Model-Based Interpretation of Cardiac Beats by Evolutionary Algorithms

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Abstract

This work presents current progress of a new system for cardiac beat interpretation, combining model-based reasoning and evolutionary computing. As a difference from other model-based systems, the proposed approach directly integrates ECG signals with a cardiac model. Model-based reasoning is formalized as the minimization of an error function defined between the observation and the model's output. This paper presents a new adaptation process permitting the reproduction of a sequence of cardiac beats and the generation of beat interpretations by means of ladder diagrams. Results show the application of the proposed approach to two pathological rhythms from the MIT-BIH arrhythmia database. Although some limitations persist, preliminary results are encouraging and show the potentiality of this approach to exploit anatomic and physiological knowledge in order to explain underlying conduction disorders.

1. Introduction

Automatic interpretation of cardiac beats remains as a challenging problem. Different approaches have been proposed in the literature, but no solution is still available for an effective application in clinical practice. Current rhythm interpretation systems can be classified in two classes, according to the way they represent the knowledge about the cardiac rhythm: those based on "shallow" or experiential knowledge and those based on "deep" electrophysiological knowledge. Most of the current approaches are part of the former group and their main limitations are related to the difficulty of creating and maintaining a complete knowledge base and appropriate classification rules. Deep knowledge can be introduced by means of model-based systems (MBS), in which a model of the underlying physiology is built, leading to a comprehensive and compact knowledge representation. These systems present the advantage of being able to generate a meaningful explanation of the observation, useful for diagnosis or prediction purposes. However, they require a more complex reasoning mechanism.

Current MBS for the diagnosis of cardiac arrhythmia can be summarized into three representative systems: the set of "Ticker" models [1], "EINTHOVEN" [2] and "HOLMES" [3]. These systems are based on spatio-temporal electrophysiological cardiac models, with varying degrees of detail and present a reasoning mechanism, generally based on a hypothesize-and-test paradigm followed by a pruning phase, in order to keep the most significant interpretations. Among these systems, only EINTHOVEN counts with a complete reasoning structure that has been evaluated on different cardiac rhythms [2].

Besides the still limited rhythm explanation capabilities, these systems lack a practical way of associating the modeled knowledge with clinical observations. ECG analysis is based on a set of hand-made annotations about the occurrence of atrial and ventricular activities, accompanied, in some cases (EINTHOVEN and HOLMES) with a qualitative morphological description of each observed wave. The absence of a direct automatic integration of model and observed phenomena represents an important limitation of current MBS for an on-line implementation. This paper presents current progress of a new model-based system named CARMEM (Cardiac Arrhythmia Recognition by Model-based ECG Matching), presenting such a direct signal/model integration.

2. Proposed approach

An overview of CARMEM is shown in Fig. 1. Two main processing levels can be identified: *i)* the lower level, which is responsible for detecting *P*-waves and *QRS* complexes from the observed ECG and *ii)* the higher level, in which a semi-quantitative model of the cardiac electrical activity is used to represent medical knowledge and to propose an interpretation of the observed phenomena. In order to couple these two levels, an error function is defined between a set of observed indicators (X_O) and an equivalent set of simulated indicators (X_S). Model-based reasoning can thus be formalized as an optimization problem, directed to minimize this error function.

Concerning the low-level processing, detection of *QRS* complexes and, particularly, of *P*-waves can be regarded as a very difficult problem in the presence of noisy

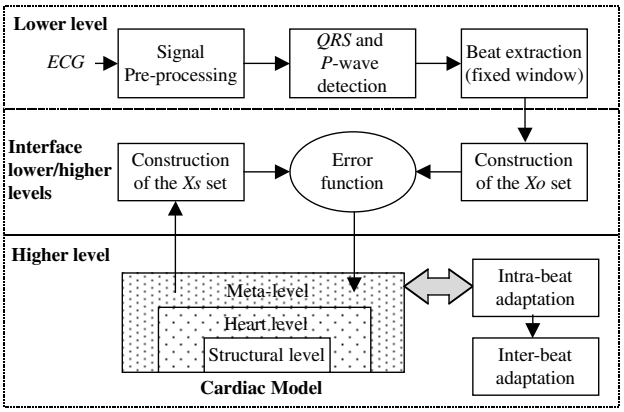

Figure 1. Overview of the CARMEM system.

data. Improvement of the detection performance in these conditions has been a research line undertaken in our laboratory and new multi-sensor approaches has been proposed [4].

The high-level processing is constituted by: *i)* a semi-quantitative, cellular automata model of the cardiac electrical activity, *ii)* an intra-beat adaptation module, which adapts the model's parameters in order to reproduce and explain individual beats and *iii)* an inter-beat adaptation module that adjusts the parameters of the model so as to reproduce the observed cardiac rhythm, by using parameters found during the intra-beat adaptation. The cardiac model in CARMEM has been presented in [5] and the intra-beat adaptation in [6]. This work recalls briefly the main components of the system and presents a preliminary inter-beat adaptation process.

2.1. Overview of the CARMEM model

CARMEM contains a dynamic, semi-quantitative, cellular-automata model of the cardiac electrical activity. This model is composed of a set of interconnected macro-cellular structures of two kinds: nodal automata (NA) and myocardial automata (MA). Each automaton can be in one of four physiological states: slow diastolic depolarization (SDD) (for NA) or idle (for MA), upstroke depolarization period (UDP), absolute refractory period (ARP) and relative refractory period (RRP). Transitions between these states are controlled by a set of internal real-valued parameters, representing the duration of each physiological phase. The basic model presents the same abstraction level as EINTHOVEN or HOLMES and is composed of 16 automata (ten NA and six MA), representing: the sino-atrial node; the upper and lower parts of internodal atrial tracts; the atrio-ventricular node; the upper and lower parts of the bundle of His; the upper and lower, left and right bundle branches; the upper and lower parts of both atria and the upper and lower, left and right ventricles. New automata can be added and connected dynamically to the basic model in order to represent other structures, such as ectopic pacemakers, accessory pathways, etc. However, as in other models presenting the same anatomo-physiological level of detail, the model in CARMEM is not able to generate some pathological rhytms like atrial or ventricular fibrillation or flutter.

The individual contribution of each MA to the vector-cardiogram (VCG) is calculated during the phases of depolarization and repolarization by a set of templates. These contributions are added in a sample-to-sample basis, in order to obtain a VCG that can be projected onto any chosen set of ECG leads. More details about the VCG/ECG synthesis process can be found in [5].

The model's meta-level allows interfacing to other physiological models (such as a model of the baroreflex), or the implementation of external algorithms to adapt the parameters for dynamic simulations. An explanation of each simulated beat, by means of ladder diagrams, is also generated in this level. The meta-level is essential to perform model-based interpretation, allowing to adapt the cardiac model in order to reproduce observed phenomena.

2.2. Signal-model interface

The low-level signal processing modules are applied to an observed ECG lead to minimize the different types of noise and to detect the instant of occurrence of *P*-waves ($\tau_o^{p_i}$) and *QRS* complexes ($\tau_o^{q_i}$) [4]. For each *QRS* detection, its associated beat (beat i) is extracted by means of simple windowing (B_o^i). The model is able to generate a simulated beat (B_s^i), as well as the instants of occurrence of the simulated *P*-waves ($\tau_s^{p_i}$) and *QRS* complexes ($\tau_s^{q_i}$). A transformation is then applied to B_o^i in order to obtain the same dynamic range as B_s^i. Two sets are constructed, one for the observed activity ($X_O^i = \left\{B_o^i, \tau_o^{p_i}, \tau_o^{q_i}\right\}$) and the other for the simulated activity ($X_S^i = \left\{B_s^i, \tau_s^{p_i}, \tau_s^{q_i}\right\}$). Finally, after the alignment of B_o^i and B_s^i with respect to their *QRS* detection instants, an error function is defined as

$$\varepsilon_i(X_O^i, X_S^i) = \sum_{M_1}^{M_2} \left|B_o^i(k) - B_s^i(k)\right| + \alpha \left|\tau_o^{p_i} - \tau_s^{p_i}\right| \quad (1)$$

where $M_2 - M_1$ is the beat window length and constant $\alpha \in [0, 1]$ allows to establish the relative weight of the error associated to the generation of the *P*-wave. If there is no available *P*-wave detection for beat *i*, the error function is only based on the morphological error between the observed and simulated beats. Detected *P*-waves that are not contained in one of the windows are considered as blocked *P*-waves and initiate a specific adaptation process.

2.3. Intra-beat adaptation

Once the signal-model interface has been defined, the interpretation of beat *i* can be seen as an optimization problem consisting of minimizing the error function $\varepsilon_i\left(X_O^i, X_S^i\right)$. Since the model automatically generates the ladder diagram of the simulated beat, an explanation of the *i*-th observed beat can be obtained from the optimal set of model parameters that minimizes this error function. However, this approach leads to an ill-posed problem. Moreover, due to the nature of the cardiac model, the error function ε_i is not differentiable with respect to the model's parameters, preventing the use of gradient descent methods.

Evolutionary algorithms (EA) have shown to be useful in the solution of such hard identification problems [7]. They are independent of the existence of the derivative of the error function and adapted to complex problems, presenting a big number of parameters and multiple local optima.

In the intra-beat adaptation EA, each individual represents an instance of the whole cardiac model and is formed as the concatenation of 21 segments, representing the 16 fundamental structures of the model, 4 NA representing ectopic foci and one MA, for the right free wall accessory pathway. Segments of nodal structures are constituted of three real values (durations of SDD, UDP and ARP). Segments associated with myocardial structures present two parameters (durations of UDP and ARP). Thus, chromosomes are composed of G=56 real values.

The initial population is constituted of 16 predefined beats (normal and pathological) and 34 random variations. This initialization technique allows integration of explicit medical knowledge, by introducing a set of beats observed often in clinical practice. Moreover, for the adaptation of beats $i > 1$, the solution of the beat $i-1$ is also included in the initial population. The evaluation of each individual is based on ε_i and the ranking method, adapted for function minimization, is used for individual selection [7].

In order to improve convergence and to reduce computational load, specific knowledge was introduced into the genetic operators, to give a higher modification probability to some meaningful genes in certain situations [6]. The EA is driven by a mutation process (geometrical creep mutation) and by two cross-over methods (uniform and heuristic cross-over), for which the random function generator has been modified in order to take advantage of this electrophysiological knowledge.

2.4. Inter-beat adaptation

After performing the intra-beat adaptation to reproduce each observed beat, a new adaptation phase is necessary in order to reproduce the observed rhythm. A simple version of an inter-beat adaptation is presented here. It is based on three steps:

1. Model initialization: Before reproducing beat *i*, all structures of the model are reset to their resting state (for MA) and to the beginning of the slow diastolic depolarization (for NA). Parameters obtained from the intra-beat adaptation algorithm for beat *i* are then copied in the corresponding structures of the model.
2. Pacemaker structure identification and calculation of its SDD: The solution obtained from the intra-beat adaptation process for beat *i* allows identification of its active pacemaker structure (*i.e.* the sinus node for normal beats). The SDD period for this structure is identified in order to reproduce the observed *PP* interval between beats *i*-1 and *i* (or the *RR* interval, in the case of ventricular beats).
3. Beat simulation and Lewis diagram generation: The model is used to synthesize beat *i* stopping at the end of the last simulated wave. The Lewis diagram is also generated.

3. Results and discussion

A recent work of our group has been focused on the evaluation of the intra-beat adaptation process for the reproduction and explanation of different beats from the MIT-BIH database [6]. This work showed that, even if the ladder diagrams may differ slightly for different replicas of supra-ventricular beats (with or without conduction disorders), the interpretation proposed by the model remains coherent and coincided with the annotations of the database. For ectopic beats of ventricular origin the pacemaker structure of the proposed solution was correctly identified in all cases. However, some limitations were found for the explanation of the conduction path. Most of the convergence errors observed for the intra-beat adaptation were related to the reproduction of premature ventricular complexes (PVC) and were a consequence of the limitations of the synthesis phase of the model, specially for the reproduction of T-waves [6].

The intra-beat adaptation results presented in [6] have been used in this work to test the proposed inter-beat adaptation phase. Figures 2 and 3 show the reproduction and beat interpretations of two segments obtained from records 100 and 111 of the MIT-BIH arhythmia database [8]. In each case, the upper panel shows the observed ECG (ECG_o), the middle panel shows the ECG simulated by the model (ECG_s) after intra and inter-beat adaptations and the lower panel presents the ladder diagram.

Figure 2 shows a sinus rhythm with an A-V block and a left bundle branch block. For this example, the morphological reproduction of each beat is relatively accurate and ladder diagrams generated by the system correspond to beat annotations. This is an example of the easiest scenario for the inter-beat adaptation phase, in which the model parameters of individual beats present low beat-to-beat variations and the proposed approach performs

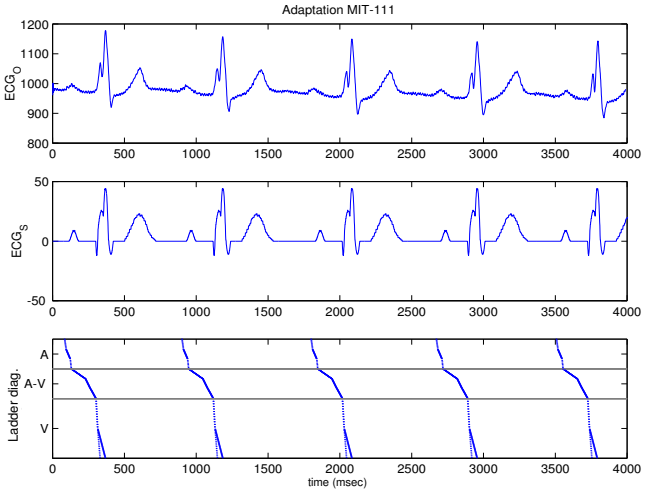

Figure 2. Model adaptation to a beat sequence taken from the MIT-BIH arrhythmia database record # 111.

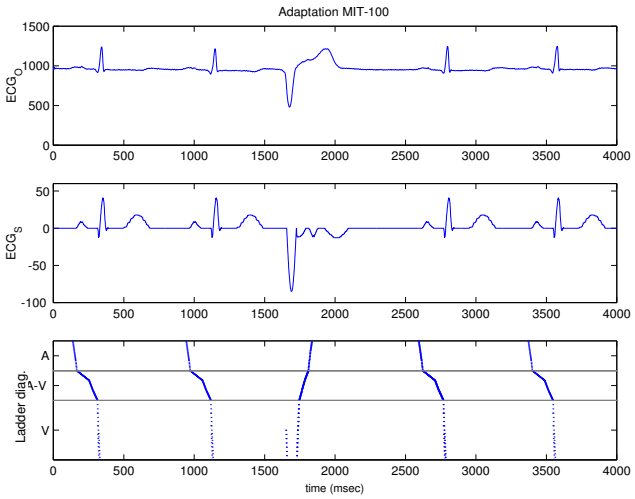

Figure 3. Model adaptation to a beat sequence taken from the MIT-BIH arrhythmia database record # 100.

straightforwardly. The example in figure 3 presents four sinus beats and a PVC. The morphological reproduction of the PVC is not accurate, particularly the *T*-wave and, although the ladder diagram shown in this example is correct, this was not the case for other tests applied to the same rhythm. These aspects illustrate the limitations mentioned earlier and are part of our current developments. However, one interesting element can be noticed on the synthesized PVC, where a retrograde *P*-wave generated by the model coincides with that of the observed beat (which is very difficult to discern). This element suggests how it is feasible to take advantage of knowledge within the model to generate valid hypotheses on wave locations, especially for *P*-waves.

Concerning the inter-beat adaptation for record 100, the presence of the PVC implies a rupture in the parameter sequence. Adapting the SDD parameter of the ectopic focus for this beat results in an appropriate beat sequence match (figure 3). However, this approach does not take into account neither the physiological phenomena governing the beat before the PVC, nor the continuous transition of the physiological state of each structure, between the end of the PVC and the next beat.

4. Conclusion

This paper presented the global functioning structure of the CARMEM system and, particularly, current progress on the inter-beat adaptation phase. Although the proposed inter-beat adaptation is still simple, it is useful for the reproduction of established rhythms and represents a promising approach for automatic cardiac rhythm interpretation. In the case of rhythm transitions or paroxysmal activity, these preliminary results allowed us to foresee the difficulties of the problem. On one hand, this adaptation has to take into account individual solutions of the intra-beat adaptation (explanation of individual beats) and, on the other hand, to preserve the global physiological state and the continuity of parameter values between consecutive beats. Current developments are directed in this sense by improving the ECG synthesis stage of the model and by completing the inter-beat adaptation phase.

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