A ROBUST SEQUENTIAL DETECTION ALGORITHM FOR CARDIAC ARRHYTHMIA CLASSIFICATION

Peter M. Clarkson, Szi-Wen Chen and Qi Fan

Biomedical Engineering Center
The Ohio State University
Columbus, OH 43210, USA

ABSTRACT

We describe a modified *sequential probability ratio test* (SPRT) for the discrimination of ventricular fibrillation (VF) from ventricular tachycardia (VT) in measured surface electrocardiograms. The algorithm uses a novel regularity measure dubbed *blanking variability* (BV) applied to threshold crossings from the measured ECG. Blanking variability corresponds to the normalized rate of change of cardiac rate as the blanking interval is varied. The algorithm has been trained and tested using separate subsets drawn from the MIT-BIH malignant arrhythmia database. BV values are modeled using a truncated Gaussian distribution, and parameter values are derived by averaging over the training component of the database. In testing, the algorithm achieved an overall classification accuracy of 95%.

1. INTRODUCTION

Ventricular fibrillation (VF) and ventricular tachycardia (VT) are life-threatening cardiac arrhythmias [1, 2]. Reduction of mortality from such cardiac causes depends on rapid detection and accurate classification of these arrhythmias. Conventional algorithms used in both surface ECG monitors and in implantable cardiovertor/defibrillators rely on simple heart rate for detection–classification. While both VF and VT have significantly higher rates than normal sinus rhythm, the rate range of VF overlaps with that of VT [3]. Thakor *et al.* [4, 5] described a *sequential probability ratio test* (SPRT) based on the *threshold crossing interval* (TCI), which is equivalent to the reciprocal of rate, for the discrimination of VF and VT. Using the malignant ventricular arrhythmias of the MIT-BIH database, we found that the TCI distributions of VF and VT overlap significantly (see Figure 1(a)), which leads to a significant error rate in the detection algorithm (see Section 3).

This work was supported by the National Science Foundation under grant number MIP-9220769.

We approach this problem by utilizing a novel feature dubbed *blanking variability* (BV) designed to provide greater separation between the feature distributions for VF and VT. BV provides a measure of the variability of heart rate with respect to the so-called "blanking interval" – the interval over which the heart is considered refractory. After computing BVs from sampled ECG data from a wide range of recorded arrhythmias, we construct probability density functions of BV for VF and VT using a *truncated* Gaussian model. Observed BV values are then subjected to an SPRT that is modified to account for the truncated Gaussian parameters.

2. DETECTION ALGORITHM

2.1. Rate Computation

In the first stage of the classifier, the instantaneous rate is derived from the interval between successive depolarizations. Threshold crossings are measured by setting a threshold equal to 20% of the peak amplitude of the ECG signal for each 1-second segment from the record, and then computing the locations of successive threshold crossings. To avoid multiple counts for a single depolarization, a *blanking interval* is set. This is a time interval following each depolarization during which further threshold crossings are ignored. This corresponds physiologically to the period following a depolarization when the heart is *refractory*, i.e., when it cannot be depolarized. Blanking intervals on the order of 50–100 ms are typical in heart rate estimation algorithms.

The product of the threshold crossing analysis is a series of *threshold crossing intervals* (TCI),[1] $\{T_i\}_{i=1}^{M}$ (measured in milliseconds). The corresponding heart

[1]The TCIs discussed here are "instantaneous", as distinct from the averaged TCIs employed by Thakor *et al.* [4, 5]. In their definition, TCIs are averaged over successive 1-second intervals.

0-7803-2431-5/95 $4.00 © 1995 IEEE

rate, $\{R_i\}_{i=1}^{M}$, can then be found simply from

$$R_i = \frac{60000}{T_i} \text{ (beats/min)}, \; i = 1, 2, \ldots, M. \quad (1)$$

2.2. Definition of Blanking Variability

The rate sequence R_i obtained from Eq. (1) depends on the choice of blanking interval. In particular, for "regular" rhythms, varying the blanking interval over the range 50–100 ms typically changes the rate only slightly. By contrast, for "irregular" rhythms, a similar variation of blanking interval can produce a very significant change in the rate. Since VT is known to be significantly more regular than VF, a measure based on blanking interval variability has the potential to give good separation of the two arrhythmias. We propose a new measure, dubbed *blanking variability* (BV), which uses the heart rate sequences obtained with three different blanking intervals, 60 ms, 80 ms, and 100 ms, respectively, and is defined as

$$BV = \frac{|\mu^{(60)} - \mu^{(80)}|}{\mu^{(80)}} + \frac{|\mu^{(80)} - \mu^{(100)}|}{\mu^{(100)}}, \quad (2)$$

where $\mu^{(60)}, \mu^{(80)}$, and $\mu^{(100)}$ represent the mean values of heart rate obtained using blanking intervals of 60, 80 and 100 ms, respectively. Each rate sequence is processed in blocks or windows of length 30. First, we apply an N-point median filter to the raw rate sequence. This removes outliers from the raw data which can significantly improve the quality of the resulting rate estimates [6]. After median filtering, the BV is computed from the three 30-sample subsequences by using Eq. (2). Then, the processing window is shifted by one sample and the BV is recomputed. After 9 successive shifts, we obtain 10 values of BV for a given ECG segment.

2.3. Modeling the Probability Density Function of Blanking Variability

Using the MIT-BIH malignant arrhythmia database, histograms of the BV values corresponding to VF and VT have been obtained. Here, we have adopted a *truncated Gaussian PDF* to model the distributions rather than the traditional Gaussian PDF. This is appropriate because from the definition of Eq. (2), BV is always *non-negative* and thus the probability of BV < 0 is zero. The truncated Gaussian PDF can be written as

$$P(x) = \frac{K}{\sqrt{2\pi\sigma^2}} e^{-\frac{(x-\mu)^2}{2\sigma^2}}, \qquad 0 \le x < \infty, \quad (3)$$

where μ and σ paramerize the distribution and K is the unit area constraint

$$K = \frac{2}{1 + \text{erf}(\frac{\mu}{\sqrt{2}\sigma})}, \quad (4)$$

where erf(x) represents the *error function.*

Eq. (3) is convenient for implementation of the SPRT. However, μ and σ are *distinct* from the distribution mean, μ_D, and standard deviation, σ_D. The relation between μ and μ_D is expressed by

$$\begin{aligned} \mu_D &= E\{X\} = \int_0^\infty \frac{Kx}{\sqrt{2\pi\sigma^2}} e^{-\frac{(x-\mu)^2}{2\sigma^2}} dx \\ &= K[\frac{\sigma}{\sqrt{2\pi}} e^{-\frac{\mu^2}{2\sigma^2}} + \frac{\mu}{2}(1 + \text{erf}(\frac{\mu}{\sqrt{2}\sigma}))]. \end{aligned} \quad (5)$$

Similarly,

$$\begin{aligned} \sigma_D^2 &= K[\frac{\mu\sigma}{\sqrt{2\pi}} e^{-\frac{\mu^2}{2\sigma^2}} + \\ &\quad \frac{(\mu^2 + \sigma^2)}{2}(1 + \text{erf}(\frac{\mu}{\sqrt{2}\sigma}))] - \mu_D^2. \end{aligned} \quad (6)$$

Substituting Eq. (4) into Eqs. (5) and (6), respectively, we have

$$\mu_D = \frac{\sqrt{2}\sigma}{\sqrt{\pi}(1 + \text{erf}(\frac{\mu}{\sqrt{2}\sigma}))} e^{-\frac{\mu^2}{2\sigma^2}} + \mu, \quad (7)$$

and

$$\sigma_D^2 + \mu_D^2 = \frac{\sqrt{2}\mu\sigma}{\sqrt{\pi}(1 + \text{erf}(\frac{\mu}{\sqrt{2}\sigma}))} e^{-\frac{\mu^2}{2\sigma^2}} + \mu^2 + \sigma^2. \quad (8)$$

Estimates of μ_D and σ_D can be computed from the BV samples and we can then obtain estimates of μ and σ by jointly using Eqs. (7) and (8).[2] After finding μ and σ, we compute the constraint constant K using Eq. (4). The modeled densities are shown in Figure 1(b). While there is some overlap between the distributions for VF and VT, this is much less than in the corresponding TCI plot of Figure 1(a).

2.4. SPRT Implementation

After obtaining the values of BV, we compute the mean and standard deviation over the database for VF and VT, respectively. Values of μ, σ and K for VF and VT are then computed as described above. The calculated values are given in Table 2. Discrimination of observed rhythms is performed via the SPRT algorithm [7, 8].

Using a median length $N = 9$, we seek to discriminate the hypotheses (see Table 2):

[2] Here, we solve for μ and σ using geometric approximation. The solution is identical to the intersection of these two equations in the μ-σ plane. Error limits of 0.01% were used for the iteration.

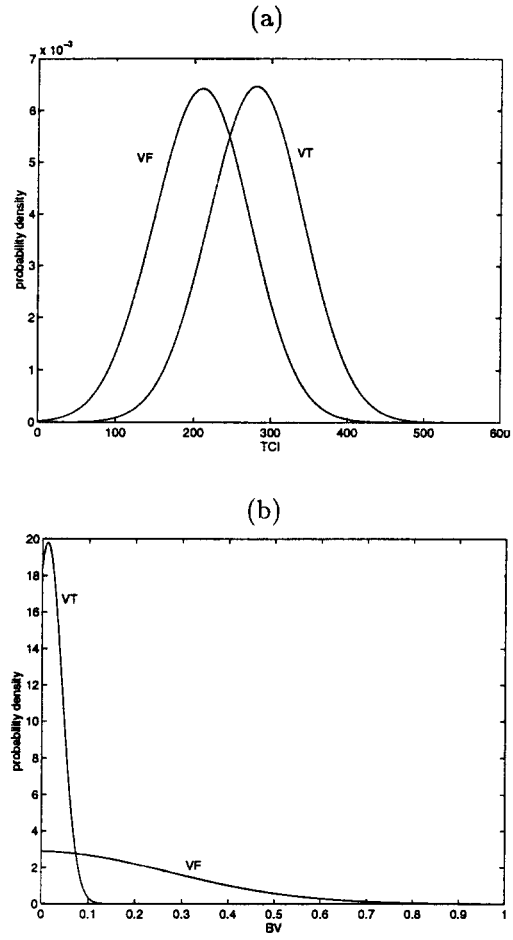

Figure 1: Approximated probability density functions for TCI and BV. (a): TCI distributions for VF and VT groups; (b): BV distributions for VF and VT groups.

H_{VF}: $\mu_{VF} = -0.0145$, $\sigma_{VF} = 0.2875$ ($K_{VF} = 2.0838$);
H_{VT}: $\mu_{VT} = 0.0118$, $\sigma_{VT} = 0.0311$ ($K_{VT} = 1.5437$).

We construct a *likelihood ratio test* (LRT) Λ, and select two thresholds, T_1 and T_2, as

$$\Lambda(BV_1, \ldots, BV_k) = \frac{f(BV_1, \ldots, BV_k \mid \text{VF})}{f(BV_1, \ldots, BV_k \mid \text{VT})}, \qquad (9)$$

and

$$T_1 = \frac{1-\beta}{\alpha}, \quad T_2 = \frac{\beta}{1-\alpha}, \quad (T_1 > T_2 > 0), \qquad (10)$$

where f is the conditional probability density function under the hypothesis H_{VF} or H_{VT}; α is the probability of rejecting H_{VT} when it is true and β is the probability of rejecting H_{VF} when it is true. Comparing the LRT Λ with the two thresholds T_1 and T_2, if $\Lambda(BV_1) \geq T_1$ (or $\Lambda(BV_1) \leq T_2$), then the algorithm selects H_{VF} (or H_{VT}) and the test is terminated. If $T_2 < \Lambda(BV_1) < T_1$, then the test is inconclusive. In this case, $\Lambda(BV_1, BV_2)$ is calculated and compared with T_1 and T_2, and so on until a decision is reached.

The logarithmic form of Eq. (9) for a test comprising m data segments can be written as

$$\begin{aligned} ln(\Lambda_m) &= ln[\frac{f(BV_1, BV_2, \ldots, BV_k \mid \text{VF})}{f(BV_1, BV_2, \ldots, BV_k \mid \text{VT})}] \\ &= m\, ln(\frac{K_{VF}\sigma_{VT}}{K_{VT}\sigma_{VF}}) + \frac{1}{2\sigma_{VT}^2}\sum_{i=1}^{m}(BV_i - \mu_{VT})^2 - \\ &\quad \frac{1}{2\sigma_{VF}^2}\sum_{i=1}^{m}(BV_i - \mu_{VF})^2. \end{aligned} \qquad (11)$$

Comparing $ln(\Lambda_m)$ with $ln(T_1)$ and $ln(T_2)$, we can formulate the decision rule at the mth stage as follows. Let

$$\begin{aligned} g(BV_1, \ldots, BV_m) &= \frac{1}{\sigma_{VT}^2}\sum_{i=1}^{m}(BV_i - \mu_{VT})^2 - \\ &\quad \frac{1}{\sigma_{VF}^2}\sum_{i=1}^{m}(BV_i - \mu_{VF})^2, \end{aligned}$$

and

$$s_1 = 2m\, ln(\frac{K_{VT}\sigma_{VF}}{K_{VF}\sigma_{VT}}) + 2\, ln(\frac{1-\beta}{\alpha}),$$

$$s_2 = 2m\, ln(\frac{K_{VT}\sigma_{VF}}{K_{VF}\sigma_{VT}}) + 2\, ln(\frac{\beta}{1-\alpha}).$$

The decision rule is

$$\begin{aligned} g(BV_1, \ldots, BV_m) \quad \geq s_1, \quad &=> \quad H_{VF}; \\ \leq s_2, \quad &=> \quad H_{VT}; \\ \text{Otherwise} \quad &=> \quad \text{continue testing.} \end{aligned}$$

The test is repeated using each successive BV value, until a decision is reached.

3. RESULTS AND DISCUSSION

To test the proposed algorithm, we used a set of ECG data vectors of VF and VT obtained from the malignant arrhythmia subset of the MIT-BIH database. For convenience, the original data were divided into two groups corresponding to episodes of VF and VT containing 30 and 70 ECG data segments, respectively. Each segment comprises a 20-second recording. In order to remove baseline drift and high frequency noise, a band-pass filter (passband = [2 Hz, 20 Hz]) was applied.

Table 1: PDF parameter and SPRT classification results for the method of Thakor *et al.*

mean of TCI (ms)	$\mu_{VF} = 210.4695, \mu_{VT} = 280.4446$
STD of TCI (ms)	$\sigma_{VF} = 62.1029, \sigma_{VT} = 61.6941$
α, β	$1.38 \times 10^{-1} \sim 1.58 \times 10^{-1}$
specified VF	27/30=90%
specified VT	57/70≈81%
total correct	84/100=84%
no decision	0%

Table 2: PDF parameter and SPRT classification results for the proposed method

median filter length	$N = 9$
mean of BV	$\mu_D^{(VF)} = 0.2242, \mu_D^{(VT)} = 0.0118$
STD of BV	$\sigma_D^{(VF)} = 0.1707, \sigma_D^{(VT)} = 0.0311$
parameters for VF	$(\mu_{VF}, \sigma_{VF}, K_{VF})$ $= (-0.0145, 0.2875, 2.0838)$
parameters for VT	$(\mu_{VT}, \sigma_{VT}, K_{VT})$ $= (0.0118, 0.0311, 1.5437)$
α, β	$2.6 \times 10^{-3} \sim 4.5 \times 10^{-3}$
specified VF	28/30≈93%
specified VT	67/70≈96%
total correct	95/100=95%
no decision	0%

The classification results obtained using the algorithm of Thakor *et al.* [4, 5] are given in Table 1.[3] We see that the detection accuracy for VF is 90%, that for VT is 81%, giving an overall correct classification rate of 84%. While reasonably high, these results do not approach the 100% accuracy achieved by Thakor *et al.* with their database. We may speculate that the MIT-BIH database includes a broader range of ventricular tachycardias, including fast tachycardias with rates that overlap those of VF. We should also point out that Thakor's method employs the "averaged" TCI as a feature used for classification. We have observed that for the MIT-BIH database such an averaging process *reduces* the differences between the TCIs obtained from VF and VT groups, compared to the use of instantaneous TCIs.

For the proposed method, the classification results are given in Table 2. We observe that the overall classification accuracy increases to 95%. Obviously, the results obtained are significantly better than those obtained previously. Finally, we note that the results obtained were *not* critically dependent on the choices for α and β implying a degree of *robustness* in the performance of the algorithm.

[3] To calculate these TCIs, we used 1-second averaging as adopted in the original paper by Thakor *et al.*

4. REFERENCES

[1] M. E. Cain, B. D. Lindsay, R. M. Arthur, J. Markham, and H. D. Ambos, "Noninvasive detection of patients prone to life-threatening ventricular arrhythmias by frequency analysis of electrocardiographic signals," in *Cardiac Electrophysiology, from Cell to Beside,* pp. 817–831, 1990.

[2] M. E. Cain, H. D. Ambos, J. Markham, B. D. Lindsay, and R. M. Arthur, "Diagnostic implications of spectral and temporal analysis of the entire cardiac cycle in patients with ventricular tachycardia," *Circulation*, vol. 83, no. 5, pp. 1637–1648, May 1991.

[3] S. C. Vlay, "Clinical recognition of cardiac arrhythmias," in *Manual of Cardiac Arrhythmias*, S. C. Vlay (Ed), Little, Brown and Company, 1988.

[4] N. V. Thakor, Y.-S. Zhu, and K.-Y. Pan, "Ventricular tachycardia and fibrillation detection by a sequential hypothesis testing algorithm," *IEEE Trans. Biomedical Engineering*, vol. 37, no. 9, pp. 837–843, 1990.

[5] Y.-S. Zhu, and N. V. Thakor, "Ventricular fibrillation detection by sequential hypothesis testing," in *Proc. IEEE/9th Annu. Conf. Eng. Med. Biol. Soc.*, pp. 918–919, 1988.

[6] Q. Fan and P. M. Clarkson, "A robust adaptive estimator of rate for cardiac arrhythmia detection," in *Proc. IEEE ISCAS*, vol. 1, pp. 822-825, 1993.

[7] A. J. Wald, *Sequential Analyses*, Dove, New York, 1947.

[8] K. Fukunaga, *Introduction to Statistical Pattern Recognition*, Academic Press, New York, 1990.