,G,H,K,M,Q,R,S,X,Z\}$$

$$V_{T_1} = \{a,b,c,d,e,f,g,h,\} \text{ and}$$

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† This section is based on the author's pubilished paper no. 6.

P_1 : K ⟶ KC|RE|SC|SG|XE|XG

R ⟶ AB|MB|QR

M ⟶ DA|HA|HB|ZA|ZB

Q ⟶ MA

Z ⟶ CD|CF

S ⟶ BA|QG|QS|RQ

X ⟶ KR|RR|SR|XQ

A ⟶ a, B ⟶ b, C ⟶ c, D ⟶ d

E ⟶ e, F ⟶ f, G ⟶ g, H ⟶ h

Example 6.3

Let us consider the first QRS complex from Table 6.4. The input string corresponding to the QRS complex is 'cfbahabec'. The parsing table using C-Y-K parsing algorithm is shown in Table 6.5. The first column of the parsing table shows that ventricular complex is 'QR'.

Table 6.5

Parsing table for the

string 'cfbahabec'

K								
K								
R	K							
	K							
	X	K						
Q		KK						
M		RK						
Z	S	MR						
C	F	B	A	H	A	B	E	C
c	f	b	a	h	a	b	e	c

Example 6.4

The parsing table for the string 'cdabhbahabhbagc' is shown in Table 6.6. The length of the string is fifteen. So the size of the parsing table is 15 X 15. The ventricular complex for the above string is RSR'S'. As R' wave and S' wave are denoted by symbol X, so RSXX appears in the first column of the parsing table.

Table 6.6

Parsing table for the string

'cdabhbahabhbagc'

K														
KK														
XKK														
XK														
X	K													
X	KK													
X	SK													
X	X	K												
S		KK												
S	R	SK												
S	X	S	K											
R			SK											
MR	Q	R	QK											
ZMR	MS	MR	MS											
CDABHBAHABHBAGC														
cdabhbahabhbagc														

6.10 Development of P-wave grammar†

P-wave configuration consists exclusively of i) an upright wave ii) an inverted wave or iii) a biphasic wave i.e, complex is partly above and partly below the isoelectric line. The string representation for different P-waves is shown in Table 6.7.

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† This section is based on the author's pubilished paper no. 3.

Table 6.7

P-wave complexes and

their representation

Sl.No.	P-wave	String
1.	Upright	cdabec
2.	Inverted	cfbagc
3.	PX(biphasic P-wave; negative wave followed by positive wave)	cdabhbagc
4.	XP (biphasic P-wave; positive wave followed by negative wave)	cfbahabec
5.	Notched P-wave (positive wave followed by positive wave)	cdababec

Context-free grammar in Chomsky normal form has been generated for identification of different P-wave complexes.

Here also, the grammar has been generated in such a way that inspection of first column of the parsing table will reveal the presence of subpatterns along with other nonterminals and starting symbol. The grammar derived for the problem under consideration is presented below :

$$L_P = L(G_2)$$

$$G_2 = (V_{N_2}, V_{T_2}, P_2, K)$$

$$V_{N_2} = \{A,B,C,D,E,F,G,H,K,M,P,X,Z\}$$

$$V_{T_2} = \{a,b,c,d,e,f,g,h\}.$$

and P_2 :

$K \longrightarrow PE|KC|XG$

$M \longrightarrow DA|ZA|ZB|HB|HA$

$P \longrightarrow AB|MB|PP|XP$

$X \longrightarrow MA|BA|PX$

$Z \longrightarrow CD|CF$

$A \longrightarrow a$, $B \longrightarrow b$, $C \longrightarrow c$, $D \longrightarrow d$

$E \longrightarrow e$, $F \longrightarrow f$, $G \longrightarrow g$, $H \longrightarrow h$

In the above procedure nonterminal 'X' represents the inverse P-wave.

Example 6.5

Let us consider the third wave 'PX' of Table 6.7. The string representation is 'cdabhbagc'. The parsing table for this string is shown in Table 6.8. The first column of the parsing table reflects the wave pattern. The auricular complex for the string is 'PX'. The parsing table for the notched P wave is shown is Table 6.9.

Table 6.8

Parsing table for the

string 'cdabhbagc'

```
K
KK
XKK
 XK
  X K
P   KK
MP  XK
ZMP MX
CDABHBAGC
cdabhbagc
```

6.11 Development of T-wave grammar (Taken from [148])

The T-wave is normally upright or inverted and the direction is entirely dependent on the leads in which it appear. The string corresponding to the upright T-wave is 'cdabec' and for the inverted is 'cfbagc'. The T-wave grammar, used for our

Table 6.9

Parsing table for the

string 'cdababec'

K
KK
PKK
PK
P P K
MP K
ZMPXP
CDABABEC
cdababec

problem, is presented below. Again, it may be noted that the grammar is generated in such way in Chomsky normal form that inspection of first column of parsing table will indicate the presence of T-wave.

$$L_T = L(G_3)$$

$$G_3 = (V_{N_3}, V_{T_3}, P_3, K)$$

$$V_{N_3} = \{A,B,C,D,E,F,G,K,M,T,X,Z\}$$

$$V_{T_3} = \{a,b,c,d,e,f,g,h\}$$

and P_3 :

$$K \longrightarrow XG|TE|KC$$

$$M \longrightarrow ZA|ZB|DA,\ T \longrightarrow MB|AB,\ X \longrightarrow MA|BA$$

$$Z \longrightarrow CD|CF$$

$$A \longrightarrow a,\ B \longrightarrow b,\ C \longrightarrow c,\ D \longrightarrow d$$

$$E \longrightarrow e,\ F \longrightarrow f,\ G \longrightarrow g.$$

In the above productions, nonterminal T represents positive T-wave whereas nonterminal X represents a negative T-wave.

Example 6.6

Let us consider the input string corresponding to the upright T-wave complex 'cdabec'. The parsing table for the string is shown in Table 6.10. The first column of the parsing table indicates the presence of positive T-wave.

Table 6.10

Parsing table of the string 'cdabec'.

K
KK
TKK
NTK
ZNT
CDABEC
cdabac

6.12 ECG feature measurement (Taken from [148])

The next task, after the proper identification of ECG complexes, is the measurement of different ECG wave features (Sction 6.1) those are required for the proper diagnosis of the heart diseases. In this section, a method for ECG parameter measurements based on the representations suggested in the preceding sections is proposed.

In the QRS-T complex one has to undertake eighteen different measurements viz., QRS duration, VAT, ST duration, PR

duration, ST onset, amplitude and durations, of Q,R,S,R',S' and T waves and the QT interval. Similarly, amplitudes and durations of P and X waves (if they are present) are required for studying the P-waves. If even some of the above parameters are not measured accurately, then the final diagnosis will be incorrect. The measurement program being proposed here utilizes the first column of the parsing table for measurement of amplitudes and durations of the wave complexes. This column contains useful information about absolute location and other relevent data regarding the waveforms. It has already mentioned in the previous sections that some of nonterminals of the first column of the parsing table represent subpatterns like different waves in an ECG complex. These non terminals are always formed with the combination of two or more terminals. For example, let us consider the parsing table given in Table 6.5 for the string 'cfbahabec'. Here the first column of the parsing table contains the nontermals C,Z,M,Q, R and K. Here the nonterminals Q and R represent the subpatterns of the QRS wave. The first column of the parsing table reveals that the nonterminal 'Q' is present in the fourth row and on the nonterminal 'R' is present in the seventh row. Here the nonterminal 'Q' is formed with the combination of first four terminals i.e., cfb and a. Similarly, nonterminal 'R' is formed with all the five terminals left since there is no subsequent nonterminals like Q,R,S or X. Thus the peak extremum of Q-wave is the maximum amplitude of the four sample values corresponding to four terminals. The time difference between the time of occurence of the first and fourth sample values indicate the duration of the Q-wave. The amplitude and duration of R-wave can be found

similarly.

It is now evident from the previous discussion that this method requires less time than the classical method for obtaining necessary informations about the amplitudes and durations of waves. The other measurements i.e., QRS duration, PR duration etc., can be found very easily utilising the different information already stored in different arrays' i.e., STRN-array, T4-array etc. The algorithm for ECG features measurement is given below :

Algorithm MEASUREMENT

Input : The STRN-array contains compressed string. The Y1 array and T2-array contain the sample values and time information for the compressed string. The T3-array contains the locations of different ventricular complexes. The strings for ventricular complexes are stored in L3-array. Similarly, the string for P-wave and T-wave are stored in L1-array and L2-array. The T4-array and T5-array contain the locations of P-wave and T-wave.

Output : Patient data matrix(DT-array). It contains different ECG measurements for 12-lead ECG. The random file PDM.DAT contains the copy of the DT-array.

Step 1 : Set I = 1, IG = 1 and initialize DT-array with zero. Open the random file PDM.DAT.

Step 2 : Initialize ST-array with zero.

Step 3 : If IG = 1 then continue, otherwise go to step 7.

Step 4 : Store the string corresponding to i-th QRS complex from L3-array in S1-array.

Step 5 : Obtain the parsing table for the string in S1-array using the Algorithm CYK given in section 3.9. The QRS wave grammar is used here for parsing.

Step 6 : Find the wave sub-complexes (i.e., Q, R, etc.) present in the first column of the parsing table. Measure the amplitudes and durations of sub-complexes using the method as discussed in this section. Compute the different measurements i.e., QRS duration, PR duration, ST onset etc., utilising the informations stored in STRN-array, Y1-array, T2-array and T3-array. The previous measurement of each parameters, i.e., amplitude and durations of sub-complexes, QRS duration etc., stored in the assigned locations of DT-array is added with current computed each result in the respective locations of the DT-array. Go to step 14.

Step 7 : If IG = 2 then continue, otherwise go to step 11.

Step 8 : Store the string for i-th T-wave from L2-array in S1-array.

Step 9 : Repeat step 5 using T-wave grammar.

Step 10 :Find the wave complex present in the first column of the parsing table. Compute the amplitude and duration of the wave complex utilising STRN-array, Y1-array, T2-array and T5-array. Add these measurement values with old values for the amplitude and durations of the wave complex and store each result in assigned locations of DT-array. Go to step 16.

Step 11 :Store the string for i-th P-wave from L1-array in S1-array.

Step 12 :Repeat step 9 using P-wave grammar.

Step 13 :Find the wave complexes (P and / or X) present in the first column of the parsing table. Measure the amplitude and duration of wave complex utilising the information stored in STRN-array, Y1-array, T2-array and T4-array. The content of respective locations of DT-array for this wave complex is added with this computed values and store each result in DT-array. Go to step 18.

Step 14 :If I is equal to end of L3-array then continue, otherwise set I = I + 1 and go to step 2.

Step 15 :The final result of each measurement i.e., QRS duration, amplitudes and durations of different sub-complexes (Q,R or S etc.), PR duration is divided by I. Go to step 20.

Step 16 :If I is equal to end of L2-array then continue, otherwise set I = I + 1 and go to step 2.

Step 17 :The final result of amplitude and duration of T-wave is divided by I. Go to step 20.

Step 18 :If I is equal to end of L1-array then continue, otherwise set I = I + 1, and go to step 2.

Step 19 :Repeat the step 17 for P-wave.

Step 20 :If IG = 3 then continue, otherwise set IG = IG + 1, I = 1 and go to step 2.

Step 21 :Copy the DT-array into file PDM.DAT.

Step 22 :Close the file PDM.DAT and exit.

6.13 Heart-rate measurement (Taken from [148])

The heart-rate per minute is defined as the interval in seconds (or fraction of a second) between the peaks of two successive R-waves divided by sixty seconds. This can easily be found with the empirical formula given below.

$$\text{Heart rate} = \frac{60 \times C}{t} \text{ beats/minute}$$

Where C = number of cardiac cycles.

t = time interval in seconds.

The heart-rate table is given in Table 2.1. The heart rate corresponding to any cycle duration can be found by observing the table.

In the method developed so for in this chapter, the Table 2.1 is not useful because of the different approach proposed for solving the problem. Thus, an algorithm for determining the heart rate from compressed ECG data subsequent to the procedure developed so far will now be presented.

Algorithm HEARTRATE

Input : The T4-array contains the locations of R-waves. The L2-array contains the start and end point of the corresponding R-waves in T4-array. The T2-array contains time information of the compressed string.

Output : Patient data matrix (DT-array).The file PDM.DAT.

Step 1 : Open file PDM.DAT, Set HRATE = 0

Step 2 : Set I = 1 and I1 = number of R-waves in lead under consideration.

Step 3 : Set J = T4(I), F1 = L2(J), F3 = T4(I + 1) and F2 = L2(F3).

Step 4 : Compute the value HRATE = T2(F2) - T2(F1) + HRATE.

Step 5 : If I = I1 - 1 then continue, otherwise set I = I + 1 and go to step 3.

Step 6 : Compute the value HRATE = 60 X (I1 - 1)/HRATE and store the value in DT-array as well as in file PDM.DAT.

Step 7 : Close file PDM.DAT and exit.

6.14 Measurement of the electrical axis (Taken from [148])

Electrocardiographic diagnosis may be both emperical and deductive. Emperical diagnosis is based on clinical-electro-cardiographic, as well as pathological electrocardiographic correlation. For example, an inverted T wave in a particular lead becomes known to be associated with a certain clinical or pathological state, and thereby assumes a diagnostic significance. Deductive electro -cardiographic diagnosis is based on the orientation of electrocardiographic forces or vectors; e.g. the QRS complex. It must be stressed that the emperical and deductive methods complement each other and both are, and should be, used in clinical electrocardiography.

The electrical axis of the heart has already been discussed in Section 2.9. A simple algorithm to find out the mean QRS axis will now be presented.

Algorithm AXIS

Input : x and y contains the algebric sum of amplitude R plus amplitude S in lead III and lead I respectively.

Output : Angle θ, the electrical axis of the heart.The file PDM.DAT.

Step 1 : Open the file PDM.DAT. Set $\alpha = 60^0$.

Step 2 : If y is zero continue, otherwise goto step 6.

Step 3 : If x is zero goto step 12.

Step 4 : If x is negative, set $\theta = -90^0$ and goto step 12.

Step 5 : If x is positive, set $\theta = 90^0$ and goto step 12.

Step 6 : Set $\theta = \tan^{-1}\left(\frac{y \cos \alpha + x}{y \sin \alpha}\right)$.

Step 7 : If y is negative continue, otherwise goto step 12.

Step 8 : If x is negative continue, otherwise goto step 10.

Step 9 : Set $\theta = \theta - 180^0$, goto step 12.

Step 10: If θ is positive, goto step 9.

Step 11: Set $\theta = \theta + 180^0$.

Step 12: Store θ in the file PDM.DAT.

Step 13: Exit.

Example 6.7

The patient data matrix of 12-lead ECG from a 58 year old male patient is given in Table 6.11. Assume that the example ECG obtained from a 58 year old male has already been processed by the string generation program, the string compression program, the wave locations program, the axis analysis program, measurement program and the heart rate measurement program.

The patient data matrix thus produced is shown in Table 6.11. The last row marked as 'OTHER' contains three information in the first three columns. These are age, axis of the heart and the heart rate of the patient. The other columns of that row are not used and so those contain zero values.

6.15 Concluding remarks

The feature extraction strategies of an ECG wave is presented in this chapter. All the algorithms are developed with respect to a single lead for clarity of presentation. In practice, each algorithm has to be repeated for all the leads. The set of primitives has been developed by considering the actual wave shapes consisting of three segments, Viz., horizontal, positive and negative. Eight pattern primitives are defined and context-free grammars in Chomsky normal form are generated in order to identify the sub-complexes of each detected complex. The C-Y-K parsing algorithm is used for both the syntax analysis and parameter measurement purposes. Necessary algorithms developed for different types of processing are presented.

Finally, simple algorithms for measuring the i)heart rate, and ii)electrical axis of the heart from an ECG wave have been proposed.

Table 6.11 Patient Data Matrix.

PARA METERS	LEAD NUMBERS I	II	III	aVR	aVL	aVF	V1	V2	V3	V4	V5	V6
PA	1.98	2.00	-2.00	-1.00	1.00	1.00	-1.00	2.00	2.00	1.00	1.00	1.00
PD	0.11	0.13	0.12	0.12	0.11	0.12	0.12	0.12	0.11	0.12	0.12	0.12
P'A	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
P'D	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
QA	-1.05	-1.00	0.00	0.00	0.00	-1.00	0.00	0.00	0.00	-2.00	-2.00	-2.00
QD	0.01	0.02	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.02	0.02	0.02
RA	10.00	11.00	5.00	0.00	17.00	2.95	0.00	3.00	3.00	40.00	40.00	39.00
RD	0.07	0.09	0.08	0.00	0.11	0.05	0.00	0.02	0.02	0.06	0.06	0.07
R'A	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
R'D	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
SA	-6.00	0.00	-8.00	-18.00	0.00	-11.01	-37.00	-22.00	-22.00	-12.00	-12.00	-11.00
SD	0.02	0.00	0.11	0.12	0.00	0.05	0.15	0.10	0.10	0.02	0.02	0.02
S'A	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
S'D	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
TA	2.01	3.00	1.00	-3.00	-3.00	2.00	-7.00	6.00	6.00	7.00	8.00	7.00
TD	0.11	0.12	0.11	0.12	0.12	0.12	0.12	0.12	0.11	0.11	0.12	0.13
VAT	0.05	0.06	0.05	0.00	0.07	0.04	0.00	0.01	0.01	0.07	0.07	0.07
PR	0.16	0.16	0.14	0.16	0.16	0.16	0.16	0.16	0.16	0.16	0.16	0.16
QT	0.27	0.28	0.25	0.28	0.28	0.28	0.27	0.27	0.27	0.26	0.28	0.27
ST	0.04	0.06	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04
QRS	0.11	0.12	0.11	0.12	0.11	0.12	0.12	0.12	0.12	0.11	0.12	0.12
S-Tonset	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
OTHER	58.00	-15.00	95.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Amplitude in mm. Duration in second.

Age: 58 years.
Axis: -15 degree.
Heart rate: 95 beats per minute.

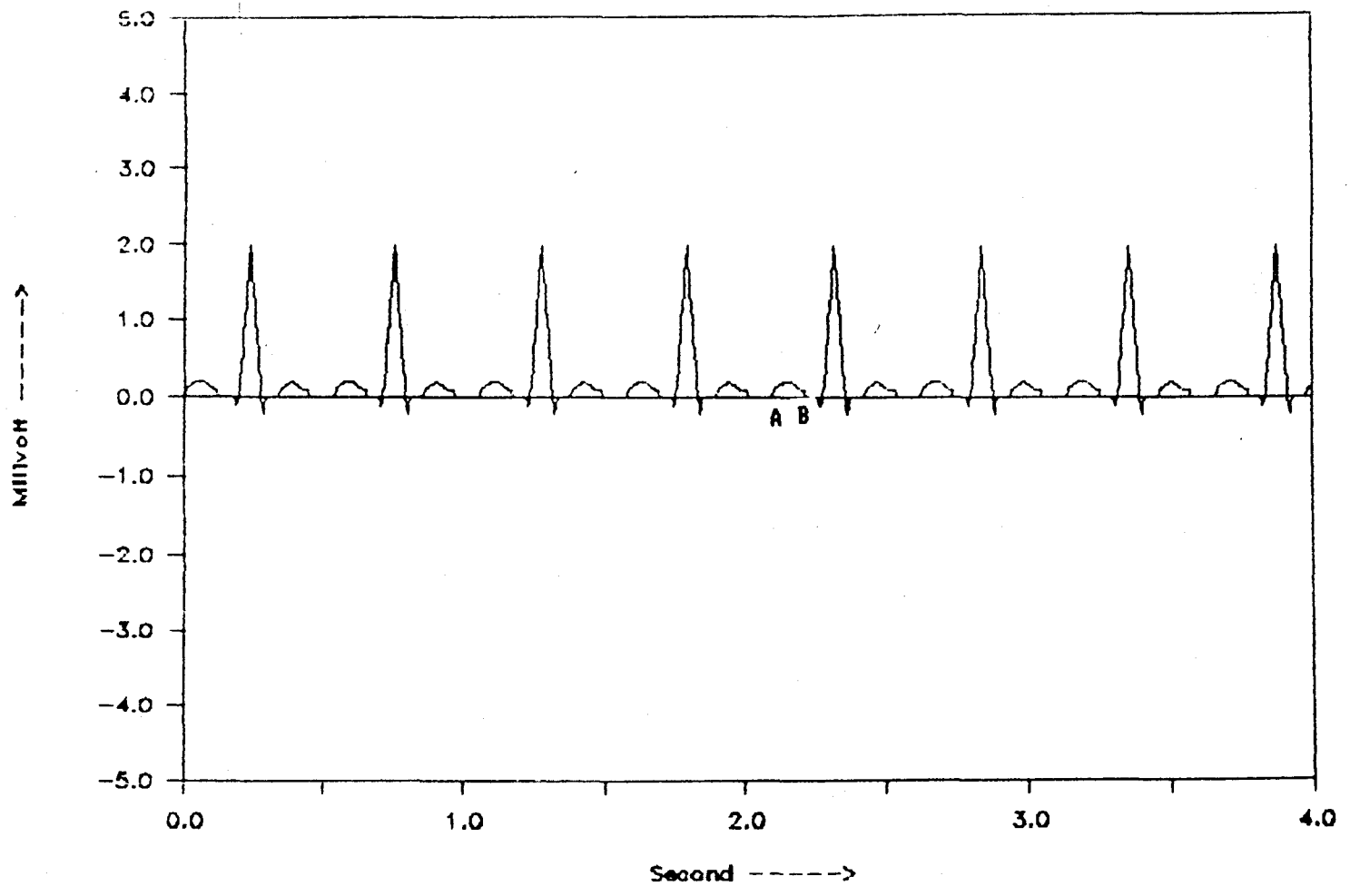

Fig. 6.1 The analog ECG signal (Lead I).

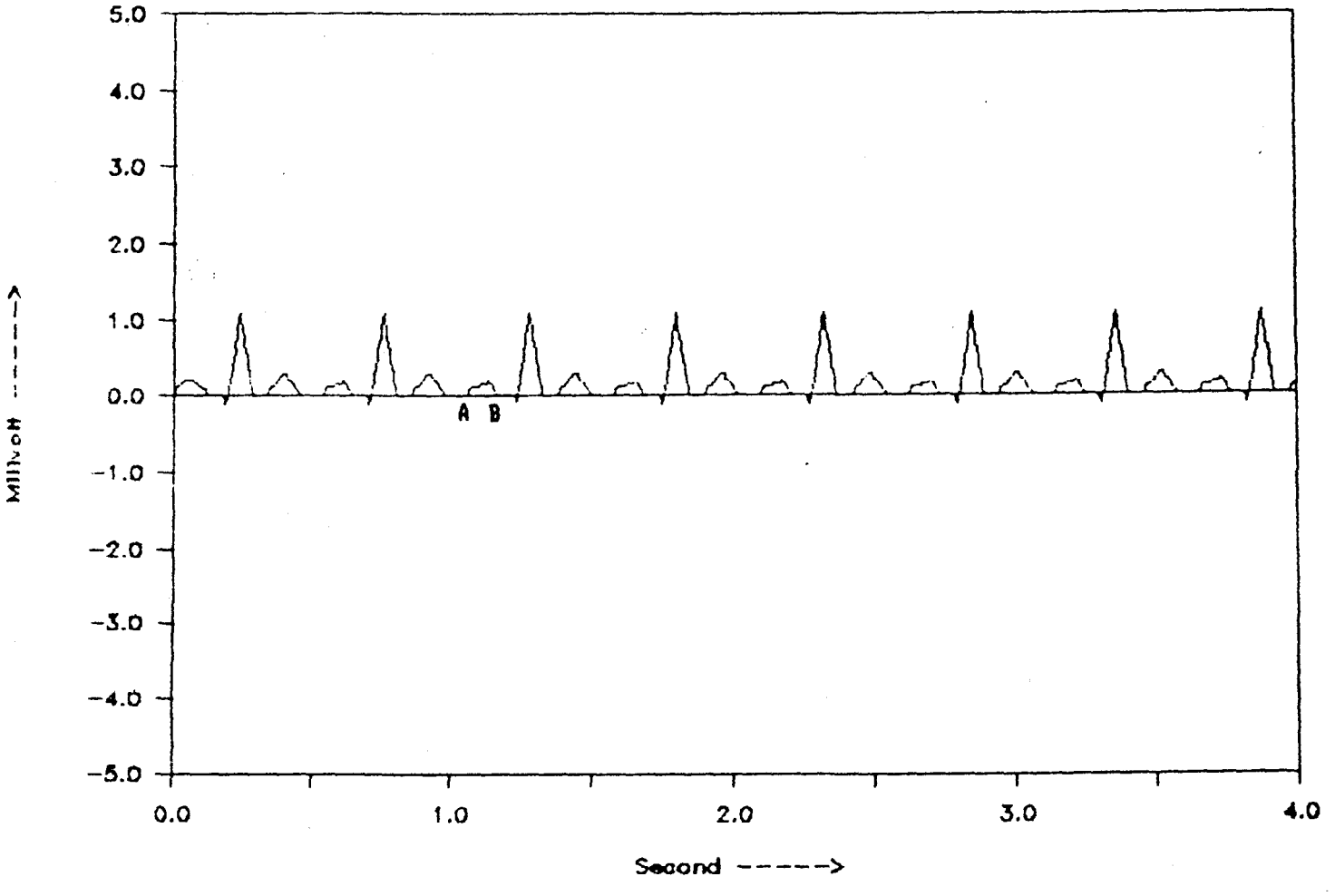

Fig. 6.2 The analog ECG signal (Lead II).

name in the Turbo Prolog program. For the sake of simplicity the file "PAT.DAT" will be called as "reply_file" henceforth.

In the so called consultation session (paradigm) of the proposed system a number of questions will be asked depending on the disease criteria and these will be answered either 'y' or 'n' by reading the reply_file. The dynamic database stores the facts relating to the diagnostic criteria as well as the diagnosed diseases. At the end of the consultation the occurances of different diseases will be displayed if they are manifested in the patient's ECG.

7.2 Selection of diseases

To demonstrate the feasibility of proposed method in diagnosis of cardiac diseases, it would be impractical to study all the many types and degrees of heart diseases that appear in ECG waveforms. As an illustration only five important diseases will be considered here, but the method presented can be extended to include any number of heart diseases. The diseases considered are listed below :

1. Left bundle branch block (LBBB).
2. Right bundle branch block (RBBB).
3. Left ventricular hypertrophy (LVH).
4. Left anterior hemiblock (LAH).
5. Left atrial hypertrophy (LAH1).

Disease is thought to occur independently in the auricles and ventricules of the heart. Monitorying of auricular electrical activity is an important part of determining the basic rhythm of the heart, but ventricular electrical activity is highly