ECG Analysis for Automated Diagnosis of Subclasses of Supraventricular Arrhythmia

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Abstract – A Markov-model based technique is proposed to automatically detect a patient's disease state into different subclasses of Supraventricular arrhythmia based upon automated ECG analysis. Separate Markov-models have been developed for each subclass using a finer resolution of P-waves that takes into account left and right atria and multiple slopes of the P-waves. ECG data from Physionet database has been used to train the Markov-models. Patient’s ECG has been transformed to a probabilistic-transition-graph. Graph based comparison has been used to match probabilistic-transition-graph derived from Patient’s ECG and Markov-models of the corresponding subclasses to identify the patient’s disease state in real time. The result correlates well with the physician's diagnosis of supraventricular arrhythmia. Algorithms and sensitivity analysis have been presented.

Keywords: Arrhythmia, ECG analysis, Markov model, Patient diagnosis, Patient monitoring

1 Introduction

As society is aging, the mortality caused by cardiovascular diseases is increasing [4]. One of the major problems is sudden death caused by arrhythmias [4, 19, 22]. During arrhythmias, heart-beat becomes rapid, irregular, and unsynchronized. Statistics from the Center for Disease Control and Prevention (CDC) estimates sudden cardiac death rates due to arrhythmias at more than 600,000 per year [4]. Arrhythmias occur suddenly with varying refractory period, may disappear, and may not be able to reproduce during regular checkup [12]. Recording and classification of the subclasses of arrhythmias when it occurs can timely save many lives for our aging yet mobile society.

Arrhythmia is broadly classified as: 1) supraventricular arrhythmia [9, 12, 14, 22] that originate due to electric impulse irregularity and atria enlargement in the upper chambers; and 2) ventricular arrhythmia [12, 21] that originate due to conduction irregularity in the ventricles. Arrhythmia classification is necessary for attending physicians after cardiac surgery as some types of arrhythmias such as supraventricular arrhythmia [9, 22] occurs frequently post-cardiac surgery [19, 20, 22], and can be fatal if not treated immediately [19, 20, 22].

Depending on the origin of electric impulses, supraventricular arrhythmia is classified into: atrial fibrillation (AFib), atrial flutter (AFlu), junctional tachycardia (JTachy), atrial-ventricular nodal reentry tachycardia (AVNRT) and ectopic atrial tachycardia (EAT).

Previous approaches for automated detection of subclasses of arrhythmias [8, 13, 17, 26] have met with limited success due to the lack of electric pulse synchronization that causes inconsistent morphological changes in P-QRS-T waveforms and their occurrence-sequence due to irregular beats. Previous works are limited to the separation of supraventricular arrhythmia from ventricular arrhythmia [2, 8, 26] and limited identification of a subclasses of arrhythmias [7, 10, 13, 17, 21].

Different subclasses of supraventricular arrhythmia are treated differently [9, 14, 22] using different medications [14, 20, 22]. Misdiagnosis of different forms of supraventricular arrhythmia can be fatal [19, 22] or mistreatment can cause serious side-effects [10, 19, 20, 22]. Hence, correct automated diagnosis of subclasses of supraventricular arrhythmia is important.

This paper describes an improvement in automated diagnosis of a patient suffering from supraventricular arrhythmia. We develop Markov-models for major subclasses of supraventricular arrhythmia, and employ these models for the diagnosis of a patient’s condition in real time.

The major technical contributions of this paper are:

1. Resolution of P-waves into four states in a Markov-model based on electric impulse traversal in left and right atria and the positive and negative slopes of P-waves. This resolution generates distinct Markov-models for each subclass of supraventricular arrhythmia.

2. Construction of distinct Markov-model for each subclass of supraventricular arrhythmia by studying Physionet public database [23]; and

3. Modeling patient’s ECG as probabilistic-transition-graph (PTG), and matching PTG with the probability-graphs corresponding to the Markov-models to identify exact disease states.

The paper is organized as follows: Section 2 describes the background information about subclasses of supraventricular
arrhythmia and needed definitions related to graph matching. Section 3 describes our approach and the training of the Markov-models with finer classification of P-waves for each subclass of supraventricular arrhythmia. Section 4 describes an algorithm to identify disease state using probabilistic-graph matching. Section 5 describes an implementation. Section 6 discusses the results. Section 7 compares this work with other related works. The last section concludes the work.

2 Background

Supraventricular arrhythmia is a rapid heart rhythm where electrical impulse travels from the upper chambers (SA-node or ectopic foci in atria) to ventricles via AV-node [9, 12]. Supraventricular arrhythmia occurs due to the lack of synchronization of depolarization and repolarization caused by rapid misfiring (or lack of firing) of SA-node, presence of a cyclic electric current in atria, and/or impulse arising from junction valves or one or more ectopic mass in atria. There are five major subclasses, namely, atrial fibrillation (Afib), atrial flutter (AFlu), junctional tachycardia (JTachy), atrio-ventricular nodal reentry tachycardia (AVNRT), and Ectopic atrial tachycardia (EAT).

2.1 Supraventricular arrhythmia subclasses

Atrial fibrillation (Afib) occurs when action potentials fire very rapidly within the pulmonary veins or atria in a chaotic manner [7, 12, 17]. The result is a very fast atrial rate (about 400-600 beats per minute). The AV-node becomes intermittently refractory and allows only a fraction of atrial action potentials to reach the ventricles.

Atrial flutter (AFlu) occurs when a reentrant electrical circuit is present in atria causing a repeated loop of electrical activity to depolarize the atrium at a rate of about 250-350 beats per minute [12, 17, 22]. This produces a characteristic "sawtooth" pattern. Only a fraction of P-waves are conducted through the AV-node. Typical AFlu rotates “counterclockwise” in direction, and results in negatively directed flutter waves in the inferior leads.

Junctional tachycardia (JTachy) arises from the area encompassing AV-node, his-bundle and immediately surrounding atrial tissue [12]. Depolarization proceeds towards atria. Hence P-waves in inferior leads are negative. Discharge has very little distance to travel to the AV-node. Hence, PR interval is very short. In some cases, atrial depolarization coincides with ventricular depolarization. In that case, P-wave gets buried in QRS-complex. It is also possible that atrial depolarization follows ventricular depolarization. Then P-wave occurs after QRS-complex.

Atrial-ventricular nodal reentry tachycardia (AVNRT) is a common form of nodal arrhythmia [9, 12, 14]. In AVNRT, atrial depolarization is conducted through AV-node via two tracts instead of one [9, 12, 14]. One tract functions normally and other conducts the impulse slowly. An impulse travels over the slow pathway towards the ventricles and returns via the faster pathway to the atria. The retrograde P-wave is embedded inside QRS-complex or appears after the QRS-complex.

Ectopic atrial tachycardia (EAT) has discrete foci in the main mass of atria outside SA-node and junctional region [9, 12]. Depending on the origin of impulse atrial depolarization may (or may not) travel from right to left atria. Since the impulses travel from different ectopic foci in atria, P-wave axis keeps changing. In this case, P-wave is negative in one of the following leads I, II, III or V5 or V6.

2.2 Definitions

A weighted-graph has weighted-edges. An unweighted-edge is denoted as source-node \( \rightarrow \) destination-node. A weighted-edge is denoted as a pair of the form (source-node \( \rightarrow \) destination-node, weight). A probability-graph is a weighted-graph with probability as edge-weights. Markov-model [24] is a probabilistic finite-state automata that is modeled as a probability-graph that has one or more initial and final states. The edges in the probability-graph for a Markov-model shows the transition-probability from one state to another. A probability-graph is represented using a transition matrix such that the value in a cell \((i, j)\) represents the transition-probability from the state \(i\) to state \(j\), where \(i \leq j\). The column-id of cell with the highest value in a row gives the next most-probable transition state. The probability of a path in the probability-graph is given as the product of the edge-weights in the path.

Probabilistic-transition-graph, denoted by PTG, is a probability-graph that is constructed by analyzing a patient's ECG for a finite duration of real-time monitoring.

Most-probable-path, denoted by MPP, is the path with highest edge-weights from the initial state to the final state in a probability-graph. The edge-weights of MPP are maximum of the outgoing-edges from the corresponding source-nodes of the edges. The probability of an MPP in PTG is closest to the maximum value of 1.0 when compared to other paths.

Probability-difference, denoted as \(\delta_i\) (1 \(\leq i \leq \) number of edges in a path), is the absolute-difference \(|\beta_{i1} - \beta_{i2}|\) where \(\beta_{i1}\) and \(\beta_{i2}\) are edge-weights of the corresponding edges in the two paths of probability-graphs. Path-difference is defined as the sum of probability-differences \(\Sigma_i\) of the corresponding paths in two probability-graphs. Path-difference acts as a metrics of dissimilarity for the comparison of MPP and the corresponding path of a probability-graph: lower path-difference means that PTG is more similar to the probability-graph. It can be mathematically shown that path-difference between MPP in PTG and the corresponding path in a probability-graph is a close approximation of the absolute-difference of transition-probabilities \(\prod_i|\beta_{i1} - \beta_{i2}|\) (1 \(\leq i \leq \) number of edges in the MPP) since \(\delta_i \leq \beta_{i1}\) and \(\delta_i \leq \beta_{i2}\) in the MPP, and subterms containing factors \(\delta_i\) can be dropped from the product expansion during path-comparison as they have very small value. Similarly, the factors \(\beta_i\) is limited by the value \(\delta_i\) since \(\beta_i\) is less than and close to 1.0.
3 Approach

The overall approach is: 1) develop a Markov-model that captures all the variations of electric-impulse travel in upper chambers; 2) train the Markov-models for each subclass of supraventricular arrhythmia using well-annotated public database such as Physionet [23] that contains large number of cases of supraventricular arrhythmia; 3) perform real-time analysis of patient's ECG to get a probabilistic-transition-graph (PTG); 4) identify the most-probable-path in a PTG; and 5) develop graph matching algorithms to identify the best matching probability-graph corresponding to subclasses of supraventricular arrhythmia and the PTG. Best match is obtained using the annotations obtained through wave-peak detections ($P_{11}$, $P_{12}$, $P_{21}$, $P_{22}$, Q, R, S and T), wave-onsets and wave-offsets (Iso1, Iso2). For some cases, observed waveform could be either T-wave (in case of missing ST-segment) or elevated ST-segment (T-wave superimposed with ST-segment). Those waveforms are marked as ST/T-node in the Markov-model (see Figures 1.a and 1.b).

3.2 Trained Markov-models

Markov-models were trained using the Supraventricular Arrhythmia Database available at Physionet [23] using approximately 15 cases for each Markov-model. Approximately 1800 heartbeats were used for training each Markov-model.

![Figure 1. Trained Markov-models](image-url)
Figure 1.a describes a trained Markov-model for atrial fibrillation (AFlib). The transitions are: Iso3→P11 (P-wave present, probability 0.1); Iso3→Iso1 (P-wave missing, probability 0.9); P11→P22 (superimposed P-waves, probability 0.31); P11→P12→P21→P22 (P-wave splitting, probability 0.69); P22→Iso1 (always when P-wave occurs); Iso1→Q (Q-wave present, probability 0.91); Iso1→R (Q-wave missing, probability 0.09); Q→R (probability 1.0), R→S→Iso2 (S-wave present, probability 0.67); R→Iso2 (S-wave missing, probability 0.33); Iso2→T→Iso3 (T-wave present, probability 0.87); and Iso3→Iso1 (T-wave missing, probability 0.13). Multiple sites within atria depolarize independently. Low amplitude action-potentials fire rapidly resulting into missed P-waves as shown by the transition Iso3→Iso1.

Figure 1.b describes a trained Markov-model for atrial flutter (AFlu). The discharge of depolarizing current from the re-entrant loop may produce large negative deflections in the inferior leads causing negative P-waves. P-waves are missed occasionally due to fast atrial activity. Negative P-waves are shown by the transition-sequence P12→P11→P22→P21. The transition P21→P22 is due to the possibility of more than one P-wave for one QRS-complex. Sometimes T-wave gets superimposed with the next P-wave that shows up as missing T-wave as illustrated by the direct transition Iso3→Iso1.

Figure 1.c describes a trained Markov-model for junctional tachycardia (JTachy). The probability transition-sequence P12→P11→P22→P21 is due to the presence of negative P-waves in the inferior leads. The P-waves occasionally coincide with the QRS-complexes as illustrated by transition Iso3→Q. In some cases, P-wave appears after QRS-complex as illustrated by the transition from S→P12.

Figure 1.d describes a trained Markov-model for AV nodal reentrant tachycardia (AVNRT). The transition Iso3→Iso1 illustrates retrograde P-wave due to the superposition with QRS-complex. The transition S→P11 shows P-wave appearing after QRS-complex. T-wave appearing after P-wave is shown by the transition P22→T.

Figure 1.e describes a trained Markov-model for ectopic atrial tachycardia (EAT). Transition from Iso3 may go to P11 (for positive P-wave) or to P12 (negative P-wave). Since origin of impulse is not SA-node, impulse traveling from AV-node is weak causing undetectable low amplitude Q-waves. Hence, the transition Iso1→R occurs with sufficient probability (0.24).

4 Algorithm to identify patient’s state

Probabilistic-transition-graph (PTG) for patients are constructed from ECG waves in real-time using a moving window of 30 seconds to monitor a patient in real-time. The problems of identifying patient’s disease state reduces to matching the PTG with the probability-graphs corresponding to Markov-model of each arrhythmia-subclass and identifying the closest match.

The algorithm to match the PTG with the probability-graphs has four steps:

Step 1: identifying the subset of probability-graphs corresponding to the Markov-models of arrhythmia-subclasses that contain all the edges of PTG. If any edge in PTG is missing from a probability-graph, then the corresponding arrhythmia-subclass is ruled out;

Step 2: deriving the most-probable-path (MPP) in PTG;

Step 3: pairwise matching the MPP in PTG with the subset of probability-graphs derived in Step 1;

Step 4: sorting the path-differences of the matched paths to identify the probability-graph with the smallest path-difference.

Path-difference between MPP in PTG and the corresponding path in a probability-graph is calculated by iteratively summing up the probability-difference $\delta_i$ (difference in the edge-weights) between the corresponding edges in two paths.

An algorithm is described in Figure 2. The probability-graphs are represented as transition-matrices denoted by $T_i$ ($1 \leq i \leq n$ of number of transition-matrices). The cell values in $T_i$ represent the transition-probabilities. PTG is modeled as a transition-matrix denoted by $T^p$. The cell-value in the $i$th row and $j$th column of $T^p$ is denoted by $T^p(i, j)$, and shows the weight of the edge $i\rightarrow j$. A row in a transition-matrix contains the edge-weights of outgoing-edges from a node; and the highest cell-value in a row gives the next node in the MPP.

The set of probability-graphs that contain PTG as a subgraph are denoted by $S^m$. PTG is identified as a subgraph of one or more probability-graphs by testing that the set of unweighted-edges $S^p$ in the transition-matrix $T^p$ is a subset of the set of unweighted-edges $S_i$ in the transition-matrices $T_i$ ($1 \leq i \leq n$ of number of probability-graphs). If there exists an edge $E \in S^p$ such that $E \notin S_i$ then the corresponding $T_i$ is not included in the set $S^m$.

The pseudo-code to derive MPP is based upon: 1) starting from the initial state $Iso3$; and 2) iteratively finding the outgoing weighted-edge with highest weight ($cur_state \rightarrow next_state$, max $prob$) and including the weighted-edge in the accumulator $ptg\_mpp$ until the $Iso3$ (final state) is reached again. $Iso3$ is both initial and final state since P-QRS-T cycle repeats. The variable $ptg\_mpp$ accumulates the sequence of edges in the MPP.

To match the MPP in PTG and the corresponding path in a probability-graph, the variable $ptg\_mpp$, is copied in the variable $edge\_set$. The edges in $edge\_set$ are matched with the edges in edge-set $S_i$ of $T_i$ using an iterative-loop. Next edge, denoted by the variable $cur\_edge$, is extracted from the $edge\_set$, and the corresponding outgoing-edge $E$ is identified in the edge-set $S_i$. The absolute-difference of the weights of the two edges $|w_1 - w_2|$ is added to an accumulator $path\_diff$. After the variable $edge\_set$ becomes empty, all the edges in the MPP have been compared, and the variable $path\_diff$ contains the path-difference between two paths. The pair ($path\_diff$, $D_i$) is inserted into a set $matched\_set$ where $D_i$ is the name of the corresponding disease-state.

After pairwise comparing MPP and the corresponding paths of the probability-graphs, the elements on the set $matched\_set$ are sorted in the ascending order of path-difference values. The corresponding disease state is identified as the second field of the first element in the sorted-sequence.
Algorithm Diagnose-patient-state

Input: 1. Transition-matrix $T^p$ for the patient’s PTG;
2. Set of transition-matrices $\{T_1, \ldots, T_M\}$ for the probability-graphs;
3. Set of the corresponding disease-states $\{D_1, \ldots, D_M\}$;
Output: Diagnosed disease-state $D^p$;

{ % Find the probability-graphs that include PTG
  $S^p = \text{set of unweighted-edges in the transition-matrix } T^p$; $S^M = \{ \}$;
  for each $T_i$, ($1 \leq i \leq M$) do { % identify probability-graphs
    $S_i = \text{set of unweighted-edges in } T_i$;
    if($S^p \subseteq S_i$) $S^M = S^M + T_i$;
  }

  % Find the most-probable-path in the transition-matrix $T^p$;
  initial_state = 'Iso 3'; final_state = 'Iso3';
  cur_state = initial_state; ptg_mpp = \{ \};
  do { max_prob = maximum($T^p(cur_state, col)$ for $1 \leq col \leq 13$);
    next_state = col such that $T^p(cur_state, col) = \text{max_prob}$;
    ptg_mpp = ptg_mpp + (cur_state $\rightarrow$ next_state, max_prob);
    cur_state = next_state; }
  until (cur_state == final_state);

  % Match the MPP in PTG with the probability-graphs
  matched_set = \{ \}; % initialize matched_set to an empty set
  for each $T_i$ in $S^M$ do { % find matching path in probability-graph
    edge_set = ptg_mpp; path_diff = 0.0;
    $S_i = \text{set of weighted-edges in } T_i$;
    while (non_empty(edge_set)) {
      cur_edge = next_element(edge_set); % get next edge
      cur_edge = next_element(edge_set); % get next edge
      let $E$ be of the form $(\text{src} \rightarrow \text{dest}, w)$;
      search the edge $E$ of the form $(\text{src} \rightarrow \text{dest}, w) \in S_i$;
      path_diff = path_diff + absolute_value($wi - w2$);
      edge_set = edge_set $\rightarrow$ cur_edge;
    }
    matched_set = matched_set + (path_diff, $D_i$);
  }
  sorted_set = ascending_sort(matched_set);
  $D^p = \text{second_field}(\text{first_element(sorted_set)})$;
  return($D^p$);

Figure 2. Matching patient’s PTG with Markov-models.

Example 1

The ECG of a patient was procured from the MIT Physionet database [23]. Patient is a 36-year-old female with a heart rate of 270 bpm (beats per minute). She had a prior history of atrial fibrillation, and was suffering from right atrial hypertrophy. The PTG is shown in Figure 3. The path with bold edges shows the MPP $\text{Iso}_1 \rightarrow P_{11} \rightarrow P_{22} \rightarrow \text{Iso}_1 \rightarrow Q \rightarrow R \rightarrow S \rightarrow \text{Iso}_2 \rightarrow T \rightarrow \text{Iso}_3$.

The edge $P_{22} \rightarrow \text{Iso}_1$ is missing from the probability-graphs of AFib, JTachy and EAT. The edge $P_{11} \rightarrow P_{22}$ is missing from the probability-graph of AVNRT. Hence, the arrhythmia-subclasses AFib, JTachy, EAT, and AVNRT are ruled out. All the edges of PTG are present only in the probability-graph of AFib. Hence, the patient’s disease state is identified as atrial fibrillation that matches with the clinical interpretation. The overall path-difference between the MPP of PTG and the corresponding path in AFib is 1.42.

5 Implementation

The software implementation consists of five interconnected modules: 1) module-1: P-QRS-T-waveform detection and annotation; 2) module-2: slope detection and annotation of $P_{11}, P_{12}, P_{21}$ and $P_{22}$; 3) module-3: development of transition matrix for Markov-model from P-QRS-T annotation; 4) module-4: development of transition matrix for analyzing patient’s ECG; and 5) module-5: graph matching algorithm. The software used available C-library functions in WFDB (Waveform Database) library [28] (available at http://www.physionet.org/physiotools/wfdb.shtml#dowloadng) for module 1. The output of this software gave us the onset, offset and amplitude of P-waves, QRS-complex and T-waves. Remaining modules were developed in C-language to be consistent with WFDB library [28].

The output from the module 1 and the ECG data-file were used as input to the module-2. Module-2 derived slopes of P-waves; split QRS-complex into Q-slope, R-slope, and S-slope; and split P-wave into four segments: $P_{11}, P_{12}, P_{21}$, and $P_{22}$. P-wave split was identified using differentiation of the waveform and comparing the point(s) of zero-slope (slope = 0) with the offset-point of P-wave. The presence of two zero-slope (slope = 0) points describes P-wave split into P-wave from the right atrium followed by P-wave from the left atrium. In the case of P-wave split, first rising edge was called $P_{11}$, followed by first falling edge as $P_{12}$, followed by the second rising edge as $P_{12}$, followed by the second falling edge as $P_{22}$. In the absence of second zero-slope point, the P-waves from left and right atrium were superimposed; the first rising edge was labeled as $P_{11}$, and the following falling edge was labeled $P_{22}$. In the case of P-wave inversion, shown by first edge as falling edge, first falling edge was labeled as $P_{12}$, and the following rising edge was labeled as $P_{22}$.

The observations (amplitudes and durations of waveforms) from ECG signal were used to derive transition probabilities for each state. Markov-model was developed for each subclass by obtaining transition probabilities using Baum-Welch Algorithm [24]. Baum-Welch algorithm is an expectation-maximization technique. Using this technique, those edges with very small probability below a threshold (threshold-probability < .001) were discarded to reduce noise. The graph-matching algorithm was coded in C-language.

5.1 Database

The data for training the Markov-model was obtained from MIT Physionet database [23]. The database contains 48 fully annotated half-hour excerpts of two-channel ambulatory ECG recordings. The recordings were digitized at 360 samples per second per channel.
6 Results and discussions

In this section, we compare the statistics based upon our analysis of the patients' information available in a public database available at Physionet [23] and St. Petersburg 12-lead database [25]. The data was extracted and analyzed by an expert cardiologist to identify various subclasses of supraventricular arrhythmia. The data of 30 patients were automatically analyzed using multiple windows of 30 seconds to generate PTGs of the patient's condition. The ECG in the windows was reconfirmed for the correctness by the physician, and was automatically analyzed using our graph matching algorithm. The result of sensitivity analysis (Sensitivity = true positives/ (true positives + false negatives)) is summarized in Table I.

Table I. Statistics of ECG diagnosis

<table>
<thead>
<tr>
<th>Disease State</th>
<th>Number of Patients</th>
<th>Sensitivity</th>
</tr>
</thead>
<tbody>
<tr>
<td>AFib</td>
<td>30</td>
<td>92%</td>
</tr>
<tr>
<td>AFlu</td>
<td>30</td>
<td>89%</td>
</tr>
<tr>
<td>AVNRT</td>
<td>30</td>
<td>90%</td>
</tr>
<tr>
<td>JTachy</td>
<td>30</td>
<td>84%</td>
</tr>
<tr>
<td>EAT</td>
<td>30</td>
<td>81%</td>
</tr>
</tbody>
</table>

Table I shows that the subclasses of supraventricular arrhythmia are identified with high percentage of accuracy. JTachy and EAT are difficult to identify due to occasional and asynchronous superimposition of P-waves in QRS waveforms or T-waves. Few misclassification of AFib into AFlu or AVNRT are due to the close probability of QRS-complex in the case of missing P-wave. Misclassification of AFlu into: 1) EAT are due to negative P-waves; and 2) AFib are due to similar transition probability of QRS-complex in case of missing P-waves. Misclassifications of AVNRT into AFib are due to similar transition probability of QRS-complex. Misclassification of JTachy into AFlu or EAT are due to the negative P-waves. Misclassifications of EAT into AFlu are due to the negative P-waves and missing Q-waves. Misclassifications can be reduced by performing statistical analysis on multiple PTGs derived from the same patient and increasing the size of the training database.

The overall analysis time varied between 60 – 100 milliseconds based upon the number of ECG waveforms present in 30 second window. Due to the varying frequency of waveforms present in different patients at different times, the analysis time was different for different cases. However, the analysis is done in real-time.

7 Related works

ECG analysis has been done for wave detection, wave segmentation and arrhythmia classification using various techniques including Hidden Markov-model [2, 6, 8, 26], Wavelet transform [13, 17], and combination of Hidden Markov-model and wavelet transform [3].

Some algorithms have been developed based on wavelet transform [5, 13, 18] for detecting ECG characteristic points that can distinguish between high P-wave, T-wave, QRS-complex and baseline drifts. Some techniques [3] combine wavelet transform and Hidden Markov-model to get precise segmentation and classification including P, QRS and T, waveform detection, identification of normal waves, and premature ventricular contractions. Some techniques [27] detect morphology changes in waveforms using HMM that can classify beats between normal and premature electrical activity based on QT interval analysis [10].

Coast [8] presented arrhythmia analysis using HMM for the first time. The importance of P-wave detection for supraventricular arrhythmia along with QRS detection for ventricular arrhythmia was realized and addressed by using P-wave detection technique [7, 15]. However, these techniques do not precisely diagnose and identify all arrhythmia subclasses due to the insufficient P-wave modeling in HMM. Abnormality of P-wave is one of the important attributes to be considered while classifying supraventricular arrhythmia. None of the previous works identify exhaustively different subclasses of arrhythmia.

P-wave analysis by Clavier [7] combines Markov-model, slope observation and coefficients of ECG wavelet transform. Then P-wave delineation is done to get the positive and negative slopes of the ECG. These are represented as P1 for the positive slope of atrial activation and P2 for the negative slope of atrial activation. Then classification is done based on four parameters: time, space, spectral and wavelet entropy. Similarly QRS-complex is broken into Q1 for positive slope of ventricular activation and Q2 for negative slope of ventricular depolarization. T-wave is broken into T1 and T2 for positive and negative slope of ventricular repolarization. Then Markov-model is developed on state transition probabilities obtained from a database. Their work is limited as they do not take into account P-waves from left and right atria and P-wave inversions.

In our proposed Markov-model, the finer decomposition of P-waves into four different states based upon P-wave splitting and atria traversal captures different possibilities of electric impulse travel in upper chambers. We present a clear graph matching algorithm-based most-probable-path in patient's Markov-model to identify a subclasses of arrhythmia. We extend the work by Clavier [7] by introducing four different states using both left and right atria and P-wave inversions.

8 Conclusions and future work

In this paper, we have proposed a new Markov-model to diagnose different subclasses of supraventricular arrhythmia. The trained Markov-models have high sensitivity to identify patient's disease state during real-time monitoring. The approach when augmented with morphological analysis [10, 27], improved statistical analysis of multiple PTGs from a patient and bigger training database will facilitate automated identification of various subclasses of supraventricular arrhythmia with a high confidence factor. Currently, we are refining Markov-model to include morphological data such as amplitude, interval, inversion of T-wave, and change in
isoelectric line. We are also extending the model to identify subclasses of ventricular arrhythmia [21].

9 References


