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Automated Musical Rhythm Transcription of ECG RR Interval Time Series as a Tool for Representing Rhythm Variations and Annotation Anomalies in Arrhythmia Heartbeat Classifications

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Abstract

We introduce a linear time algorithm for transcribing RR intervals into musical rhythms using approximate common divisors (ACDs). The technique maps ACDs to nodes on a graph, node transitions represent heart rate variations; a balance must be struck between rhythmic changes and heart rate variation. Possible transcriptions correspond to paths in the ACD graph. Given a set of weights, a shortest path algorithm finds the optimal transcription. The representation facilitates efficient pattern recognition and extraction. The transcription technique is applied to the Physionet Long Term Atrial Fibrillation Database to demonstrate how it shows the rhythmic variation within heartbeat subsequences having the same labels, and its utility in detecting potential labelling errors on its own and via a rhythm simplex. Further work may explore prospective applications to arrhythmia stratification.

1. Introduction

The burgeoning popularity of wearable devices has led to an explosion in the quantity of electrocardiographic (ECG) data collected by every day consumers whilst, on the other hand, implantable loop recorders provides long, continuous monitoring on the order of years. Both multitudinous individual short recordings and an abundance of very long recordings give rise to the need for robust and efficient ways to process ECG data at scale for pattern search, characterisation of short term and long term dependencies, and for automatic categorisation of cardiac arrhythmias and their subtypes.

Quantisation is a dimension reduction technique that is employed in many domains to map continuous, infinite values to a smaller and finite set of discrete values. This improves storage capacity and search efficiency. Quantisation is at the heart of the music transcription process. In common practice music, a periodic beat, like the sinus rhythm, marks time. Rhythm notation maps musical events, which occur on the real timeline to a discretised grid limited to simple subdivisions of the beat. This abstraction allows music to be written down for faithful replication [1]. In music information research, such symbolic representation facilitates fast algorithms for rapid detection of repeated patterns like motives [2], similar segments [3], and hierarchical structure [4].

Researchers have noted the musicality of arrhythmic heart rhythms [5, 6]. Like music, the heart has a natural pacemaker that generates a regular pulse. The RR interval and its reciprocal, the heart rate (HR), is constrained by properties of the sinus node and autonomic nervous system [7], and also tend towards simple ratios of their neighbors [8]. Traditional time-frequency measures of RR variability include computing of its high frequency and low frequency power components and spectral analysis. These measures require assumptions of signal stationarity and do not apply in situations with transient activity as in the case of most arrhythmias. Thus, RR intervals are a feature that is exploited in computational cardiology for arrhythmia detection [9, 10].

In this paper, we present a method for mapping RR intervals to musical rhythms. The advantage of the rhythm encoding is the representation of proportional time relationships between consecutive RR intervals. This is conceptually similar to, but more nuanced than, turning ECGs to sequences of discrete categorical labels of heartbeat types [9] or ECG parts [11]. To obtain the rhythm notation automatically, we propose an algorithm for rhythm transcription originally designed for music, but applied to RR intervals, to get a representation of the heart rhythm. We then show how this stream of symbols can be used to characterise and detect arrhythmias.

In the next sections, we present the method, including approximate common divisors and the shortest path problem, then we apply the technique to RR intervals from recordings of atrial fibrillation, and discuss the results, us-

ing a rhythm simplex and arrhythmic norm to find outliers.

2. Methodology

We transfer the methodology for representing rhythms in time to ECG RR intervals. In music, time is measured in units called the *tatum* [12, 13], which is the smallest interval of time required to capture all the events in a temporal sequence. The tatum is a meaningful subdivision of the beat, aka the *tactus*, to capture the events in between. The duration of the tatum may be fixed for a period of time or adapt as necessary to the changing tempo. The rhythm of a series of events over time can then be represented by the tempo and in tatum units. For example, to represent an event of duration $0.5\,\mathrm{s}$ followed by another of duration $1\,\mathrm{s}$, we set the tatum to $0.5\,\mathrm{s}$ and say that the first event has a duration of 1 tatum and the second a duration of 2 tatums, i.e. the rhythm is $(1, 2)$. If a slight variation occurs and the second duration is not exactly two tatums long, say its duration is $1.01\,\mathrm{s}$, we can consider the tempo changed so that the tatum is now $0.505\,\mathrm{s}$.

This same way of representing durations as rhythms using a time-varying grid, the tatum, can be applied directly to RR intervals. Normal sinus may produce an homogeneous rhythm of $(1, 1, 1, ...)$ and a tatum that varies slightly according to the RR intervals. However, in arrhythmic sequences, we may get more varied rhythms like, for instance, $(2, 4, 3)$, that show the heart's abnormal rhythmic behaviour. Thus, we will propose an algorithm for transcribing rhythmic sequences that may be used to describe and detect abnormal rhythms. In order to achieve that, we first introduce the notion of *approximate common divisors*.

2.1. Approximate common divisors

Given a series of onset times, $T = (t_0, t_1, ..., t_n)$, and beat durations, $D = (d_1, d_2, ..., d_n)$, the objective is to find a tatum value a such that $t_i \approx m_i a$ for some $m_i \in \mathbb{N}$ where $|t_i - m_i| < \tau$ for some small threshold $\tau > 0$. Every a is associated with an error measure,

$$\varepsilon_T(a) = \max_n \min_{m \in \mathbb{Z}} |t_n - am| \,. \tag{1}$$

Definition 1: Let $T = (t_0, t_1, ..., t_n)$ be a series of onset times. $a > 0$ is an *approximate common divisor* (ACD) of T with threshold $\tau > 0$ if
1. $\epsilon_T(a) \leq \tau$; and,
2. ϵ_T has a local minimum at a.

For a given ACD, a, we extract the rhythm by getting the difference between consecutive values of m that minimise the error $|t_n - am|$.

Example 1: Consider the sequence of arrhythmic heartbeats represented by $D = (0.640\,\mathrm{s}, 0.359\,\mathrm{s}, 0.875\,\mathrm{s})$. The onset times are $T = (0\,\mathrm{s}, 0.640\,\mathrm{s}, 0.999\,\mathrm{s}, 1.874\,\mathrm{s})$. If the threshold $\tau = 0.05\,\mathrm{s}$, we have the ACDs $0.319\,\mathrm{s}$, $0.205\,\mathrm{s}$, $0.168\,\mathrm{s}$, $0.159\,\mathrm{s}$, ... For the ACD $a = 0.205\,\mathrm{s}$, the error minimising m values are $(0, 3, 5, 9)$. By computing the differences, we get the rhythm $(3, 2, 4)$.

Note that, in this case, the ACD is the same for all three beats. The following section describes the ACD graph, which allows the ACD to vary in ways that make overlapping consecutive subsequences of timestamps compatible one with another.

With this definition, there exists an ACD for every sequence, but if the ACD is too small (e.g. nearly zero), the representation will be nearly equivalent to the original RR intervals with the tatum being the time resolution. This is why, in practice, we set a lower limit for the ACD, and sometimes there may not be a feasible ACD.

2.2. ACD graph

When dealing with a long sequence of RR intervals, we will almost certainly not be able to find a single ACD that works for the whole sequence, or the ACD could be too small to be useful. What we do is split the sequence into smaller stretches and compute the rhythms separately. For continuity and coherence, we require that the subsequences overlap. For convenience, we set the subsequence length to two durations. For coherence, the common duration must be the same between two overlapping subsequences. This will be modelled using a graph.

For each subsequence indexed i, we have a collection of ACDs, $(a_1^i, a_2^i, ..., a_{k_i}^i)$. This are the nodes of our graph. For two consecutive subsequences, we connect an ACD of the former segment with an ACD of the latter one if they have a common duration. Figure 1 shows the graph resulting from the first 9 beats of record 01 from the PhysioNet Long Term AF Database (LTAFDB) [14, 15], with $\tau = 0.05\,\mathrm{s}$ and a lower limit of $0.15\,\mathrm{s}$ for the ACDs.

With this construction, each transcription becomes a path in the ACD graph, e.g. the red path in Figure 1 gives the transcription $(2, 3, 2, 3, 2, 3, 2, 1, 2)$, where the common durations are merged to obtain the sequence.

2.3. Shortest path

To select a transcription for the sequence, we transform the problem into one of finding the shortest path. To do this, we must first add two extra nodes, a source and a sink, that will connect all the first nodes and all the last ones, respectively. This way, the problem becomes one of finding the best path from the source to the sink. There may be several solutions, so we assign weights to each edge to get a shortest path problem. There are several ways to assign nodes. Here, we propose at least two: to use the local transcription error as weight, or to use the tempo variation across subsequences.

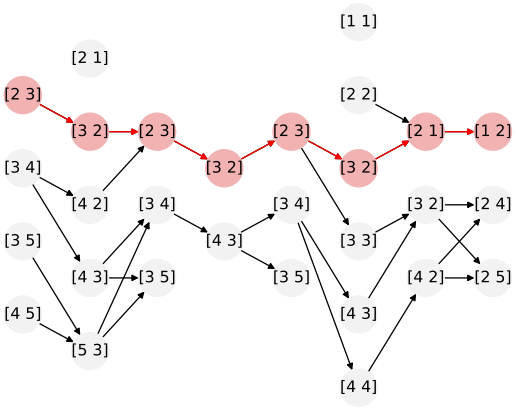


Figure 1: Example ACD graph with outlined path giving a transcription of the duration sequence.

2.3.1. Local error of the transcription

The local error of the transcription is $\varepsilon_k^i := \varepsilon_{T_i}(a_k^i)$. This measures the degree of accuracy of the transcription for the segment. To assign a weight, we use a linear function $w_\tau^{\text{err.}}(\varepsilon) = \frac{\varepsilon}{\tau}$. We assign this weight to the edges entering the node corresponding to the a_k^i ACD. Other weights may be explored and used as needed.

2.3.2. Tempo variation across stretches

When connecting two nodes by an edge, we are changing the ACD of the rhythm and then the tempo. We choose to penalise an edge if the tempo changes too fast: we assign a low weight when the tempo change is low and a large one when the tempo change is big. Here, we choose the $\log 2$ distance between ACDs $w^{\text{t.var.}}(a_k^i, a_{k'}^{i+1}) = |\log_2(\frac{a_k^i}{a_{k'}^{i+1}})|$.

For each edge, the total weight w will be the weighted sum, $w = a^{\text{err.}} w^{\text{err.}} + a^{\text{t.var.}} w^{\text{t.var.}}$. Here, we use $a^{\text{err.}} = a^{\text{t.var.}} = 1$, but other weights are also possible.

2.4. Solving the shortest path problem

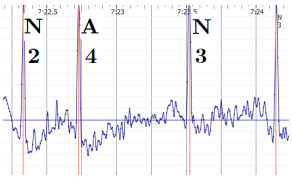
Shortest path problems can be difficult to solve in complex graphs. However, we have a directed acyclic graph (DAG), which then has a topological ordering that enables the shortest path problem to be solved in linear time [16]. The computation time, $\mathcal{O}(n+m)$, is linear in n, the number of nodes, and m, the number of edges.

3. Rhythm transcription for arrhythmias

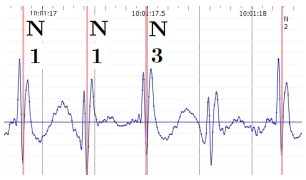
Next, we apply rhythm transcription to the LTAFDB, and compare the transcriptions to the assigned beat labels. Table 1 shows the beat labels corresponding to the extracted rhythm pattern $(2, 4, 3)$. Note that 95% of this pattern resulted from the N-A-N sequence, an atrial ectopic (A) followed by a compensatory pause, surrounded by normal (N) beats. Two were due to the similar N-V-N. Several were from A-A-N and, surprisingly, N-N-N.

Table 1: Beat category labels for the rhythm pattern 2-4-3 in LTAFDB Record 06.

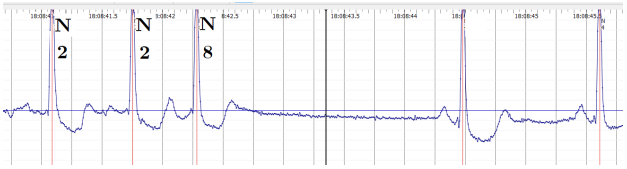
Labels	Nb. of 2-4-3	Percentage	Total count
A-A-N	87	3.93 %	309
N-A-N	2104	95.03 %	3869
N-N-N	21	0.95 %	91839
N-V-N	2	0.09 %	3



(a) Example of a N-A-N pattern aligned with a 2-4-3.



(b) Missing beat in a 1-1-3 sequence.



(c) A 2-2-8 sequence with long (2.195 s) RR interval labelled as normal.

Figure 2: Examples of ECGs of certain rhythmic patterns.

Figure 2b and 2c were each labeled N-N-N but with extremely unlikely rhythms. On closer inspection, the transcription revealed a missed annotation and an abnormally long pause that suggests a labelling error. Thus, rhythm transcription may have some utility for finding both typical patterns as well as for improving automatic labelling.

To further study the results of the transcription, we introduce the *rhythm simplex* and the *arrhythmic norm*.

3.1. Visualising transcriptions of triplets

We visualise the rhythm transcriptions of three-interval rhythms using the 2-dimensional *rhythm simplex*, first proposed for studying perceived rhythm equivalence classes [17, 18]. Each three-interval rhythm is normalised to sum to one, and represented as a unique point on the rhythm simplex. Figure 3 shows one such mapping of the rhythms associated with subsequences labeled N-N-N.

We also use the rhythm simplex to assess the arrhythmicity of a sequence via the arrhythmic norm. For any point (x, y, z) in the rhythm simplex, where $x+y+z = 1$,

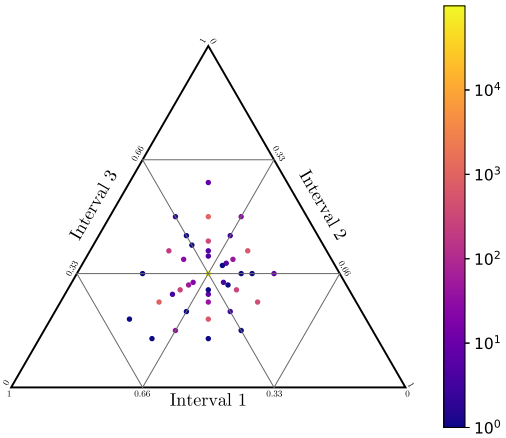


Figure 3: Rhythm simplex of rhythms labelled N-N-N from LTAFDB Record 00.

the *arrhythmic norm* is

$$||(x, y, z)||_{\mathrm{R}} = ||(x, y, z) - (\frac{1}{3}, \frac{1}{3}, \frac{1}{3})||_2\,, \qquad (2)$$

which measures the irregularity of the RR intervals. Sinus rhythm will result in norm values at or close to zero; e.g. the rhythm $(\frac{1}{3}, \frac{1}{3}, \frac{1}{3})$ has a norm of 0.

The arrhythmic norm can be used to identify outliers that reveal errors. Amongst rhythms for beats labeled N-N-N, $(1, 1, 3)$ from LTAFDB Record 00 has a high arhythmic norm. Figure 2b shows that the number 3 is due to a missing annotation. The transcription also revealed beats that may have been erroneously labelled as N. Figure 2c shows the rhythm $(2, 2, 8)$ with the highly unlikely RR interval (duration $2.195\,\mathrm{s}$) is probably not a normal beat.

4. Conclusions

We have introduced an automatic method for rhythm quantisation using ACD graphs, and applied it to rhythm transcription of the LTAFDB. The transcription technique has potential for use in improving automated labelling. Future work may explore applications in arrhythmia stratification.

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