

Real-time Decision Policies with Predictable Performance

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Abstract—As methods and tools for Cyber-Physical Systems grow in capabilities and use, one-size-fits-all solutions start to show their limitations. In particular, tools and languages for programming an algorithm or modeling a CPS that are specific to the application domain are typically more usable, and yield better performance, than general-purpose languages and tools. In the domain of cardiac arrhythmia monitoring, a small, implantable medical device continuously monitors the patient's cardiac rhythm and delivers electrical therapy when needed. The algorithms executed by these devices are *streaming algorithms*, so they are best programmed in a streaming language that allows the programmer to reason about the incoming data stream as the basic object, rather than force her to think about lower-level details like state maintenance and minimization. Because these devices are resource-constrained, it is useful if the programming language allowed predictable performance in terms of processing runtime and energy consumption, or more general costs. StreamQRE is a declarative streaming programming language, with an efficient and portable implementation and strong theoretical guarantees. In particular, its evaluation algorithm guarantees constant cost (runtime, memory, energy) per data item, and also calculates upper bounds on the per-item cost. Such an estimate of the cost allows early exploration of the algorithmic possibilities, while maintaining a handle on worst-case performance, on the basis of which hardware can be designed and algorithms can be tuned.

Index Terms—Quantitative Regular Expressions, Streaming languages, Arrhythmia monitoring, Tachycardia, Real-time

I. INTRODUCTION

THE last few years have witnessed an explosion of IoT systems in applications such as smart buildings, wearable devices, and healthcare. A key component of an effective IoT system is the ability to make decisions in real-time in response to data it receives. For instance, a gateway router in a smart home should detect and respond in a timely manner to security threats based on monitored network traffic, and a healthcare system should issue alerts in real-time based on measurements collected from all the devices for all the monitored patients. Programming the desired logic as a deployable implementation is challenging due to the volume of data and hard constraints on available memory, power usage, and response time.

In current practice, a general-purpose imperative language such as C is used to program real-time decision making policies. Due to the challenges in analyzing such code, this approach does not lead to *predictable* performance and does not facilitate *exploration of design options* at early stages. A specialized language for specifying these policies in a declarative manner, with programming abstractions suitable for processing data streams with performance guarantees, can be a potential solution to both these challenges. It can play

the same role as *model-based design* does for safety-critical embedded control software [1], [2], [3], [4].

To specify the decision logic based on computing quantitative summaries of data streams we advocate *Quantitative Regular Expressions (QREs)* [5], [6]. The language allows the computation to be expressed as a streaming composition of stages. The core QRE combinators, which are quantitative extensions of operations in classical regular expressions, can be used to impart to the input data stream a logical hierarchical structure facilitating modular specifications (for instance, to view patient data as a sequence of episodes and to view network traffic as a sequence of Voice-over-IP sessions). The QRE compiler translates a high-level query into a streaming algorithm with precise complexity bounds on per-item processing time and total memory footprint. The StreamQRE library, an implementation in Java, has been shown experimentally to have superior performance compared to other existing high-performance engines for processing streaming data [6]. This experimental evaluation involved workloads that are representative of clickstream analysis (Yahoo streaming benchmark [7]) and real-time analytics for business event streams (NEXMark benchmark [8]). A variant of StreamQRE (called NetQRE) has been shown to be useful for network monitoring [9].

Medical devices offer an ideal test-bed for exploring the applications of formal methods in system design due to their safety-critical nature that demands predictable operation [10]. Recently, the implantable pacemaker has been used to illustrate the benefits of model-based design [11], [12], [13]. This involves specifying the algorithms for detecting slower-than-normal rhythms used by pacemakers using formal modeling languages, such as timed automata [14] and hybrid automata [15], and verifying correctness requirements using a model checker such as UPPAAL [16].

While this previous work dealt with pacemakers, Implantable Cardioverter Defibrillators (ICDs) and Insertable Loop Recorders (ILRs) are a more sophisticated class of implantable cardiac devices that must do *multi-beat rhythm classification*, not only detect whether a beat was missing, like pacemakers do. The goal of such an Arrhythmia Monitoring Algorithm (AMA) is to detect undesirable patterns in the (discretized) input signal being monitored. We argue that such a classification task is best viewed as a matching algorithm over streaming data, and the desired decision logic can be naturally expressed using QREs.

In particular, we program a representative AMA, used in an ICD by Boston Scientific [17], using the QRE language. The

1 QRE compiler then generates the low-level implementation
 2 whose space complexity and per-item processing time com-
 3 plexity are constant — that is, independent of the number of
 4 samples processed so far (see Section 4 of [6]). Furthermore,
 5 we show how the QRE compiler can *statically* compute an
 6 upper bound on the cost of processing each item, where the
 7 cost can be, for example, the energy consumption on a specific
 8 platform. This assures predictable real-time performance. Such
 9 estimates, provided early in the design cycle, allow one to
 10 compare design alternatives (that is, different variants of the
 11 monitoring algorithm) statically in terms of their achievable
 12 worst-case costs. Such analysis complements average-case
 13 analysis (i.e., measured performance when running the al-
 14 gorithm on a typical load). We demonstrate the latter type of
 15 analysis by profiling the energy consumption of the QRE on
 16 a signals database on a given hardware platform.

17 The paper is organized as follows. Section II gives a back-
 18 ground on cardiac function, necessary for understanding the
 19 complexity of arrhythmia monitoring. Section III motivates the
 20 programming of AMAs in QREs, and Section IV introduces
 21 the QRE formalism and the Java library that implements it.
 22 This library is available online at [18]. Section V describes
 23 one representative AMA and Section VI details its QRE
 24 implementation. The Java library is used in Section VII to
 25 illustrate the implemented AMA on a database of arrhythmia
 26 episodes. Section VIII describes how to compute upper bounds
 27 on QRE cost, like per-item energy consumption. Section IX
 28 summarizes related work and Section X concludes the paper.

30 II. BACKGROUND ON CARDIAC FUNCTION

31 To understand the arrhythmia monitoring algorithm pre-
 32 sented in this paper and appreciate its complexities, it is
 33 necessary to first understand some basics of cardiac electro-
 34 physiology: how the heart beats normally, why it could go
 35 into arrhythmia, and what measurements are available to an
 36 implantable device to detect this.

39 A. Cardiac electrophysiology

40 The heart has two upper chambers called the *atria* and
 41 two lower chambers called the *ventricles* (see Fig. 1). The
 42 synchronized contractions of atria and ventricles assure an
 43 adequate supply of oxygenated blood to the rest of the body.
 44 This contraction is driven by electrical activity in the heart,
 45 which originates in the right atrium, floods the atria first,
 46 then conducts down to the ventricles and floods those in
 47 turn. The cardiac muscle contracts as it is being traversed by
 48 the electrical wavefront, i.e., as it *depolarizes*. In a first ap-
 49 proximation which is sufficient for understanding AMAs, we
 50 may consider that this contraction is an instantaneous event,
 51 and refer to it as an (atrial or ventricular) *beat*. This normal
 52 pattern of electrical activity is referred to as Normal Sinus
 53 Rhythm (NSR), after the *sino-atrial node* where the electricity
 54 normally originates. Disturbances of NSR are referred to as
 55 *arrhythmias*. They can arise because of structural defects in
 56 the cardiac muscle, like a re-entrant circuit around which the
 57 electrical waveform circulates very fast, or because of irritable
 58 tissue that starts to depolarize faster than the sino-atrial node.

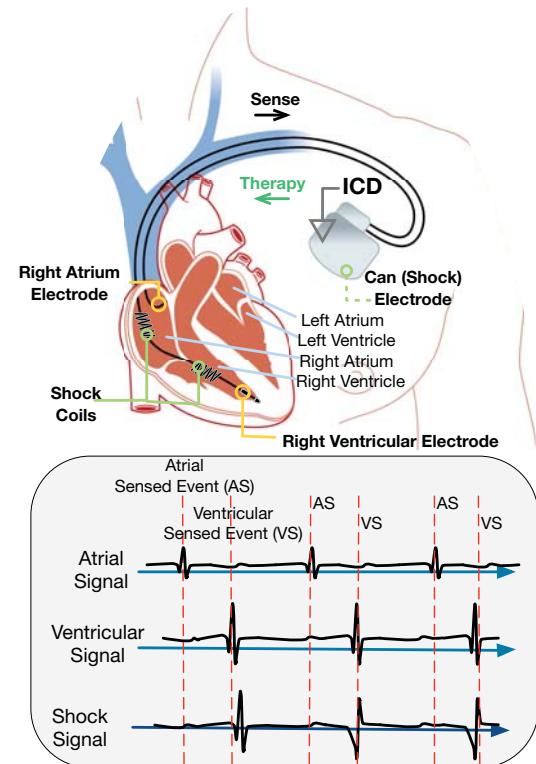


Fig. 1: ICD and its connection to the heart

Ventricular Tachycardia (VT) is an example of an arrhythmia originating in the ventricles, in which the ventricles depolarize at a very high rate and effectively drive the rhythm. This high rate of depolarization doesn't give enough time for the muscle to contract and relax properly, which can result in insufficient blood supply. If the VT is sustained, or degenerates into *Ventricular Fibrillation (VF)* (Fig. 2), it is fatal within a minute. An abnormally fast heart rate that originates in the atria and/or the conduction system above the ventricles is referred to as a *Supra-ventricular Tachycardia (SVT)*. An SVT causes patient discomfort but is not fatal in the short-term and does not require device treatment. Most fast arrhythmias fall under these two categories: VT or SVT.

69 B. Implantable devices

70 Two types of implantable devices monitor a heart's rhythm
 71 continuously to detect abnormally fast arrhythmias, aka *tachy-
 72 cardias*. The first is Implantable Cardioverter Defibrillators
 73 (ICDs). An ICD is inserted under the pectoral muscles, and
 74 has one or two leads that are directly implanted in the cardiac
 75 chambers, and through which it measures local electrical
 76 activity - see Fig. 1. The measured signals are known as
 77 *electrograms*, or EGMs, and are termed 'atrial' or 'ventricular'
 78 depending on the chamber where they are measured¹. See
 79 Fig. 3. An ICD uses EGMs to distinguish a wide range of
 80 tachycardias. If it detects a potentially fatal tachycardia, then
 81 it delivers therapy to the heart in the form of either low-energy

¹In this paper, we will ignore the so-called 'shock EGM' as it will not be used in describing arrhythmia monitoring algorithms.

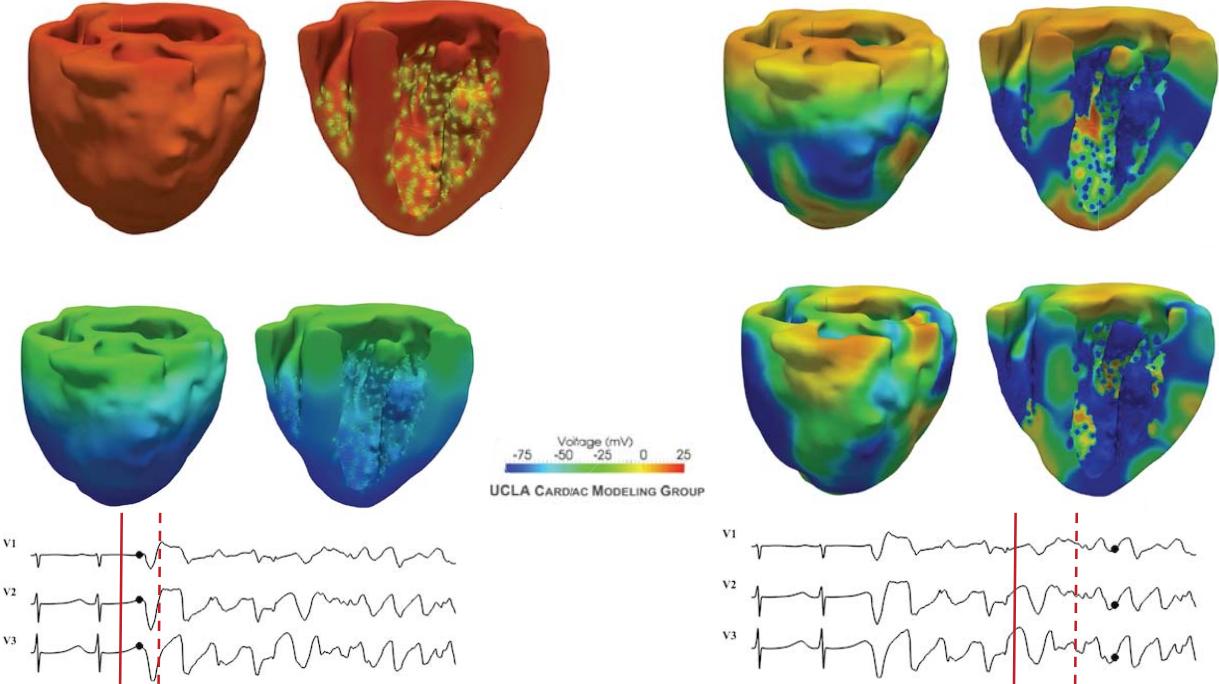


Fig. 2: Electrical activity during Normal Sinus Rhythm (NSR) and Ventricular Fibrillation (VF). The color scale runs from blue = rest state to red = excited (aka depolarized) state. (Colors in digital version). In the top left, the ventricles are shown from two different angles, during a phase of NSR. The ventricles are fully excited. The bottom left panel shows a later phase of the same beat, where the ventricles are progressively relaxing, starting with the apex (the pointed tip of the heart). This orderly propagation ensures adequate muscle contraction and blood flow. Three surface ECGs are shown beneath the left column, with red bars indicating the timing of the two snapshots. Note the periodic pattern. The right column shows two snapshots during VF (earlier snapshot on top). Note the disorganized nature of the electrical activity, wavefront breakup, and the multiple regions of depolarization. Note also the change in the surface ECG from periodic and regular (early on) to disorganized. The AMA reads two such signals (obtained, however, intra-cardially and not from the surface) and tries to detect fibrillation. [Snapshots obtained from video of a simulation of the ventricles at UCLA, courtesy of Luigi Perotti [19]]

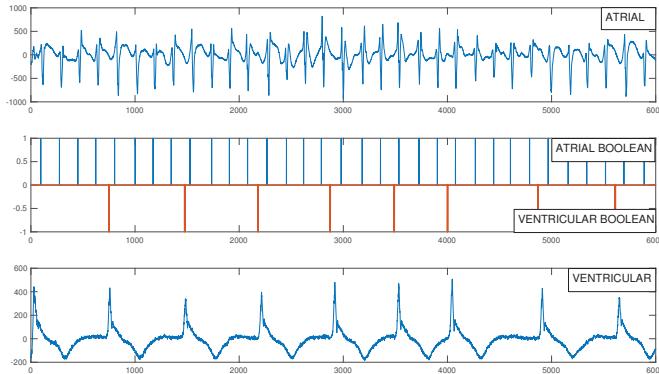


Fig. 3: EGMs (top and bottom panels) and corresponding boolean beat signals (middle) during atrial tachycardia. Beats correspond to peaks in the EGMs.

pacing sequences or (possibly more than one) very high-energy shock. Either way, the goal of the therapy is to stop the current rhythm and allow a normal rhythm to start. VTs and SVTs can share similar heart rates and other characteristics, so an SVT can be mis-diagnosed as a VT. This is problematic because shock therapy used to stop a VT can deliver between 30-60 Joules of energy at around 700 Volts in under 15ms [20], directly to the heart, which is very painful to the patient², and

²Patients compare the shock to a “horse kicking you in the chest”.

has been shown to increase morbidity [21]. Therefore, one of the biggest challenges for ICDs is to discriminate between VF and sustained VT that typically requires a shock, and SVT that typically should not be shocked [22]. This paper will present one particular ICD AMA in detail in Section V.

The second type of device that monitors tachycardias is the Insertable Loop Recorder (ILR) (also known as Implantable Cardiac Monitor). An ILR is a small device (the smallest ILR on the market is smaller than a key) that is inserted subcutaneously, and monitors surface ECG signals. It uses these signals to compute a number of long- and short-term statistics of the rhythm, and in particular to detect Atrial Fibrillation (AF) episodes. AF is an abnormally fast and disorganized atrial rhythm that can lead to fainting spells, and which, in the long term, contributes to blood clot formation. These clots can cause a stroke upon reaching the brain. The ILR does not have any therapeutic functions, but only monitors the heart rhythm. As an example, Biotronik’s BioMonitor [23] calculates and stores the following daily quantities, in a sliding window of 240 days where the oldest day drops out of the window. The quantities include 1) the average daily heart rate, 2) the daily minimum average heart rate, where the averages are calculated over consecutive blocks of 10 mins in the day, 3) daily heart rate variability, defined as the standard deviation of the sliding 5-minute averages, and 4) the rate histogram, where each heartbeat is binned into bins of width

10 beats-per-minute (bpm). In addition, the BioMonitor will take consecutive windows of n beats and count the number of cycle lengths that fall below a fixed value in each window.

Remote continuous monitoring has recently been shown to improve treatment outcomes [24] and to reduce time-to-treatment for patients with atrial tachycardia burden [25], so it is important to develop algorithms that can monitor over longer periods of time and/or compute more advanced statistics that can better detect the arrhythmia burden.

12 C. Device measurement: from real-valued to boolean signal

13 Formally, an EGM is a uniformly-sampled, discrete-time
 14 real-valued bounded signal. An EGM signal can be characterized by the *timing of beats* that produced it, and the
 15 *morphology of the signal itself*. To detect the beat timing (i.e.,
 16 when the chamber is contracting), the peaks of the EGM are
 17 detected [26]. The output of peak detection is a discrete-time
 18 boolean signal, where a 1 indicates a beat. See Fig. 3. Beat
 19 timing is crucial to an arrhythmia's detection, since it is used
 20 in all discriminators.

21 The 'morphology' refers to the shape of the EGM. The so-
 22 called 'shock' EGMs during an atrially-driven rhythm look
 23 different from the shock EGMs during a ventricularly-driven
 24 rhythm. The ICD uses this to help it determine whether the
 25 current arrhythmia is an SVT or VT. In this paper, and in order
 26 to keep the exposition simple, we will only work with the beat
 27 signal, i.e., the boolean signal produced by peak detection on
 28 the local atrial and ventricular channels, as shown in Fig. 3.

31 III. STREAMING ALGORITHMS FOR ARRHYTHMIA 32 DETECTION

33 An AMA is naturally viewed as a *pipeline of streaming*
 34 *algorithms*, where each node of the pipeline performs a
 35 streaming calculation on its input signal, and passes its output
 36 signal to the next node. So what is a streaming algorithm?
 37 And why view arrhythmia monitors as streaming algorithms?
 38 The main characteristics of a streaming algorithm are that
 39 it views its input as a sequence, or *stream*, of items from
 40 some data domain, arriving one at a time. It gets to process
 41 each item only once, after which it discards it and moves on
 42 to the next item in the input stream. After processing each
 43 item, the algorithm produces an output value (which might
 44 also be null). A streaming algorithm has limited memory
 45 available (much smaller than the length of the stream which,
 46 for practical purposes, may be regarded as infinite), and
 47 limited processing time. Section IV gives several examples
 48 of streaming calculations.

49 The following considerations, which govern the design and
 50 execution of an AMA, establish the suitability of the streaming
 51 model of calculation for AMA. First, an AMA's input is a
 52 uniformly sampled discrete-time electrical signal that arrives
 53 in real-time, one sample at a time, and thus can be viewed
 54 as a stream. Second, when running on an ICD, the AMA
 55 has a delay constraint. Namely, not much time must elapse
 56 between the onset of a fatal VT and the moment that the AMA
 57 detects it, because this delays the delivery of therapy. This
 58 requirement translates directly into a requirement of small
 59 processing time per item of the input signal.

60 processing time per item of the input signal, which is a key
 61 constraint on streaming algorithms. Third, ICDs and ILRs
 62 share a power consumption concern. Indeed, power is the
 63 *main* non-functional design factor for these devices. Even
 64 for today's ICDs, which can have a battery life between
 65 7 and 11 years, an additional 3 months of battery life are
 66 still worth pursuing [27], since they can mean the difference
 67 between having to surgically replace the ICD or not. Because
 68 most ICD and ILR recipients are older patients with health
 69 complications [28], it is desirable to prolong battery life and
 70 reduce the likelihood of a replacement [27]. The power in
 71 an ICD is consumed by the monitoring algorithms, the shock
 72 therapy, and the pacing therapy. Although shocks are the single
 73 most power-hungry event, over an average device's lifetime,
 74 they will only consume 3% of the battery, and it is exceedingly
 75 rare that they consume more than 36% [29]. The rest is shared
 76 between pacing and monitoring. Thus it is important to reduce
 77 the power cost of monitoring. For ILRs, because they do not
 78 have any therapeutic functions, most of the power is consumed
 79 by monitoring. Thus an AMA has a more general *small cost-per-item constraint*.

80 If AMAs are viewed as streaming algorithms, then it follows
 81 that they are best programmed using a *streaming*
 82 *programming language*. That is, a language that is expressly
 83 designed and optimized for describing streaming algorithms
 84 and automatically generating efficient code from the program
 85 description. Indeed, it is important to note the productivity
 86 gains achievable by using a Domain Specific Language (DSL).
 87 It is generally agreed that programming in a DSL results in
 88 greater productivity for the development teams producing the
 89 software - see, e.g., [30] and [31] where development time
 90 reductions of 5-7x are routinely reported. During the *design*
 91 *exploration stage* when AMAs are developed, tweaked and
 92 compared, it is helpful to program in a language that allows
 93 high-level reasoning about the stream as the basic object of
 94 manipulation and easy capture of patterns in the stream.

95 The StreamQRE language [18], [6] permits such a declarative
 96 way of programming. StreamQRE (pronounced 'stream
 97 query') allows the developer to create Quantitative Regular
 98 Expressions (QREs), which are a quantitative extension of
 99 regular expressions. A QRE declares how the stream should
 100 be divided up (by matching against a regular expression) and
 101 which arbitrary operations should be executed on the matching
 102 pieces. Similarly to regular expressions, QREs can be
 103 combined using quantitative extensions of regular combinators
 104 to form more complex computations. QREs are described
 105 in detail in the next section. QREs also provide theoretical
 106 guarantees on the memory, time and energy consumed to
 107 process a data item by the resulting algorithm. Specifically, a
 108 QRE has per-item memory and time complexities and energy
 109 consumption that are independent of the length of the stream,
 110 and depend only on the size of the query. Thus, a QRE
 111 program automatically gives a baseline implementation with
 112 constant cost per data item. One also automatically gets a
 113 static upper bound on the per-item cost of a QRE. This allows
 114 a cost comparison to choose between similarly-performing
 115 algorithms. Such early feedback on cost allows early design
 116 exploration, at a point in the design cycle where algorithmic

1 changes are easy and can be correlated to cost decrease, and
 2 where it is well-established that the most gains are possible.
 3

4 Of course, during design exploration, AMAs can also be
 5 programmed in a general purpose language like C++, and in
 6 a non-streaming fashion, e.g., by keeping a sliding window
 7 big enough to store the entire signal segment of interest
 8 and repeating all computations with every new sample that
 9 enters the window. However, this requires the programmer to
 10 explicitly think of keeping state information and minimizing
 11 it, and to think of various sources of delay in her code
 12 and minimize those. Moreover, it is much harder to obtain
 13 upper bounds on cost (whether power, memory or processing
 14 time) of free-form code than the cost of QREs, which have
 15 sufficient structure to enable the above analysis. Finally, when
 16 it is possible, analysis of cost at code-level enables late-stage
 17 implementation changes whose effect on cost will typically be
 18 small compared to early-stage algorithmic changes.

19 **On adopting a domain-specific language.** In general,
 20 learning a new language incurs overhead for the engineers.
 21 This is true for *any* programming language, not only a DSL
 22 like StreamQRE, and the above-cited studies indicate the
 23 overall productivity gains that can be achieved after the initial
 24 learning curve. For instance, Regular Expressions are familiar
 25 to database developers who favor them over writing C code for
 26 querying databases. In our project, we had two teams: Team M,
 27 consisting of the first author and two other engineers, coded
 28 the AMA in Matlab. Matlab was chosen because Team M
 29 are very familiar with it, it is an easy language to work in,
 30 and has a very rich development environment and IDE. After
 31 understanding the algorithm, it took Team M approximately
 32 three weeks to code it and check its operation (amount of time
 33 estimated from github commits). Team Q, consisting of the
 34 second and third author, took one week to code the same AMA
 35 in StreamQRE. Thus our experience validates the general point
 36 that using a DSL can unlock productivity gains.

37 In summary, the advantages of describing AMAs in a
 38 streaming language, and more specifically in StreamQRE, over
 39 describing them in a general purpose language, are:

- 40 • A more natural way to reason about the algorithm's
 41 streaming operation, which highlights opportunities to re-
 42 use computation results.
- 43 • A declarative way to program the algorithm, which en-
 44 ables reasoning at the stream level and how it needs to
 45 be divided hierarchically and processed, rather than get
 46 bogged down in item-level computations.
- 47 • An automatic implementation of the algorithm that guar-
 48antees bounded memory, runtime, and energy consump-
 49 tion per data item that is independent of the input signal
 50 length. The algorithm designer is relieved from having to
 51 explicitly maintain state.
- 52 • An automatic way to obtain an upper bound on the cost of
 53 a QRE as a function of the costs of the basic operations.
 54 This cost can model power consumption, for example.

55 IV. INTRODUCTION TO QREs

56 This section is an introduction to the language of *Quan-*
 57 *tative Regular Expressions* (QREs). First, we present the

5 semantic model of streaming functions for describing stateful
 6 streaming transformations. Then, we introduce the language
 7 of QREs and define some derived constructs that will be used
 8 later to specify the arrhythmia detection algorithm. Finally, we
 9 discuss an efficient implementation of QREs as a Java library.

A. Streaming functions

10 We introduce here the basic semantic objects for our lan-
 11 guage, called *streaming functions*, which are partial functions
 12 from sequences of input data items to an output value. Each
 13 streaming function has an associated *rate* that captures its
 14 domain, that is, as the function reads the input data stream,
 15 the rate characterizes the prefixes that trigger the production
 16 of the output. In our language, the rates are required to be
 17 *regular*, captured by symbolic regular expressions, which lead
 18 to decision procedures for constructing well-typed expressions.

19 As a motivating example, consider a stream that consists of
 20 integers and special separator symbols #:

21 3 -5 4 1 -3 # 7 -2 9 # 1 -4

22 Given such an input data stream, suppose we want to specify
 23 the transformation illustrated below that outputs at every occur-
 24 rence of the # symbol the sum of all integers from the start
 25 of the stream.

26 input : 3 -5 4 1 -3 # 7 -2 9 # 1 -4
 27 output : 0 14

28 This transformation can be modeled by a streaming function,
 29 i.e. a partial function $f : D^* \rightarrow \mathbb{Z}$, where $D = \mathbb{Z} \cup \{\#\}$ is the
 30 set of input data items. For example, $f(3 -5 4 1 -3 \#) = 0$ and
 31 $f(3 -5 4 1 -3 \# 7 -2 9 \#) = 14$. The rate of f is the
 32 set of all finite sequences over D that end with $\#$, which
 33 is denoted by the regular expression $D^* \cdot \#$. This rate is also
 34 captured by the equivalent expression $(\mathbb{Z}^* \cdot \#)^+$, where $\mathbb{Z}^* \cdot \#$
 35 matches a block of integers terminated by a # symbol.

36 Suppose now that we want to process further the output
 37 stream produced by f in order to emit at every occurrence of
 38 a negative output of f the count of all negative outputs of f so
 39 far. This second processing state is described by a streaming
 40 function $g : \mathbb{Z}^* \rightarrow \mathbb{N}$, whose rate is denoted by the regular
 41 expression $\mathbb{Z}^* \cdot \mathbb{Z}^{<0}$, that counts the number of negative input
 42 elements and emits the count at every occurrence of a negative
 43 input item. We write $\mathbb{Z}^{<0}$ for the set of negative integers. The
 44 overall computation is described by the *streaming composition*
 45 $f \gg g$, which supplies the stream of outputs produced by f
 46 as the input stream to g .

B. Quantitative Regular Expressions

47 We will introduce now the language of *Quantitative Regular*
 48 *Expressions* (QREs) for representing stream transformations.
 49 For brevity, we also call these expressions *queries*. A query
 50 represents a streaming transformation whose domain is a
 51 regular set over the input data type.

52 To define queries, we first choose a typed signature which
 53 describes the basic data types and operations for manipulating
 54 them. We fix a collection of *basic types*, and we write A, B, \dots
 55 to range over them. This collection contains the type \mathbb{B} of

boolean values, and the unit type \mathbb{U} whose unique inhabitant is denoted by def . It is also closed under the cartesian product operation \times for forming pairs of values. Typical examples of basic types are the natural numbers \mathbb{N} , the integers \mathbb{Z} , the rationals \mathbb{Q} , and the real numbers \mathbb{R} . We write $a : A$ to mean that a is of type A . For example, we have $\text{def} : \mathbb{U}$.

We also fix a collection of *basic operations* on the basic types, for example the k -ary operation $op : A_1 \times \dots \times A_k \rightarrow B$. The identity function on D is written as $\text{id}_D : D \rightarrow D$, and the operations $\pi_1 : A \times B \rightarrow A$ and $\pi_2 : A \times B \rightarrow B$ are the left and right projection respectively. We assume that the collection of operations contains all identities and projections, and is closed under pairing and function composition. To describe derived operations we use a variant of lambda notation that is similar to Java's lambda expressions [32]. That is, we write $(A x) \rightarrow t(x)$ to mean $\lambda x : A. t(x)$, which is an (anonymous) function that takes an argument x of type A and returns the value $t(x)$. We write $(A x, B y, C z) \rightarrow t(x, y, z)$ to mean $\lambda x : A, y : B, z : C. t(x, y, z)$. For example, the identity function on D is $(D x) \rightarrow x$, the left projection on $A \times B$ is $(A x, B y) \rightarrow x$, the right projection on $A \times B$ is $(A x, B y) \rightarrow y$, and $(D x) \rightarrow \text{def}$ is the unique function from D to \mathbb{U} . We will typically use lambda expressions in the context of queries from which the types of the input variables can be inferred, so we will omit the types as in $(x, y) \rightarrow x$.

For every basic type D , assume that we have fixed a collection of *atomic predicates*, so that the satisfiability of their Boolean combinations (built up using the Boolean operations: and, or, not) is decidable. We write $\varphi : D \rightarrow \mathbb{B}$ to indicate that φ is a predicate on D , and we denote by $\text{true}_D : D \rightarrow \mathbb{B}$ the predicate that is always true. The predicate $((\mathbb{Z} x) \rightarrow x > 0) : \mathbb{Z} \rightarrow \mathbb{B}$ is true of the strictly positive integers.

Example 4.1: We consider a Boolean ventricular heart signal, where the data items are values of type $\mathbb{B} = \{0, 1\}$. A value 1 indicates a ventricular contraction of the heart, and a value 0 indicates the absence of a contraction. The signal is sampled uniformly with a sampling rate of f Hz. The predicates $\neg\text{isV}$ and isV test if a Boolean value is zero or one respectively. \square

For a type D , we define the set of *symbolic regular expressions over D* [33], denoted $\text{RE}\langle D \rangle$, with the grammar:

$r ::= \varphi \mid$	[predicate on D]
$\varepsilon \mid$	[empty sequence]
$r \sqcup r \mid$	[nondeterministic choice]
$r \cdot r \mid$	[concatenation]
r^*	[iteration].

The concatenation symbol \cdot is sometimes omitted, that is, we write rs instead of $r \cdot s$. The expression r^+ (iteration at least once) abbreviates $r \cdot r^*$. We write $r : \text{RE}\langle D \rangle$ to indicate the r is a regular expression over D . Every expression $r : \text{RE}\langle D \rangle$ is interpreted as a set $\llbracket r \rrbracket \subseteq D^*$ of finite sequences over D :

$$\llbracket \varphi \rrbracket \triangleq \{d \in D \mid \varphi(d) \text{ is true}\}$$

and the rest of the regular construct have their usual interpretations. Two expressions are said to be *equivalent* if they denote the same language.

Example 4.2: The symbolic regular expression $(\neg\text{isV})^* \cdot \text{isV}$ denotes sequences of samples that contain a single ventricular beat (contraction) at the end. \square

A string can be matched efficiently against a regular expression if there's only one way in which it could match the expression. Intuitively, this reduces the number of possible matches that have to be kept track of. The notion of *unambiguity* for regular expressions [34] is a way of formalizing the requirement of uniqueness of parsing. The languages L_1 , L_2 are said to be *unambiguously concatenable* if for every word $w \in L_1 \cdot L_2$ there are unique $w_1 \in L_1$ and $w_2 \in L_2$ with $w = w_1 w_2$. The language L is said to be *unambiguously iterable* if for every word $w \in L^*$ there is a unique integer $n \geq 0$ and unique $w_i \in L$ with $w = w_1 \dots w_n$. The definitions of unambiguous concatenability and unambiguous iterability extend to regular expressions in the obvious way. Now, a regular expression is said to be *unambiguous* if it satisfies the following:

- 1) For every subexpression $e_1 \sqcup e_2$, e_1 and e_2 are *disjoint*.
- 2) For every subexpression $e_1 \cdot e_2$, e_1 and e_2 are *unambiguously concatenable*.
- 3) For every subexpression e^* , e is *unambiguously iterable*.

Example 4.3: Consider the finite alphabet $\Sigma = \{a, b\}$. The regular expression $r = (a \sqcup b)^* b (a \sqcup b)^*$ denotes the set of sequences with at least one occurrence of b . It is ambiguous, because the subexpressions $(a \sqcup b)^* b$ and $(a \sqcup b)^*$ are not unambiguously concatenable: the word $w = ababa$ matches r , but there are two different splits $w = ab \cdot aba$ and $w = abab \cdot a$ that witness the ambiguity of parsing. The regular expressions $a^* b (a \sqcup b)^*$ and $(a \sqcup b)^* b a^*$ are both equivalent to r , and they are unambiguous. \square

Checking whether a regular expression is unambiguous can be done in polynomial time. For the case of symbolic regular expressions this results still holds, under the assumption that satisfiability of the predicates can be decided in unit time [35].

After these preliminaries, we now define quantitative regular expressions, or queries, recursively. Informally, a query f is a symbolic regular expression, called the *rate* of f and written $\text{R}(f)$, with a way to compute quantities over the strings that match the expression. The rate denotes the domain of the transformation that f represents. The definition of the query language has to be given simultaneously with the definition of rates (by mutual induction), since the query constructs have typing restrictions that involve the rates. We annotate a query f with a type $\text{QRE}\langle D, C \rangle$ to denote that the input stream has elements of type D and the outputs are values of type C .

1) Atomic queries: The basic building blocks of queries are expressions that describe the processing of a single data item. Suppose $\varphi : D \rightarrow \mathbb{B}$ is a predicate over the data item type D and $op : D \rightarrow C$ is an operation from D to the output type C . Then, the *atomic query* $\text{atom}(\varphi, op) : \text{QRE}\langle D, C \rangle$, with rate φ , is defined on single-item streams that satisfy the predicate φ . The output is the value of op on the input element.

Notation: It is very common for op to be the identity function, and φ to be the always-true predicate. So, we

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abbreviate the query $\text{atom}(\varphi, \text{id}_D)$ by $\text{atom}(\varphi)$, and the
query $\text{atom}(\text{true}_D)$ by $\text{atom}()$.

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Example 4.4: For the Boolean ventricular heart signal, the
query that matches a single item that is a heartbeat and returns
nothing is $f = \text{atom}(\text{isV}, x \rightarrow \text{def})$. The type of f is $\text{QRE}(\mathbb{B}, \mathbb{U})$
and its rate is isV . \square

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2) Empty sequence: The query $\text{eps}(c) : \text{QRE}(D, C)$, where
 c is a value of type C , is only defined on the empty sequence
 ε and it returns the output c .

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3) Iteration: Suppose that we want to iterate a computation
 $f : \text{QRE}(D, A)$ over consecutive subsequences of the input
stream and aggregate all these output values sequentially using
an initial value $c : B$ and an aggregation operation $op : B \times A \rightarrow B$. The iteration query

$$\text{iter}(f, c, op) : \text{QRE}(D, B)$$

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describes this computation. More specifically, we split the
input stream w into subsequences $w = w_1 w_2 \dots w_n$, where
each w_i matches f . The output values $a_1 a_2 \dots a_n$ with
 $a_i = f(w_i)$ are combined using the list iterator *left fold* with
start value $c : B$ and aggregation operation $op : B \times A \rightarrow B$.
This can be formalized with the combinator

$$\text{fold} : B \times (B \times A \rightarrow B) \times A^* \rightarrow B,$$

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which takes an initial value $b : B$ and a stepping map $op : B \times A \rightarrow B$, and iterates through a sequence of values of A :

$$\text{fold}(b, op, \varepsilon) = b$$

$$\text{fold}(b, op, \gamma a) = op(\text{fold}(b, op, \gamma), a)$$

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for all sequences $\gamma \in A^*$ and all values $a \in A$. For example,
 $\text{fold}(b, op, a_1 a_2) = op(op(b, a_1), a_2)$.

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In order for $\text{iter}(f, c, op)$ to be well-defined as a function,
every input stream w that matches $\text{iter}(f, c, op)$ must be
uniquely decomposable into $w = w_1 w_2 \dots w_n$ with each w_i
matching f . This requirement can be expressed equivalently
as: the rate $R(f)$ is unambiguously iterable.

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Example 4.5: For the Boolean heart signal, the query g
below matches a sequence of data items that are not heartbeats
and returns their count:

$$f : \text{QRE}(\mathbb{B}, \mathbb{B}) = \text{atom}(\neg \text{isV})$$

$$g : \text{QRE}(\mathbb{B}, \mathbb{N}) = \text{iter}(f, 0, (x, y) \rightarrow x + 1)$$

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The rate of f is $\neg \text{isV}$, and the rate of g is $(\neg \text{isV})^*$. \square

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4) Combination and application: Assume the queries f
and g describe stream transformations with outputs of type
 A and B respectively that process the same set of input
sequences, and op is a function of type $A \times B \rightarrow C$. Then,

$$\text{combine}(f, g, op) : \text{QRE}(D, C)$$

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describes the computation where the input is processed according
to both f and g in parallel and their results are combined
using op . This computation is meaningful only when both
 f and g are defined on the input sequence. So, we demand
w.l.o.g. that the rates of f and g are equivalent.

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This binary combination construct generalizes to an arbitrary
number of queries. For example, we write

$$\text{combine}(f, g, h, (x, y, z) \rightarrow op(x, y, z))$$

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for the ternary variant. In particular, we write $\text{apply}(f, op)$
for the case of one argument.

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Example 4.6: For the Boolean heart signal, suppose g counts
all heartbeats seen so far and h counts all data items. Then,
the query k below computes the ratio of these values.

$$f : \text{QRE}(\mathbb{B}, \mathbb{N}) = \text{atom}(\text{true}_\mathbb{B}, x \rightarrow \text{if } x \text{ then } 1 \text{ else } 0),$$

$$g : \text{QRE}(\mathbb{B}, \mathbb{N}) = \text{iter}(f, 0, (x, y) \rightarrow x + y)$$

$$h : \text{QRE}(\mathbb{B}, \mathbb{N}) = \text{iter}(\text{atom}(), 0, (x, y) \rightarrow x + 1)$$

$$k : \text{QRE}(\mathbb{B}, \mathbb{Q}) = \text{combine}(g, h, (x, y) \rightarrow x/y)$$

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The rate of f is true^* and the rates of the queries g , h and k
are all equal to true^* . \square

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5) Quantitative concatenation: Suppose that we want to
perform two streaming computations in sequence: first execute
the query $f : \text{QRE}(D, A)$, then the query $g : \text{QRE}(D, B)$, and
finally combine the two results using the operation $op : A \times B \rightarrow C$. The query

$$\text{split}(f, g, op) : \text{QRE}(D, C)$$

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describes this computation. More specifically, we split the
input into two parts $w = w_1 w_2$, process the first part w_1
according to f with output $f(w_1)$, process the second part w_2
according to g with output $g(w_2)$, and produce the final result
 $op(f(w_1), g(w_2))$ by applying op to the intermediate results.

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In order for this construction to be well-defined as a
function, every input w that matches $\text{split}(f, g, op)$ must be
uniquely decomposable into $w = w_1 w_2$ with w_1 matching f
and w_2 matching g . In other words, the rates of f and g
must be unambiguously concatenable.

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The binary split construct extends naturally to more than
two arguments. For example, the ternary version would be
 $\text{split}(f, g, h, (x, y, z) \rightarrow op(x, y, z))$.

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Example 4.7: For the Boolean heart signal, suppose that
 g matches sequences that end with a heartbeat and h counts
the size of sequences without any heartbeat. Then, the query k
below outputs the time that has elapsed since the last heartbeat.

$$f : \text{QRE}(\mathbb{B}, \mathbb{U}_t) = \text{iter}(\text{atom}(), \text{def}, (x, y) \rightarrow \text{def})$$

$$g : \text{QRE}(\mathbb{B}, \mathbb{U}_t) = \text{split}(f, \text{atom}(\text{isV}), (x, y) \rightarrow \text{def})$$

$$h : \text{QRE}(\mathbb{B}, \mathbb{N}) = \text{iter}(\text{atom}(\neg \text{isV}), 0, (x, y) \rightarrow x + 1)$$

$$k : \text{QRE}(\mathbb{B}, \mathbb{N}) = \text{split}(g, h, (x, y) \rightarrow y)$$

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The rate of f is true^* , that of g is $\text{true}^* \cdot \text{isV}$, the rate of h
is $(\neg \text{isV})^*$, and the rate of k is $\text{true}^* \cdot \text{isV} \cdot (\neg \text{isV})^*$. \square

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6) Streaming composition: A natural operation for query
languages over streaming data is streaming composition: given
two streaming queries f and g , $f \gg g$ represents the computa-
tion in which the stream of outputs produced by f is supplied
as the input stream to g . Such a composition is useful in setting
up the query as a pipeline of several stages. We allow the
operation \gg to appear *only at the top-level* of a query. So, a
general query is a pipeline of \gg -free queries. At the top level,
no type checking needs to be done for the rates, so we do not
define the function $R()$ for queries $f \gg g$.

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Example 4.8: For the Boolean heart signal, suppose we
want to emit at every heartbeat the average heart rate over the
entire stream. We will describe this computation as a two-stage

1 pipeline. The first stage (query h below) produces a sequence
 2 of natural numbers which correspond to the number of 0's
 3 between two consecutive 1's (heartbeats).
 4

```

 5   f : QRE<B, N> = iter(atom( $\neg$ isV), 0,  $(x, y) \rightarrow x + 1$ )
 6   g : QRE<B, N> = split(f, atom(isV),  $(x, y) \rightarrow x$ )
 7   h : QRE<B, N> = split(iter(g, def,  $(x, y) \rightarrow \text{def}$ ),
 8                           g,  $(x, y) \rightarrow y$ )
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11 The rate of f is $(\neg\text{isV})^*$, the rate of g is $(\neg\text{isV})^* \cdot \text{isV}$, and
 12 the rate of h is $((\neg\text{isV})^* \cdot \text{isV})^+$. The second stage (query n
 13 below) processes a stream of these numbers to compute the
 14 average heart rate in beats per minute.

```

15   k : QRE<N, N> = iter(atom(), 0,  $(x, y) \rightarrow x + y$ )
16   l : QRE<N, N> = iter(atom(), 0,  $(x, y) \rightarrow x + 1$ )
17   m : QRE<N, Q> = combine(k, l,  $(x, y) \rightarrow x/y$ )
18   n : QRE<Q, Q> = apply(m,  $x \rightarrow (60 \cdot f)/x$ )
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21 where f is the sampling rate in Hz. The query m computes
 22 the average number of samples between two consecutive
 23 heartbeats. The top-level query is the pipeline $h \gg n$. \square

24 7) **Global choice:** Given queries f and g of the same type
 25 with disjoint rates r and s , the query $\text{or}(f, g)$ applies either f
 26 or g to the input stream depending on which one is defined.
 27 The rate of $\text{or}(f, g)$ is the union $r \sqcup s$. This *choice* construction
 28 allows a case analysis based on a global regular property of
 29 the input stream.

30 *Example 4.9:* In our Boolean heart example, suppose we
 31 want to compute a statistic across days, where the contribution
 32 of each day is computed differently depending on whether or
 33 not an abnormally short interval between consecutive heart-
 34 beats occurred or not. Then, we can write a query summarizing
 35 the daily activity with a rate capturing normal days (the ones
 36 without any short interval) and a different query with a rate
 37 capturing abnormal days, and iterate over their disjoint union.

38 Consider the stream of interval lengths between consecutive
 39 heartbeats, i.e. the output stream of query h defined in Exam-
 40 ple 4.8. We assume that T is the threshold for an abnormally
 41 short interval between two consecutive heartbeats. Query h
 42 below computes the smallest interval length for sequences with
 43 at least one abnormally short interval:

```

44   f : QRE<N, Q> = iter(atom( $x \rightarrow x > T$ ),  $\infty$ , min)
45   g : QRE<N, Q> = iter(atom(),  $\infty$ , min)
46   h : QRE<N, Q> = split(f, atom( $x \rightarrow x \leq T$ ), g, min)
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```

49 The rate of f is $(x > T)^*$, the rate of g is true^* , and the rate
 50 of h is $(x > T)^* \cdot (x \leq T) \cdot \text{true}^*$. Query m below computes
 51 the average interval length for sequences with no abnormally
 52 short interval:

```

53   k : QRE<N, N> = iter(atom( $x \rightarrow x > T$ ), 0,  $(x, y) \rightarrow x + y$ )
54   l : QRE<N, N> = iter(atom( $x \rightarrow x > T$ ), 0,  $(x, y) \rightarrow x + 1$ )
55   m : QRE<N, Q> = combine(k, l,  $(x, y) \rightarrow x/y$ )
56
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58 The rates of k , l and m are all equal to $(x > T)^*$. The top-level
 59 query is then $\text{or}(h, m)$. \square

C. Derived constructs

The core language of Section IV-B is expressive enough to
 describe many common stream transformations. We present
 below several derived constructs.

1) **Matching without output:** Suppose r is an unambiguous
 symbolic regular expression over the data item type D . The
 query $\text{match}(r)$, whose rate is equal to r , does not produce
 any output when it matches. This is essentially the same as
 producing def as output for a match. The match construct
 can be encoded as follows:

```

  match( $\varphi$ )  $\triangleq$  atom( $\varphi, x \rightarrow \text{def}$ )
  match( $r_1 \sqcup r_2$ )  $\triangleq$  or( $\text{match}(r_1)$ ,  $\text{match}(r_2)$ )
  match( $r_1 \cdot r_2$ )  $\triangleq$  split( $\text{match}(r_1)$ ,  $\text{match}(r_2)$ ,  $(x, y) \rightarrow \text{def}$ )
  match( $r^*$ )  $\triangleq$  iter( $\text{match}(r)$ ,  $\text{def}$ ,  $(x, y) \rightarrow \text{def}$ )
```

An easy induction establishes that $R(\text{match}(r)) = r$.

2) **“Until” Iteration:** Suppose that ϕ and ψ are disjoint
 predicates on the input data type D , the function $op : C \times D \rightarrow$
 C is an aggregation operation, and $c : C$ is the initial
 aggregate. The query $\text{iterUntil}(\phi, \psi, c, op)$ aggregates a
 sequence of data items that satisfy ϕ and stops when an item
 that satisfies ψ is found. It is encoded as:

```

  iterUntil( $\phi, \psi, c, op$ )  $\triangleq$  split(iter(atom( $\phi$ ),  $c, op$ ),
                                         atom( $\psi$ ),  $(x, y) \rightarrow x$ )
```

The query has type $\text{QRE}(D, C)$ and rate $\phi^* \cdot \psi$.

3) **Stream Annotation:** Suppose that the input stream has
 items of type D , f is a query of type $\text{QRE}(D, C)$, and we
 want to produce an output stream with items of type E in the
 following way: when the query f produces an output (upon
 consumption of the input stream) apply $op_2 : D \times C \rightarrow E$ to
 the last input element and its output to get the final result,
 and when the query f is undefined apply $op_1 : D \rightarrow E$ to
 the last input element. This computation is described by
 the query $\text{annt}(f, op_1, op_2) : \text{QRE}(D, E)$ with rate D^+ . This
 annotation query can be encoded using the regular constructs
 of Section IV-B, but the encoding is complex and inefficient,
 so we provide a custom efficient implementation.

a) **Tumbling windows:** The term *tumbling windows* is
 used to describe the splitting of the stream into contiguous
 non-overlapping subsequences [36]. Suppose we want to de-
 scribe the streaming function that iterates f at least once and
 reports the result given by f at every match. The following
 query expresses this behavior:

```

  iterLast( $f$ )  $\triangleq$  split( $\text{match}(R(f))^*$ ,  $f$ ,  $(x, y) \rightarrow y$ ).
```

The rate of $\text{iterLast}(f)$ is equal to $R(f)^+$.

4) **Efficient Sliding Windows:** Suppose we want to apply
 the query $f : \text{QRE}(D, A)$ to consecutive nonoverlapping parts
 of the input, and efficiently aggregate the intermediate results
 over a sliding window of size W . That is, the W most recent
 output values of f are aggregated to produce the final output.
 The aggregation is described by an initial aggregate $c : B$ and
 three functions: an *insertion* operation $\text{ins} : B \times A \rightarrow B$ describes
 how to add a new value of type A to the aggregate
 (of type B), the *removal* operation $\text{rmv} : B \times A \rightarrow B$ describes

```

1
2 // Process a single value: rate Double
3 QRe<Double, Double> f =
4     Q.atomic(x -> true, x -> x);
5
6 // Sum of sequence of values: rate Double*
7 QRe<Double, Double> sum =
8     Q.itter(f, 0.0, (x,y) -> x+y);
9
10 // Length of sequence of values: rate Double*
11 QRe<Double, Long> count =
12     Q.itter(f, 0L, (x,y) -> x+1);
13
14 // Average of sequence of values: rate Double*
15 QRe<Double, Double> avg =
16     Q.combine(sum, count, (x,y) -> x/y);
17
18 Iterator<Double> stream = ... // input stream
19
20 // evaluator for the query
21 Eval<Double, Double> e = avg.getEval();
22
23 // execution loop
24 Double output = e.start();
25 // e.start() returns null, if undefined
26 while (stream.hasNext()) {
27     Double d = stream.next();
28     output = e.next(d);
29     // e.next(d) returns null, if undefined
30 }

```

Fig. 4: StreamQRE Library in Java: Computing the average of a sequence of values.

how to remove a value from the aggregate, and the *finalization* operation $op : B \rightarrow C$ computes the final result from the aggregate. This computation is described by the query

$wnd(f, W, c, ins, rmv, op) : QRE\langle D, C \rangle$,

whose rate is equal to $R(f)^+$. This query can be encoded using the regular constructs of Section IV-B and an additional data type for FIFO queues (in order to maintain the buffer of values of type A that are currently in the active window).

D. A Java Library of QREs

StreamQRE has been implemented as a Java library [18] in order to facilitate the easy integration with user-defined types and operations. The implementation covers all the core constructs of Section IV-B, and also provides optimizations for the derived constructs of Section IV-C (matching without output, “until” iteration, stream annotation, etc.).

Figure 4 gives a simple example that illustrates how to program with the StreamQRE Java library. The query `avg` describes the computation of the average of a sequence of values of type `Double`. The method `getEval`, which stands for “get evaluator”, is used to obtain an object that encapsulates the evaluation algorithm for the query. On this evaluator object, the methods `start` and `next` are used to initialize the algorithm and consume data items respectively.

V. AN ICD ARRHYTHMIA MONITORING ALGORITHM

We now describe in details an Arrhythmia Monitoring Algorithm (AMA) found in one of the ICDs on the market

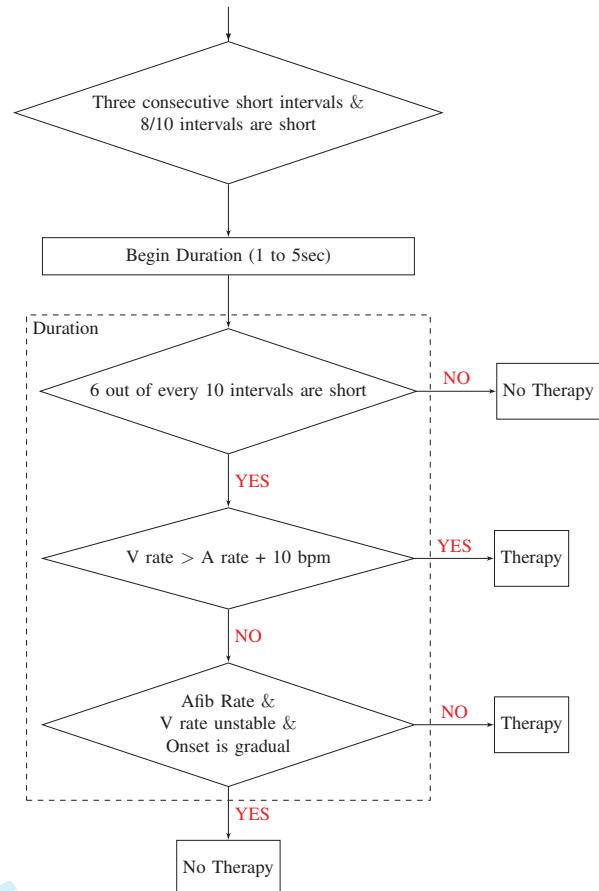


Fig. 5: Boston Scientific discrimination algorithm

today [17]. All ICD AMAs on the market today take the form of a decision tree, such as the one in Fig. 5. Each node in the tree is a *discriminator*, which computes one feature of the input signal and decides, on its basis, how to branch. Thus, each discriminator returns a decision, Yes or No. We chose to present this particular AMA because variants on its discriminators can be found in the AMAs of all devices on the market. For example, all devices measure average heart rate, compare atrial and ventricular rates, measure rate variability, onset of arrhythmia, etc. The differences are in how variability is defined (variance or sum of absolute differences, for example), the size of windows for computing quantities, the way they are combined in the decision tree, etc.

A. Discriminators

Recall that the input to the AMA is a discrete-time boolean signal, which is obtained by running a peak detector on the discrete-time real-valued EGM signal. The peak detector outputs a 1 at peaks, and 0 otherwise. The signals we work with in this paper have a sampling period of 1ms. Formally, let $\mathbb{B} = \{0, 1\}$. At every time $t \in \mathbb{N}$, the AMA receives a data item s of the following form

$$s = (V, A, t) \in D := \mathbb{B} \times \mathbb{B} \times \mathbb{N} \quad (1)$$

where $V = 1$ indicates there is a ventricular beat at time t (and $V = 0$ indicates that there is not). Similarly for A . We

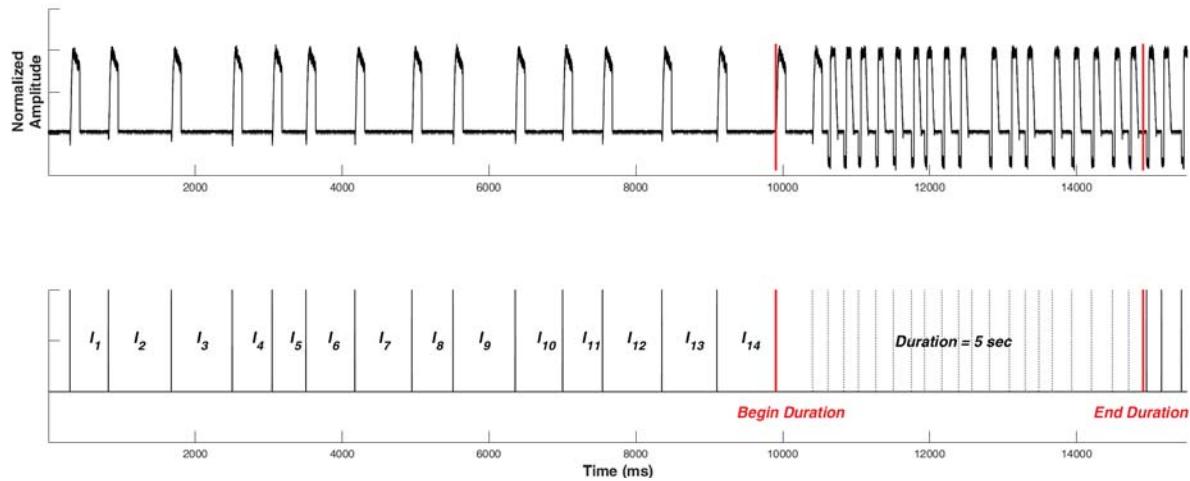


Fig. 6: Input stream from one channel. Measured electrogram (top figure) and corresponding Boolean stream (bottom figure). In the Boolean stream, spikes represent beats, and I_k is an interval of time between beats. Duration is a fixed time period, here set to 5 seconds.

will find the need to refer to the ventricular boolean signal separately, and we write $\mathbf{V} \in \mathbb{B}^*$ to denote it. It will also be called the ventricular *channel*. Similarly, $\mathbf{A} \in \mathbb{B}^*$ is the *atrial channel*. See Fig. 6. Given an item s , the function call $s.\mathbf{V}$ returns its first element; similarly for $s.\mathbf{A}$ and $s.\mathbf{t}$.

An (atrial or ventricular) *interval* in a given channel is the interval of time between two consecutive beats. Its length is denoted by I , and is always an integer measured in milliseconds (ms). The average (atrial or ventricular) *rate* is the inverse of the average interval length.

The decision tree of the AMA we describe is shown in Fig. 5. It is made up of the following discriminators.

1) **Three Consecutive Short Intervals:** Three consecutive short intervals are required to initiate rhythm analysis, as they indicate a potentially accelerating rhythm. Therefore, this discriminator checks if three consecutive intervals are shorter than some pre-specified threshold T_{csi} . Referring to Fig. 6:

$$CSI := (I_5 < T_{csi}) \wedge (I_6 < T_{csi}) \wedge (I_7 < T_{csi}) \quad (2)$$

2) **8/10 Short Intervals:** A rhythm that becomes fast for a few beats then slows down again is not fatal and so should not cause therapy to be delivered. To estimate whether the current rhythm is sustained, this discriminator checks whether 8 out of 10 intervals are shorter than some threshold $T_{8/10}$. Referring to Fig. 6:

$$\text{Short8outof10} := |\{I_k : 5 \leq k \leq 14, I_k < T_{8/10}\}| \geq 8 \quad (3)$$

3) **Sudden Onset:** Ventricular Fibrillation (VF), which is fatal, usually occurs suddenly, whereas a tachycardia that accelerates gradually is usually non-fatal. The Onset discriminator quantifies the suddenness of tachycardia onset as follows. It operates in two steps, which process a window of $2m$ intervals. To help explain this discriminator using Fig. 6, we will assume $m = 4$. In the first step, it detects the ventricular beat in the first 4 intervals (I_1, \dots, I_4) at which the interval length decreased the most. This is the *pivot* beat. If the amount of

decrease is greater than some threshold, Step I declares Onset. In the second step, the algorithm computes the differences between the average of 4 pre-pivot beats ($(I_1 + \dots + I_4)/4 := \mu$) and each of 4 post-pivot beats (I_5, \dots, I_8). I.e., it computes $d_5 = \mu - I_5, \dots, d_8 = \mu - I_8$. If at least 3 of these 4 differences d_5, \dots, d_8 is greater than a threshold, Step II declares Onset. If both stages declare Onset, the discriminator declares Sudden Onset. In our implementation, we simplify things by taking the pivot to be the middle beat in the window of $2m = 8$ intervals. So SuddenOnset is computed as:

$$\text{SO-StepI} := I_{post-pivot} < \alpha \cdot I_{pre-pivot} \quad (4)$$

$$\text{SO-StepII} := |\{d_k : d_k > T_{o2}\}| \geq 3 \quad (5)$$

$$\text{SuddenOnset} := \text{SO-StepI} \wedge \text{SO-StepII}$$

When both Three Consecutive Short Intervals and 8/10 Short Intervals match, then a *Duration* is started. A Duration is a fixed-length time period (e.g., 5sec) during which the algorithm will continue to monitor the rhythm to see whether the arrhythmia is sustained, or it slows down and dies out. In the latter case, no therapy is delivered. See Fig. 6. During Duration, the following four discriminators are evaluated.

4) **A/V Rate Comparison:** If the ventricles have more beats than the atria, this is an almost sure sign that the arrhythmia is ventricular in origin (i.e., the ventricles are driving the atria and not the other way around). This discriminator compares the average ventricular heart rate r_V with the average atrial heart rate r_A , where the average is computed over the last 10 intervals in the Duration window:

$$\text{AVRate} := r_V > r_A + 10\text{bpm}$$

5) **Sliding 6/10:** Sometimes an arrhythmia terminates on its own, which is preferable to having the device terminate it with a shock. This discriminator continuously checks whether

6 out of every 10 intervals are short; if any 10 intervals fails this check, the discriminator declares No Therapy.

Sliding6outof10 := For every 10 intervals I_1, \dots, I_{10}

$$|\{I_k : I_k < T_{6/10}\}| \geq 6$$

6) **Stability:** VF is an unstable rhythm, meaning that the interval lengths during fibrillation vary greatly. The Stability discriminator defines rhythm stability as being the variance in ventricular intervals' lengths during Duration. If variance is below a threshold T_{stab} , then the rhythm is deemed stable. With \bar{I} denoting the average interval length,

$$\text{Stability} := \frac{1}{n} \sum_{k=1}^n (I_k - \bar{I})^2 \leq T_{stab}$$

7) **AFib Rate:** Atrial Fibrillation (AF) is an atrially-driven rhythm with a high rate, and is one possible source of misclassification for the AMA. To circumvent this issue, this discriminator measures the atrial rate throughout the Duration. As long as at least 4/10 intervals are shorter than the AF threshold T_{af} , this discriminator decides that the current rhythm is in fact AF and therapy should be withheld.

SlidingAFib := For every 10 interval lengths I_1, \dots, I_{10}

$$|\{I_k : I_k < T_{af}\}| \geq 4$$

VI. QRE IMPLEMENTATION OF THE ARRHYTMIA MONITORING ALGORITHM

The QRE implementation of the BSC algorithm of Section V is divided into four main stages. The first two stages annotate the input signal with additional information: the lengths of the intervals between heartbeats, and some sliding-window statistics over them. The annotated stream is passed to the later stages in order to compute the discriminators for deciding whether therapy should be delivered or not. We give a high-level overview of each stage in Section VI-A, as well as more detailed descriptions and QREs implementations in Sections VI-B to VI-E.

A. Overview of Implementation Stages

All discriminators described in Section V use the interval lengths between consecutive heartbeats. In order to simplify the later computations, it is useful to annotate the stream with this extra information so that it is readily available in the next processing steps. Similarly, there are some sliding-window statistics that are required for the discriminators "A/V Rate Comparison", "Sliding 6/10" and "AFib Rate". These quantities require looking at the 10 previous intervals to be computed. The specification of the algorithm is much easier if this information is already present in the stream, which obviates the need to look back 10 intervals into the past. This motivates our design choice to always annotate the stream with these useful sliding-window statistics.

The ICD's AMA receives beats from the atrium and the ventricle. The input stream consists of data items that are of the form shown in (1). The implementation is a multi-stage pipeline, where each stage is a QRE. Each stage feeds its

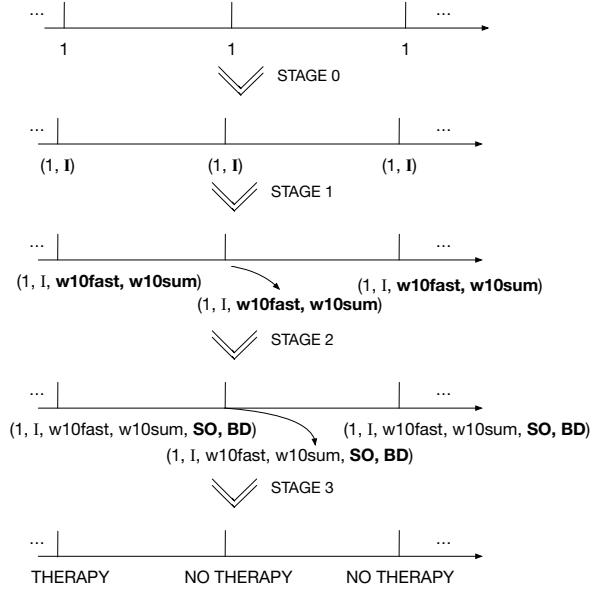


Fig. 7: The overall detection algorithm, shown for the ventricular channel and with the timestamp sequence omitted. The top stream gives the input boolean signal. Streams below it are annotated with the information in bold font. I = Interval Length, w10fast = number of last 10 intervals that are short, w10sum = sum of last 10 interval lengths, SO = Sudden Onset flag, BD = Begin Duration flag.

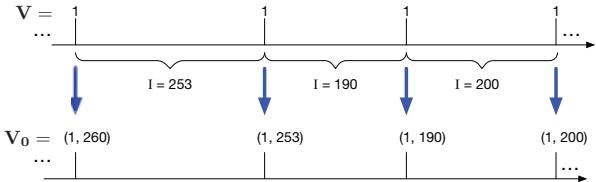


Fig. 8: Stage 0 annotates both channels V and A with interval lengths, i.e. the number of 0s between 1s. Here it is shown operating on the ventricular channel.

output stream to the following stage for further annotation and processing. They are:

- **Stage 0:** pre-processing stage which annotates the input stream s with the lengths of the ventricular and atrial intervals. See Figure 8. The output from this stage will be used in all subsequent stages. Call the output stream of this stage s_0 .
- **Stage 1:** augments its input stream s_0 with two pieces of information. The first is the total duration of every window of 10 consecutive intervals, in both channels. This will be used for the A/V Rate Comparison discriminator. The second piece of information is the number of short³ intervals in every window of 10 consecutive intervals, in both channels. This will be used for the Sliding 6/10 and AFib Rate Comparison discriminators. See Figure 9 for

³I.e., those that are shorter than a pre-defined threshold $T_{6/10}$.

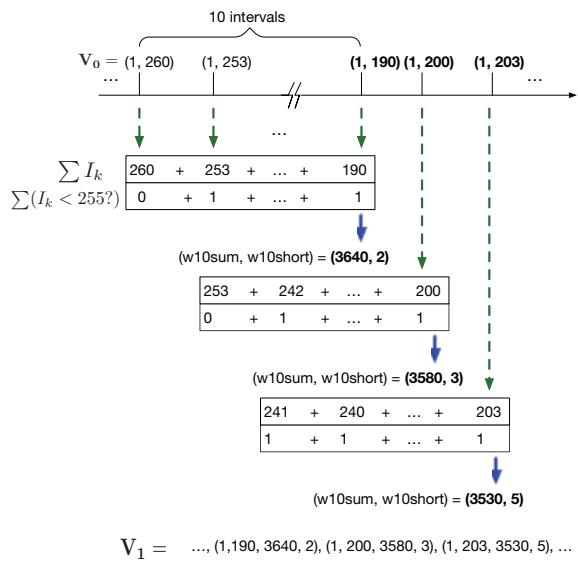


Fig. 9: Stage 1, shown acting on the V channel, augments V_0 with the total duration counter $w10sum$ and the short intervals counter $w10short$, computed over the last 10 intervals. Here, the threshold $T_{6/10} = 255$.

the computation of both quantities on the V channel. Call the output stream of this stage s_1 .

- **Stage 2:** detects the beginning of Duration, the period of time during which the rhythm is monitored for a fixed amount of time to confirm whether a suspected arrhythmia is indeed sustained and ventricular in origin. For Duration to be declared and monitored, both the Three Consecutive Short Intervals and 8/10 Short Intervals discriminators must return Yes. If Duration is initiated as a result, the input stream s_1 is annotated with a **BD** marker to indicate the start of Duration. See Fig. 10. This stage also computes the Onset discriminator and annotates the stream with flag $SO = 1$ if it is met. Call the output stream of this stage s_2 .
- **Stage 3:** final stage, has input stream s_2 . It computes all discriminators in Duration: Stability, Sliding 6/10, AV Rate Comparison, and AFib Rate. Based on all these and the value of Onset, the stage makes a final decision of Therapy or No Therapy. See Figure 10.

REMARK. Because a QRE describes a streaming algorithm, each of the above stages operates continuously and issues an output with every new data item (including \perp if the string so far doesn't match). So for example, it is possible for Stage 2 to declare the start of Duration several times in a row, i.e., to output $BD = 1$ several times. See Fig. 14 for an example. The first Duration to end in a Therapy decision in Stage 3 will cause therapy to be scheduled, and the other Durations in progress are aborted. On the other hand, if the first Duration does not end in therapy, the subsequent ones continue to be monitored to their conclusion. Thus one important consequence of this streaming implementation is that it is possible for the QRE to track *multiple simultaneous* potential

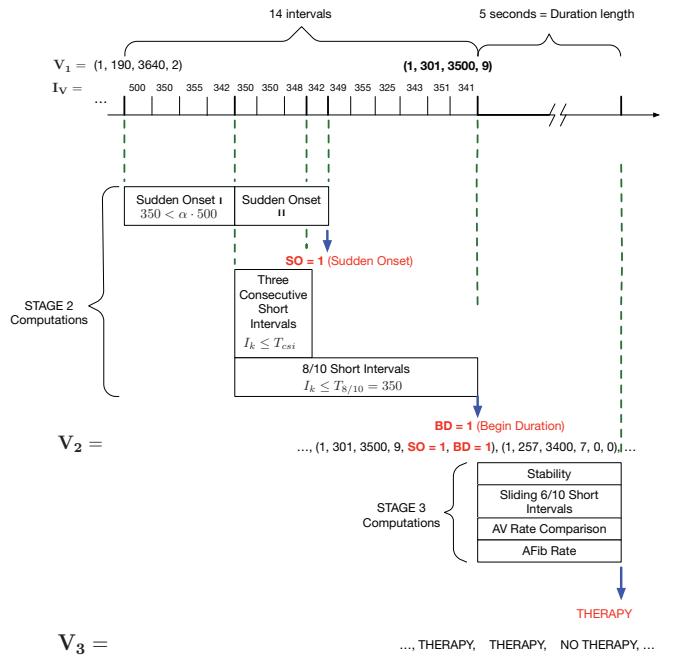


Fig. 10: Stages 2 and 3. The rectangles show the computed discriminators, and their width covers the part of the input stream used in the computation. E.g., “8/10 Short Intervals” uses the 10 intervals above its box, while Stability uses all intervals in the Duration window. Downward blue arrows indicate when a quantity is computed. E.g., the BD marker is computed every 14 intervals. SO and BD are added to stream V_1 to obtain stream V_2 . The A channel is not shown, though it enters in the calculation of AV Rate Comparison discriminator.

arrhythmias. In this way, no potentially fatal arrhythmia is missed.

We will explain now each stage in detail, and present the precise implementation in the StreamQRE language. Recall the QRE constructs of Section IV and the type of the input data items (1). Some computations are performed in the same way both on the atrial and the ventricular channel. In such cases we will only give the queries that describe the processing of the ventricular channel for the sake of brevity.

B. Stage 0: Annotate interval lengths

This stage annotates the stream with heartbeat interval lengths, that is, the lengths of the sequences between two consecutive heartbeats. So, the length of an interval of the form $100 \dots 001$ is the number of 0s between the 1s. This computation is performed both for the ventricular and atrial channel. The regular expression that describes a signal that has a single heartbeat at the end is 0^*1 . The query for computing the ventricular interval lengths is the following:

```

lincr = (x, y) -> x + 1, of type  $\mathbb{N} \times \mathbb{N} \rightarrow \mathbb{N}$ 
intV = iterUntil( $\neg isV, isV, 0, lincr$ )
allIntV = iterLast(intV) // rate  $((\neg isV)^* \cdot isV)^+$ 
annt0V = annt(allIntV,  $x \rightarrow x, (x, c) \rightarrow x[I_V := c]$ )
stage0 = annt0V >> annt0A

```

The query `intV` iterates over the 0s of the ventricular channel (predicate $\neg \text{isV}$) while incrementing a counter until it encounters a 1 (predicate `isV`). The query `allIntV` iterates `intV` over consecutive nonoverlapping subsequences, thus processing all ventricular intervals. The query `annt0V` annotates the input elements with the interval values I_V calculated by `allIntV`, and `annt0A` does the same with the atrial channel. See Fig. 8. Therefore, the output stream s_0 from this stage consists of data items of the following form:

$$s_0 = (V, I_V, A, I_A, t) \in D_0 = (\mathbb{B} \times \mathbb{N})^2 \times \mathbb{N} \quad (6)$$

C. Stage 1: Sudden Onset and Short Intervals

The input stream for this stage consists of items of the form shown in (6). In this state, we first calculate the sum of interval lengths over a sliding window that consists of 10 intervals, and we annotate the stream with this information (see Fig. 9):

```
21 blockV = split(match(( $\neg \text{isV}$ ) $^*$ ), isV,  $(x, y) \rightarrow y.I_V$ )
22 wndSumV = wnd(blockV, 10, 0,  $(x, y) \rightarrow x + y$ )
23 stg1SumV = annt(wndSumV,  $x \rightarrow x$ ,  $(x, c) \rightarrow x[SumV := c]$ )
```

The query `blockV` matches 0^*1 in the ventricular channel and returns the length of the interval that ends with the matched 1. The query `wndSumV` executes `blockV` over a sliding window of size 10 and accumulates the interval lengths by summing them up. The query `stg1SumV` annotates the stream with all these sliding-window sums.

In the second part of this stage we also calculate the number of short ventricular intervals over a sliding window of size 10, where “short” is defined as being of length less than $T_{6/10}$.

```
36 shortV = apply(blockV,
37            $x \rightarrow \text{if } (x \leq T_{6/10}) \text{ then } 1 \text{ else } 0$ )
38 wndShortV = wnd(shortV, 10, 0,  $(x, y) \rightarrow x + y$ )
39 stg1ShortV = annt(wndShortV,  $x \rightarrow x$ ,
40                    $(x, y) \rightarrow x[ShrtV := c]$ )
```

The query `shortV` applies a thresholding operator to the output of `blockV`. As before, `shortV` is run in a sliding-window fashion using the `wnd` construct, and the output is annotated onto the stream using `annt`.

The same two computations are performed on the atrial channel, but with a different threshold, T_{afib} , for `stg1ShortA`. The final query for this state is the streaming composition of the above channel-specific computations:

```
51 stage1 =
52   stg1SumV  $\gg$  stg1ShortV  $\gg$  stg1SumA  $\gg$  stg1ShortA
```

The output stream s_1 of this stage consists of items (with re-arrangement) of the following form:

$$s_1 = (V, I_V, SumV, ShrtV, A, I_A, SumA, ShrtA, t) \in D_1 = (\mathbb{B} \times \mathbb{N}^3)^2 \times \mathbb{N} \quad (7)$$

D. Stage 2: Sudden Onset and Begin Duration

This stage computes the Sudden Onset discriminator and Begin Duration (**BD**) marker at every ventricular beat. In order to do this, the last 14 ventricular intervals I_1, I_2, \dots, I_{14} have to be considered, as shown in Fig. 10.

- The first 4 intervals I_1, I_2, I_3 and I_4 are used for Step I of “Sudden Onset”, defined in (4).
- The next 4 intervals I_5, I_6, I_7 and I_8 are used for Step II of “Sudden Onset”, defined in (5).
- The intervals I_5, I_6, I_7 are used for the “Three Consecutive Intervals” discriminator, defined in (2).
- The last 10 intervals I_5, I_6, \dots, I_{14} are used for the “8/10 Short Intervals” discriminator, defined in (3).

This stage splits the stream into consecutive intervals, and evaluates all the relevant discriminators over the last 14 intervals using the operation $opStage2 : \mathbb{N}^{14} \rightarrow \mathbb{B} \times \mathbb{B}$. The input to $opStage2$ is a vector of 14 ventricular interval lengths, and the output is a pair of Boolean values: the first component indicates the presence of “Sudden Onset” (SO), and the second component indicates the presence of “Begin Duration” (BD).

```
sobd = split(blockV, ..., blockV,
               $(x_1, \dots, x_{14}) \rightarrow opStage2(x_1, \dots, x_{14})$ )
wndsobd = split(match(R(blockV) $^*$ ), sobd,  $\pi_2$ )
stage2 = annt(wndsobd,  $x \rightarrow x$ ,
                   $(x, \langle c_1, c_2 \rangle) \rightarrow x[SO := c_1, BD := c_2]$ )
```

The query `sobd` : $QRE\langle D_1, \mathbb{B}^2 \rangle$ matches 14 consecutive ventricular intervals, and applies the function $opStage2$ to their lengths in order to compute the Boolean flags for “Sudden Onset” and “Begin Duration”. This computation is executed in a sliding-window fashion and the output is used to annotate the stream. The output stream s_2 from Stage 2 contains data items of the following form:

$$s_2 = (s_1, SO, BD) \in D_2 = D_1 \times \mathbb{B}^2$$

E. Stage 3: Therapy Decision

This stage uses the four discriminators shown in Fig. 10 to make the final decision whether to apply therapy or not. Whenever “Begin Duration” (**BD**) is detected by the previous stage, the algorithm considers the window of N data items following **BD**, and the discriminators are computed using the information contained within this window. For example, if the Duration window is programmed to be 5 seconds, and the sampling rate is 256Hz, then the window contains $N = 5 \times 256 = 1280$ items. The query

```
stage3 = wnd(atom(),  $N, 0, \text{ins}, \text{rmv}, \text{discr}$ )
```

describes a sliding-window computation that maintains a buffer with all ventricular and atrial beats of the duration period. The function `ins` adds a new item to the buffer, the function `rmv` removes an expiring item from the buffer, and the operation `discr` computes the discriminators and the final therapy decision using only the items contained in the buffer.

1 F. Overall AMA Query

2 The top-level query for this Arrhythmia Monitoring Algorithm
 3 is the streaming composition of all stages (see Fig. 7):
 4

5 $\text{AMA} = \text{stage0} \gg \text{stage1} \gg \text{stage2} \gg \text{stage3}.$

6 VII. ILLUSTRATIVE EXAMPLES

7 A. Sample executions

8 Two examples will serve to illustrate the details of the
 9 query execution. Fig. 11 shows a Ventricular Fibrillation (VF)
 10 EGM signal along with the corresponding boolean beat stream.
 11 The results of running stage2 on this signal are presented
 12 in a Fig. 12. At times 12,572 ms and 12,811 ms the start
 13 of Duration is detected ($BD = 1$). At the end of the first
 14 initiated Duration (at 17,572 ms), the A/V Rate Comparison
 15 discriminator and Sliding 6/10 discriminator are satisfied and
 16 the AMA outputs Therapy. This is consistent with the decision
 17 tree in Fig 5.

18 Fig 14 shows an Atrial Fibrillation (AF) signal. The
 19 algorithm never outputs therapy. Before time 15,529 ms the
 20 rhythm is not determined to be fast (Three Consecutive Short
 21 Intervals and 8/10 Short Intervals are never satisfied together).
 22 The first time when the fast rhythm is detected is at 15,529ms.
 23 Therefore, the first $BD = 1$ flag happens at time 15,529 ms
 24 and Duration starts. At the end of this Duration (20,529 ms),
 25 A/V Rate Comparison is not satisfied. Moreover, the rhythm
 26 is determined to be unstable with gradual onset and AFib Rate
 27 condition is satisfied. Therefore, no therapy is delivered at this
 28 point. The same thing occurs for the next ventricular beat time
 29 point (15,867 ms), and no therapy is detected again.

30 B. Validation of the QRE Implementation

31 To validate the correctness of our QRE implementations, we
 32 created three versions of the AMA in Fig. 5. These three versions
 33 will also be used in the power analysis of Section VIII.
 34 The baseline version, presented in Section V, includes all
 35 discriminators and has a Duration length of 5sec. The second
 36 version does not use the Sudden Onset discriminator. This
 37 discriminator is Off by default when the device ships. The
 38 third version reduces Duration length to 1sec. Accuracy is
 39 measured using the Specificity and Sensitivity of detection,
 40 defined respectively as

$$41 \text{Specificity} = \frac{\# \text{ correctly detected SVTs}}{\# \text{ true SVTs}} \times 100\%$$

$$42 \text{Sensitivity} = \frac{\# \text{ correctly detected VTs}}{\# \text{ true VTs}} \times 100\%$$

43 where the denominators are the number of true SVTs and VT,
 44 respectively.

45 The three versions were run on a database of 960 EGMs,
 46 equally divided into 480 SVTs and 480 VTs. The beat timing
 47 in the EGMs (in other words, the boolean stream s) was
 48 generated by the heart model of [37],[38]. Briefly, this model
 49 can simulate beat generation and propagation at different rates,
 50 from different locations in the heart. E.g., it can simulate a
 51 Normal Sinus Rhythm (NSR) which originates in the sino-
 52 atrial node and conducts down, or a fast ventricular rhythm

53 TABLE I: Database-averaged detection accuracy for three versions
 54 of AMA. Throughput measured on a standard desktop with Intel i5
 55 processor running Ubuntu.

Measurements:	Algorithm		
	Baseline	No Onset	Duration = 1s
Throughput [items/sec]	674.602	714.206	914.746
Sensitivity	100%	100%	100%
Specificity	92.5%	93.13%	88.54%

56 that starts in the ventricles and conducts up to the atria. The
 57 model can also simulate different conduction pathways and
 58 conduction delays between locations. In this manner, it is
 59 capable of simulating a wide range of VTs and SVTs. These
 60 simulated arrhythmia episodes are automatically labelled by
 61 the model so that we know whether they should be treated by
 62 the device or not, thus allowing us to compute specificity and
 63 sensitivity.

64 The validity of the simulated beat stream is guaranteed
 65 in three complementary ways: 1) The model implements
 66 well-known clinical principles of arrhythmia generation, such
 67 as re-entrant circuits [22], and the implementation has been
 68 reviewed by two cardiologists. 2) Key output stream character-
 69 istics, like the rate, are guaranteed to fall in the clinically
 70 observed ranges. And finally, 3) a representative sample of
 71 model outputs has been validated as correct by two cardiolo-
 72 gists.

73 Table I shows the results of running these three versions on
 74 the signals database. It also includes throughput, which is the
 75 number of data items processed per second. First, we note that
 76 the Sensitivity of all three algorithms is 100%, which matches
 77 the reported sensitivity of ICDs in the literature. Indeed, miss-
 78 ing a true VT or VF can have a debilitating or fatal effect on
 79 the patient, so the algorithms are programmed to err on the side
 80 of safety and guarantee 100% sensitivity. Second, we note that
 81 turning off Sudden Onset has a negligible effect on Specificity,
 82 which justifies its being turned off by default in real devices.
 83 Finally, shortening Duration further decreases Specificity, as
 84 expected: when Duration is shorter, the algorithm is leaving
 85 less time for the arrhythmia to terminate on its own, and is
 86 taking a Therapy decision for signals that shouldn't be treated.

8 VII. UPPER BOUNDS ON QRE COST

9 Power consumption is an important consideration when de-
 10 signing the software and hardware of an implantable medical
 11 device. Replacing an implantable device requires surgery, and
 12 most ICD and ILR recipients are older patients with various
 13 health issues [28], so reducing the likelihood of a replacement
 14 by prolonging battery life is highly desirable [27].

15 It is generally true that the higher the abstraction level at
 16 which power consumption is estimated, then the easier it is to
 17 correlate algorithmic changes to power changes and the more
 18 questions can be answered analytically. However, the estimates
 19 are then less accurate in absolute terms. Conversely, at a lower
 20 abstraction level, the power model is more accurate, but is
 21 much harder to correlate to algorithmic changes, especially if
 22 it is tied to a particular target processor.

23 In this section, we provide a way to compute an *upper bound*
 24 on the energy consumed by a QRE per data item. The per-item

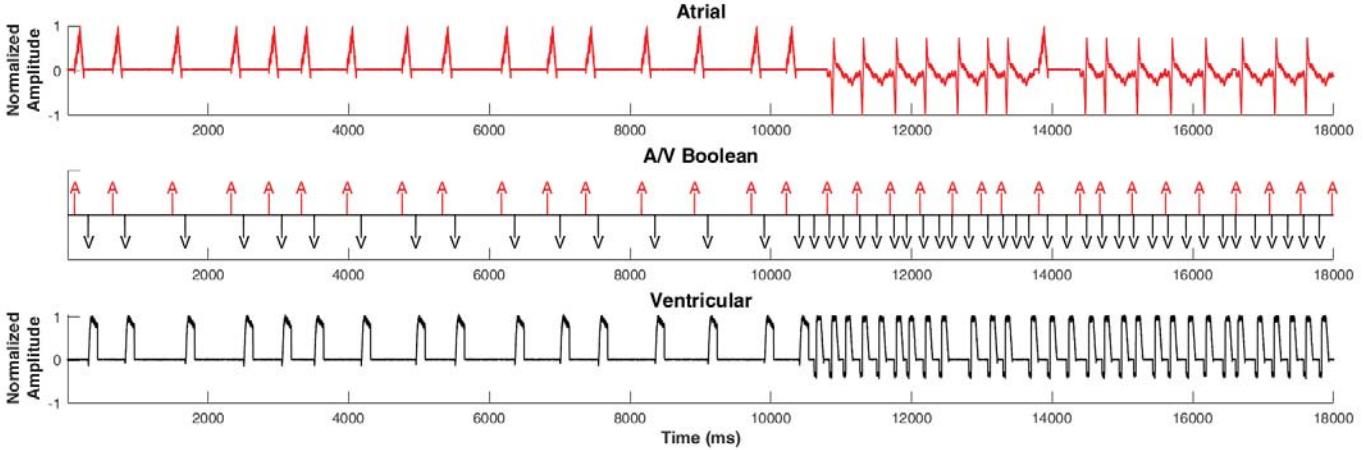


Fig. 11: EGM during a VF. Top panel shows the atrial EGM. Bottom panel shows the ventricular EGM. The middle panel shows the sensed boolean signal that is part of the input stream s to the AMA. Spikes above the x-axis indicate atrial beats, and spikes below it are the ventricular beats.

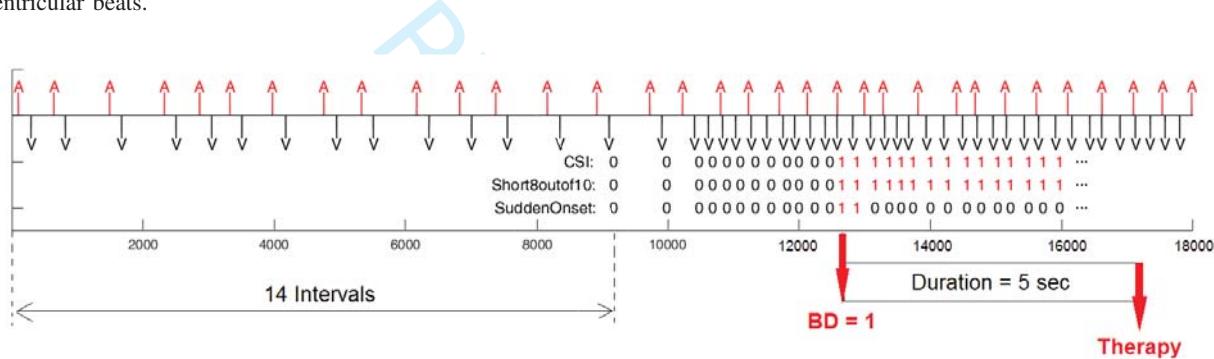


Fig. 12: Boolean beat stream from Fig. 11 and the streaming output of QRE stage2 (which calculates CSI, Short8outof10 and SuddenOnset).

consumption is the appropriate unit of measurement since a stream can be arbitrarily long. Being an upper bound, it allows the algorithm developers to compare design options very early on based on worst-case cost, and hardware engineers to provision battery capacity and electronics that are suitable for the expected worst-case energy draw. The upper bound is obtained by first measuring the per-item energy consumption of all the predicates and *ops* that appear in the QRE. These will be referred to as the *basic costs*. Then the QRE evaluator itself is used to combine these basic costs into the worst-case cost of the query. It is possible to do this for programs written in the StreamQRE language because of the well-understood syntactical restrictions it imposes, in particular, the restriction that computation results cannot be used in predicates. Note that these analyses apply trivially to any other additive cost, such as processing time, and not just power.

The upper-bound energy analysis described in the previous paragraph is meant to provide only a crude estimate of energy consumption for early design space exploration. It is not meant to replace a more fine-grained analysis (such as a WCET analysis) that takes the hardware and the input data into account. Such a high-precision analysis is useful for finetuning the performance of a production implementation, but a more rough analysis is still useful in the early design stage.

A. An upper bound based on the evaluator

We first need to understand roughly how the QRE evaluator works. The evaluator is the algorithm that evaluates a QRE on a given stream. For a query q , the evaluator first invokes a query-specific *start* routine to initialize the internal data structures appropriately. With every new data item that arrives, the evaluator invokes a query-specific *next* routine to process it. Moreover, *next* might have to pass the item to sub-queries: e.g., *split(f, g)* will pass the item to g everytime the string seen so far matches f . In such a case, *next* will need to invoke the *start* method of g . *Therefore, the cost of processing a data item is the cost of calling the QRE's next routine.*

1) *From basic cost to QRE cost:* Let $cost(\varphi)$ and $cost(op)$ be the cost of evaluating the predicate φ and operation op respectively. It is assumed that these costs are data-independent, which is true for the queries that appear in AMA. Let *start(q)* and *next(q)* be functions that return the cost of executing *start* and *next* methods of query q . The per-item cost of a QRE q can be upper-bounded using the following recursion on its structure.

$q = \text{atom}(\varphi, op) :$
 $start(q) = 0$
 $next(q) = cost(\varphi) + cost(op)$

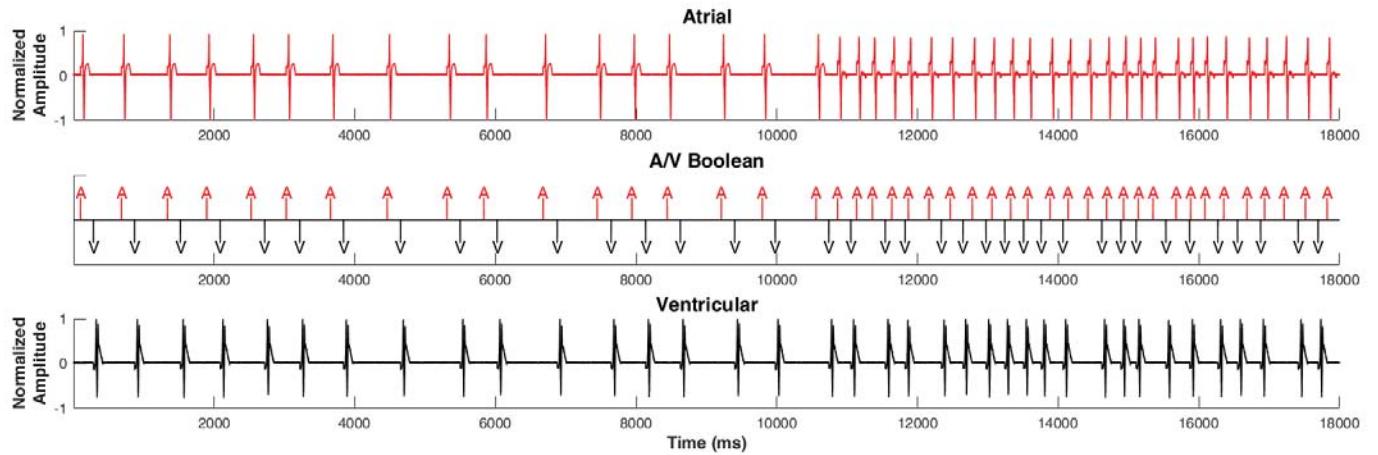


Fig. 13: Atrial Fibrillation (AF) EGMs and their boolean beat streams.

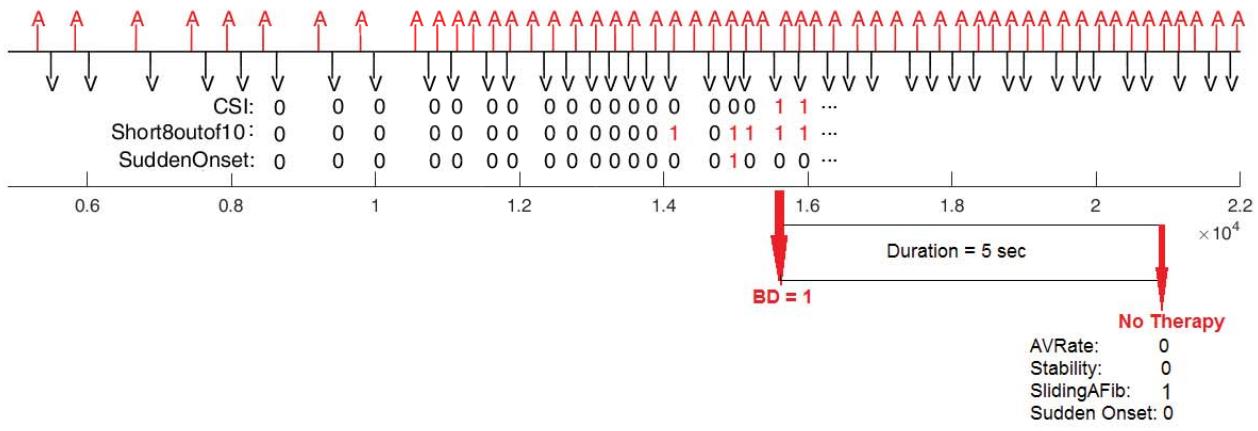


Fig. 14: Boolean beat stream from Fig. 13 and the streaming output of QRE stage2.

$q = \text{split}(f, g, op) :$

$$\begin{aligned} start(q) &= start(f) + start(g) + cost(op) \\ next(q) &= next(f) + next(g) + start(g) + cost(op) \end{aligned}$$

$q = \text{iter}(f, init, op, out) :$

$$\begin{aligned} start(q) &= start(f) + cost(out) \\ next(q) &= next(f) + cost(op) + start(f) + cost(out) \end{aligned}$$

$q = \text{iterLast}(f) :$

$$\begin{aligned} start(q) &= start(f) \\ next(q) &= next(f) + start(f) \end{aligned}$$

$q = \text{iterUntil}(\varphi, \psi, init, op) :$

$$\begin{aligned} start(q) &= 0 \\ next(q) &= cost(\varphi) + cost(\psi) + cost(op) \end{aligned}$$

$q = \text{wnd}(f, size, init, ins, rmv, out) :$

$$\begin{aligned} start(q) &= start(f) \\ next(q) &= next(f) + cost(ins) + cost(rmv) + \\ &\quad cost(out) + start(f) \end{aligned}$$

$q = \text{annt}(f, op_1, op_2) :$

$$\begin{aligned}
 \text{start}(\text{q}) &= \text{start}(\text{f}) \\
 \text{next}(\text{q}) &= \text{next}(\text{f}) + \max(\text{cost}(\text{op}_1), \text{cost}(\text{op}_2)) \\
 \text{q} = \text{f} \gg \text{g} : \\
 \text{start}(\text{q}) &= \text{start}(\text{f}) + \text{start}(\text{g}) + \text{next}(\text{g}) \\
 \text{next}(\text{q}) &= \text{next}(\text{f}) + \text{next}(\text{g})
 \end{aligned}$$

To understand this recursion, consider the case $q = \text{atom}(\varphi, op)$. Starting the evaluator doesn't cost anything in this case. When the data item arrives and it matches φ , then op is executed and we pay $\text{cost}(\varphi) + \text{cost}(op)$. Otherwise, we only pay $\text{cost}(\varphi)$. Thus an upper-bound on cost is $\text{cost}(\varphi) + \text{cost}(op)$, as indicated.

For a more involved example, consider the case $q = \text{split}(f, g, op)$. Starting q involves starting f and g , and we pay the corresponding costs. If both of them match the empty string, then we also pay $\text{cost}(op)$. So worst-case cost of start is as shown. When a data item arrives, it is passed to both f and g : f might match the string in multiple positions, and it is not possible to know ahead of time which will be the right split point, so the string is always fed to f , and we pay $\text{next}(f)$. If the string seen so far matches f then the

item is also passed to g to see if the string suffix will match it, and we pay $start(g)$. g might also be in the middle of matching a previous suffix (remember the evaluator maintains all possible matches). In that case, it will also process the new item using its $next$ routine, and we pay $next(g)$. Finally, if both f and g match, then $op([f]w, [g]w)$ is evaluated and we pay $cost(op)$. Thus in the worst-case, the cost of $next(q)$ is $next(f) + next(g) + start(g) + cost(op)$, as shown.

2) *Measuring the basic costs:* To start the above recursion, we need knowledge of $cost(\varphi)$ and $cost(op)$. For example, consider query $stage3$ defined in Section VI-E and its associated costs:

```
stage3 = wnd(atom(), N, 0, ins, rmv, discr)

start(stage3) = start(atom()) = 0
next(stage3) = next(atom()) + cost(ins) + cost(rmv)
               + cost(discr) + start(atom())
               = cost(x -> True) + cost(x -> x)
               + cost(ins) + cost(rmv) + cost(discr)
```

Therefore, it is necessary to measure the following:

$$\begin{aligned} C_1 &= cost(x -> True) \\ C_2 &= cost(x -> x) \\ C_3 &= cost(ins) + cost(rmv) + cost(discr) \end{aligned}$$

The costs of predicates and ops can be measured using jRAPL [39] for example. jRAPL provides a mean to measure the energy consumption of any snippet of Java code by enclosing it between `getEnergyStats` function calls. The `getEnergyStats` function accesses Machine-Specific Registers (MSRs) that store the energy consumed since a pre-defined datum. Thus we can measure the energy consumed by a given piece of code by comparing the register contents before and after invoking that code, e.g. as shown below:

```
EnergyCheckUtils ec = new
    EnergyCheckUtils();
double[] before = ec.getEnergyStats();
long duration =
    Queries.execute(streamlength, stream,
    myquery); //nano-sec
double[] after = ec.getEnergyStats();
double[] energy = after - before;
System.out.println("Consumed energy =
    + energy);
```

Internally, jRAPL is a Java wrapper around the RAPL library. RAPL (Running Average Power Limit) is a suite of low-level interfaces to the MSRs with the ability to monitor and control energy and power consumption of different hardware levels, and is widely supported in Intel architectures. RAPL allows energy/power consumption to be reported separately from the CPU core, package (L3 cache, on-chip GPUs, and interconnects), and DRAM.

For the example of $stage3$, Table II shows the energy values C_1 and C_2 reported by jRAPL. These operations

TABLE II: jRAPL-reported values for basic costs (Obtained by averaging over 20M execution of the operation (= 1 experiment), and over 125 experiments after a 25-experiment warm up).

Measurements:	Basic operation	
	$x -> True$	$x -> x$
DRAM [J·e-5]	0.000003244	0.00004134
CPU [J·e-5]	0.0000045418	0.0001023086
Package [J·e-5]	0.00001155	0.0002180939
Total [J·e-5]	0.000019336	0.000361745

TABLE III: jRAPL-reported energy values for $C_3 = cost(ins) + cost(rmv) + cost(discr)$, for three versions of AMA. Obtained as average of 100 experiments after a 25-experiment warm-up, each experiment having 1M runs.

Measurements:	Baseline	No Onset	Duration = 1s
DRAM [J·e-5]	0.55755	0.54573	0.182398
CPU [J·e-5]	0.549273	0.502224	0.23123
Package [J·e-5]	2.2693036	2.21987	0.726192
Total [J·e-5]	3.376137	3.267839	1.13983

are extremely cheap and their measurement can be non-deterministically affected by irrelevant processes running on the hardware (like page swaps), compiler optimizations (like discarding of unused outputs, which is why in the code listing above we print out `duration`). Therefore, and to account for this variability, we compute cost by running the same operation 20M times and averaging the energy over the runs. We call this an experiment. We run 125 such experiments in a row, and discard the first 25 experiments to take into account background noise caused by the warm up, and average the last 100 experiments. The final reported number is then the energy per predicate or op .

REMARK. As noted, measuring the cost of simple basic operations is affected by irrelevant sources of energy consumption. When the objective is to compare algorithms, it is reasonable to assume unit costs for the cheap basic operations, and proportionally larger cost to more complex operations, and compare the QREs on the basis of this cost model. The results, of course, are as good as our guess of the relative magnitudes of the various basic costs.

Table III shows the energy value C_3 , when running as part of the three versions of AMA described in section VII-B: the Baseline algorithm, version with no Sudden Onset discriminant, and version with a Duration of 1sec. The energy consumption of $discr$ depends on which algorithm it is running in because, for example, a shorter Duration implies that $discr$ is operating on fewer items, while no Onset means that the value of Sudden Onset is not used in the decision making of $discr$.

Equipped with these numbers we can upper-bound the per-item energy consumption of $stage3$ by $C_1 + C_2 + C_3$. On this basis, the Duration=1sec version is the cheapest in the worst-case, and Baseline is the most expensive. On the other hand, No Onset has a per-item cost which is only slightly smaller than that of Baseline. This can be explained by the fact that Baseline only performs one extra AND relative to No Onset, which is a cheap operation (and even that is sometimes not executed, depending on the ordering of arguments). The fact

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TABLE IV: Database-averaged jRAPL-reported energy for three version of entire algorithm. Obtained as average of 40 experiments after a warm-up of 10 experiments, each experiment having 1 run.

Measurements:	Algorithm		
	Baseline	No Onset	Duration = 1s
DRAM [J·e ⁻⁵]	1.7177	1.5836	1.1813
CPU [J·e ⁻⁵]	2.7648	2.0992	1.6067
Package [J·e ⁻⁵]	6.7009	5.9251	4.4322
Total [J·e ⁻⁵]	11.1834	9.6078	7.2203

that disabling Onset does not yield meaningful energy savings suggests that for patients that might benefit from Sudden Onset discrimination (like patients who have low frequency of SVTs), it can be enabled without any loss in device longevity.

B. Measured Energy Consumption of Entire Algorithm

In addition to the upper bounds, it is of course possible to measure the cost of a QRE on a typical workload, e.g., when processing the signals in the EGM database. The three versions of AMA and the signals database were described in Section VII. The energy is measured again using jRAPL. Because the AMA is a sufficiently costly operation and its energy measurements will not vary significantly between repeated runs, each experiment consists of a single run of the QRE on the database of signals. We still run and discard some initial experiments as warm-up.

Table IV reports the per-item energy consumption, averaged over the signals in the database. The energy numbers match expectations: the baseline version consumes the most energy. Version No Onset is second most expensive, because eliminating Sudden Onset reduces the costs of Stage 2 (which computes the Onset decision SO – see Fig. 10 and QRE stage2), and Stage 3 (which uses the SO value in an AND statement). Finally, Shortening Duration saves the most energy, since it implies shorter computations for 4 discriminators (Fig. 10).

IX. RELATED WORK

Medical device algorithms. Most of the literature on formal methods for medical device algorithms focuses on verifying and testing the functionality of the algorithm - see [40], [41], [42], [43] for examples in the specific context of implantable cardiac devices. These concerns are orthogonal to ours: the focus of this paper is the description of a *programming language* that is suitable for arrhythmia monitoring, and the *meta-functional* characteristics it automatically guarantees. It is worth nothing that the U.S. Food and Drug Administration (FDA), which regulates medical devices in the U.S.A., does not mandate particular types of validation, such as model checking [44]. Rather, it describes in generic terms the kind of evidence that should be provided. For example, it stipulates that “Software quality assurance needs to focus on preventing the introduction of defects into the software development process”, and that “software developers should use a mixture of methods and techniques to prevent software errors and to detect software errors that do occur.” [44, Section 4.2].

The FDA Guidance does not explicitly address meta-functional properties. Works in quantitative verification, such as [45] and [46], model the heart and pacemaker to verify statistically or through simulations whether some quantitative properties are satisfied. This contrasts with our approach which is model-free, and provides cost upper bounds based on the QRE code itself, not a model of it. An application of QREs to arrhythmia monitoring appeared in [26] where a peak detector is coded in an early variant of the language.

QREs are a Domain-Specific Language (DSL): they are meant for programming queries on arbitrary data streams, with strong theoretical foundations [5] and a flexible programming environment [6], [18]. DSLs have been developed for medical device development, albeit these are usually meant for the creation of the entire device, including hardware, and focus on capturing object-oriented aspects of the domain (i.e., identifying the main objects in the domain and modeling them and their relations). E.g., [47] develops a graphical language for modeling blood separator machines, along with code generators and lock-step simulators of the model and its generated code. No work has appeared in the literature on a DSL for ICDs or ILR algorithms, and more generally, rhythm monitoring algorithms.

Streaming languages. There is a large body of work on streaming database languages and systems such as Aurora [48], Borealis [49], STREAM [50], and StreamInsight [51], [52]. The query language supported by these systems (for example, CQL [53]) is typically a version of SQL with additional constructs for splitting the stream into finite windows (e.g., tumbling or sliding windows, count-based or time-based). This allows for rich relational queries, including set-aggregations (e.g. sum, maximum, minimum, average, count) and joins over multiple data streams. Such SQL-based languages are, however, limited in their ability to express properties and computations that rely on the sequence of the events such as: sequence-based pattern-matching, and numerical computation based on list-iteration when the order of the data items is significant. There are streaming engines such as IBM’s Stream Processing Language (SPL) [54], [55], ReactiveX [56], Esper [57] and Flink [58], which support user-defined types and operations, and allow for both relational and stateful sequential computation. However, none of these engines provides support for decomposing the stream in a regular fashion and performing incremental computations that reflect the structure of the parse tree, which is a central feature of the QRE language. LOLA [59] allows arbitrary computations on streams and incremental computation of statistics, but does not support regular decomposition of the stream to define the computation domains. Finally, Timed Regular Expressions [60] allow the specification of time windows during which the timed string must match a regular expression. As such they are a specification language rather than a programming language and do not support the rich computations and quantitative combinators that QREs support.

Power estimation. Since QREs are aimed at high-level programming and the cost analysis is aimed at early design exploration, we don’t review the vast literature on low-level power estimation techniques (anything below C program

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level), nor do we review analyses that focus on the impact of particular hardware choices like [61]. Such analyses occur later in the design cycle and require the availability of low-level artifacts like circuits. The interested reader can consult [62] for a recent review of such techniques.

In [63],[64] and [62], a *functional level power model* is used for estimating the power consumption of a C program without compiling it. It requires partitioning the target processor into functional units, and estimating some key parameters like the cache miss rate, external data memory access rate and the processing rate. It also depends on the user providing low-level execution details like the data mapping. This target-specific code-level analysis complements our presented bounds, which occur earlier in the design cycle and are at the algorithm level.

The approach in [65] estimates battery dissipation. It treats the processor as a black box and instead decomposes *the program* into types of basic instructions, similar to what we did to obtain the upper bounds in Section VIII. However, the basic instructions in [65] are at the instruction-set level, like integer and floating point loads and stores. And while we exploit the fact that we have a uniform evaluation algorithm for any QRE to infer bounds on the entire program's cost, the authors in [65] must establish empirically, for a given processor and program, that the program's cost is the weighted sum of the dissipations for basic instructions.

A static analysis of energy consumption of XC programs is presented in [66].⁴ After building an ISA-level power model using hardware measurements of a test suite, the XC program is translated to Horn clauses in the Ciao programming language [67]. The Ciao pre-processor can then bound the power consumption as a function of input data sizes. This technique was later extended to use a power model at the level of the compiler's intermediate representation rather than the ISA level [68]. This approach applies to programs that can be translated into a logic program. Another static analysis technique [69] uses integer linear programming to compute the worst case energy consumption, given estimates of dynamic and leakage power contributions of basic blocks in a program's control flow graph. This is inspired by well-known Worst-Case Execution Time estimation techniques.

X. CONCLUSION

This paper has argued that arrhythmia monitoring algorithms are best viewed as streaming algorithms, and that they are best programmed in the StreamQRE language. Unlike traditional streaming applications where throughput is a prime concern, here energy consumption is the primary design factor. A program written in StreamQRE automatically gets a baseline implementation with a constant memory, processing time and energy consumption per item. Moreover, the QRE evaluator automatically provides upper bounds on the per-item cost of the query, which can be used early in the design cycle to guide the choice of algorithm, and to decide whether some discriminators are worth having at all. We showed how the StreamQRE Java Library can be used to program and evaluate a query and to obtain cost upper bounds, and how these bounds correlate

⁴XC is a high-level C-based programming language.

to actual power measurements. We believe this approach to exploring and programming arrhythmia monitors, and other medical device algorithms, has the potential to greatly alleviate the device development burden. In particular, it opens the possibility of designing ILR algorithms that collect statistics over longer time durations than is currently done. Other applications that might benefit from StreamQRE include glucose monitoring [70], [71], where a mobile device periodically or continuously measures a diabetic's blood glucose and performs various filtering operations to predict hypo- or hyperglycemic episodes.

The theoretical basis of StreamQRE raises the possibility of performing static (formal) analysis of its performance. It is already possible, for queries written in a subset of the language, to answer questions such as "Does the worst-case peak power consumed by the algorithm exceed some threshold?", "Could the long-term average power consumed by the algorithm exceed some threshold?", and "Does algorithm A consume less peak/average power than algorithm B?". Answers to these questions impact the choice of electronics that must withstand the peak power draw, and the capacity of the device battery.

On the tools side, two projects are worth exploring: first, implementing the decision procedures that perform the above-described static analysis. Second, creating a compiler that compiles a QRE into C or assembly code targeting a given hardware platform. This would complete the path from algorithm to code to implementation, and would allow a reliable comparison of upper-bounds to actual energy consumption of the compiled code. In niche areas, expert coders might be able to squeeze more performance per Watt from hand-written code than a compiler could from automatically generated code. However, it is to be expected in the long run that medical devices will follow the arc of semiconductors, where automation has gradually out-performed humans, or has yielded such productivity gains that small performance losses are more than made up for by the reduced time-to-market, reproducibility and scalability of the design process, and automatic guarantees of correctness and performance.

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