IEEE Journal of Translational Engineering in Health and Medicine

Received 5 October 2023; revised 20 March 2024 and 21 April 2024; accepted 30 April 2024.
Date of publication 7 May 2024; date of current version 23 May 2024.

Digital Object Identifier 10.1109/JTEHM.2024.3397739

Detection of Non-Sustained Supraventricular Tachycardia in Atrial Fibrillation Screening

HESAM HALVAEI[1], TOVE HYGRELL[2], EMMA SVENNBERG[2], VALENTINA D.A. CORINO[3,4], LEIF SÖRNMO[1], (Life Fellow, IEEE), AND MARTIN STRIDH[1]

[1]Department of Biomedical Engineering, Lund University, 221 00 Lund, Sweden
[2]Department of Medicine, Karolinska Institutet, 171 77 Stockholm, Sweden
[3]Department of Electronics, Information and Bioengineering (DEIB), Politecnico di Milano, 20133 Milan, Italy
[4]CardioTech Laboratory, IRCCS Centro Cardiologico Monzino, 20138 Milan, Italy

CORRESPONDING AUTHOR: H. HALVAEI (hesam.halvaei@bme.lth.se)

This work was supported by European Union Horizon 2020 Research and Innovation Program through the Marie Sklodowska-Curie Grant under Agreement 766082 (MY-ATRIA).
This work involved human subjects or animals in its research. Approval of all ethical and experimental procedures and protocols was granted by the regional Ethics Committee of Stockholm under Application Nos. DNR 2015/2079-31 and 2020-01436, and performed in line with the Declaration of Helsinki.

ABSTRACT Objective: Non-sustained supraventricular tachycardia (nsSVT) is associated with a higher risk of developing atrial fibrillation (AF), and, therefore, detection of nsSVT can improve AF screening efficiency. However, the detection is challenged by the lower signal quality of ECGs recorded using handheld devices and the presence of ectopic beats which may mimic the rhythm characteristics of nsSVT. Methods: The present study introduces a new nsSVT detector for use in single-lead, 30-s ECGs, based on the assumption that beats in an nsSVT episode exhibits similar morphology, implying that episodes with beats of deviating morphology, either due to ectopic beats or noise/artifacts, are excluded. A support vector machine is used to classify successive 5-beat sequences in a sliding window with respect to similar morphology. Due to the lack of adequate training data, the classifier is trained using simulated ECGs with varying signal-to-noise ratio. In a subsequent step, a set of rhythm criteria is applied to similar beat sequences to ensure that episode duration and heart rate is acceptable. Results: The performance of the proposed detector is evaluated using the StrokeStop II database, resulting in sensitivity, specificity, and positive predictive value of 84.6%, 99.4%, and 18.5%, respectively. Conclusion: The results show that a significant reduction in expert review burden (factor of 6) can be achieved using the proposed detector. Clinical and Translational Impact: The reduction in the expert review burden shows that nsSVT detection in AF screening can be made considerably more efficiently.

INDEX TERMS Atrial fibrillation screening, signal quality, handheld ECG device, non-sustained supraventricular tachycardia.

I. INTRODUCTION

SCREENING for atrial fibrillation (AF) has received considerable attention, exemplified by the rapidly growing number of studies published in the recent years, see e.g., [1] and [2]. Screening provides an opportunity to identify patients with untreated AF and initiate anticoagulation therapy at an early stage. In a recent study [3], the screened population was found to be associated with fewer incidents (stroke and death) than the control group, i.e., patients not screened, thus emphasizing the importance of AF screening.

Previous studies have shown that subjects with excessive supraventricular arrhythmia are prone to develop AF [4], [5], [6], [7], [8], [9]. Detection of supraventricular arrhythmia has often been addressed by employing feature-based classification. The features are exemplified by RR intervals in successive short windows, wave amplitudes, wave durations, crosscorrelation to a template beat [10], [11], [12], [13], and spatial features derived from the vectorcardiogram [14]. Classification has been performed using random forests, support vector machines, linear discriminants, and neural networks [15].

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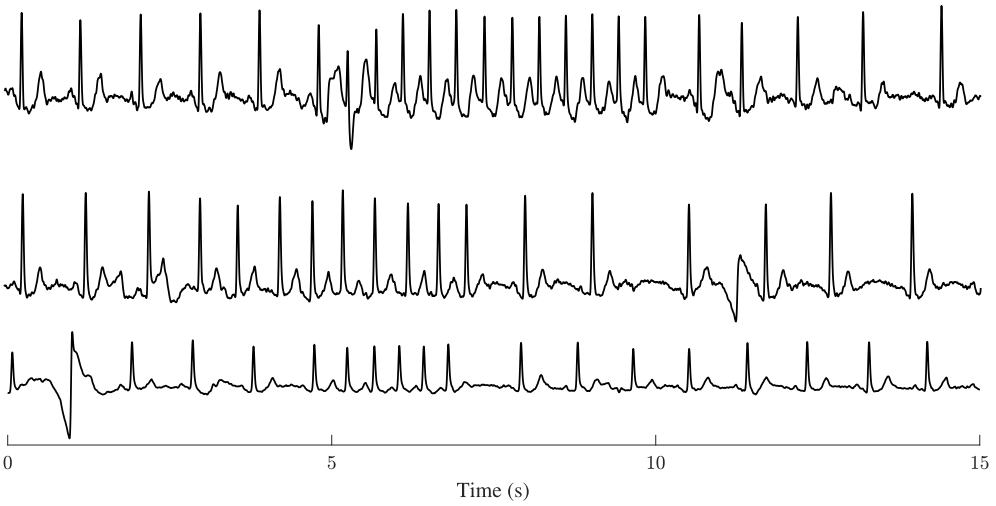

FIGURE 1. Excerpts from single-lead, 30-s screening ECGs with nonsustained supraventricular tachycardia (nsSVT), recorded using a handheld device. The nsSVT episodes, with a duration of 3 to 5 s, are surrounded by normal sinus rhythm and a few motion artifacts.

With the increasing interest in home-based AF screening using a handheld device, the prognostic implications of non-sustained supraventricular arrhythmia have gained attention. This type of arrhythmia includes frequent supraventricular beats (isolated or couplets), atrial bigeminy, and non-sustained supraventricular tachycardia (nsSVT), where nsSVT has attracted particular attention as it has been associated with a higher risk of future AF [16], [17] and stroke [4]. The presence of nsSVT can also serve as a marker of already existing but undetected AF.

The definition of nsSVT is somewhat ambiguous in the literature. The maximum duration of an episode is usually set to 30 s, see, e.g., [18], [19], [20], [21], and [22], whereas the minimum duration is usually defined by the number of beats, e.g., 4 beats [19], [22], 5 beats [21], 6 beats [23], or 10 beats [18]. Examples of nsSVT are displayed in Fig. 1.

Detection of nsSVT in ECGs recorded using a handheld device is prone to produce very large numbers of false positives. This is mainly due to falsely detected beats occurring in the presence of noise/artifacts and frequent ectopic beats [24], [25].

The present study proposes an nsSVT detector, representing a novel type of detector designed for use with single-lead, 30-s screening ECGs. The first step of the detector identifies beat sequences with similar morphology treated as candidates for nsSVT. The second step applies a set of rhythm criteria whose purpose is to sharpen the performance. The identification of similar beat sequences (SBSs) is based on machine learning, where the classifier is trained on a simulated ECG database and evaluated on two public ECG databases well-suited for SVT detection and signal quality assessment. The performance of the nsSVT detector is evaluated on a huge proprietary ECG screening database. The clinical studies [16], [17], reporting on the prognostic implications of nsSVT detection in ECG screening, serve as the translational incentive to pursue the detection problem.

The present paper is organized as follows. The databases are described in Sec. II and the nsSVT detector is described in Sec. III. Section IV presents the results, which are then subject to discussion in Sec. V.

II. DATABASES

A. SIMULATED ECG DATABASE

A simulated database (SIMDB) is generated using the simulator described in [26], containing ECGs in normal sinus rhythm or AF, varying P-wave morphology, and various types of noise. Synthetic components are used to generate simulated ECG signals, except for the noise which was taken from the MIT–BIH Noise Stress Test Database.

A total of 20,000 30-s ECGs were generated with the following two distinctly different noise levels: A set of 10,000 with a low noise level, uniformly distributed in the interval $[25, 75]$ μV, and another set of 10,000 with a high noise level, uniformly distributed in the interval $[250, 750]$ μV. In each set, 5,000 were generated in normal sinus rhythm and 5,000 in AF. The set with low noise level was used to compile episodes of detections with similar morphology, whereas the set with high noise level was used to compile episodes with one or several false detections. The upper limit of the low noise level set was chosen to 75 μV, since a higher noise level significantly influences beat morphology.

For each ECG in SIMDB, an episode containing five consecutive detections produced by a QRS detector was randomly selected. The locations of the detections were compared to the annotated beat locations provided by the simulator. If the difference between these two locations did not exceed 10 ms, the episode was annotated as an SBS. On the other hand, if the difference for at least one of the detections exceeded 75 ms, the episode was annotated as a non-SBS. All episodes with deviations between 10 and 75 ms were discarded as they did not contribute to establishing a relevant training dataset. This selection process resulted

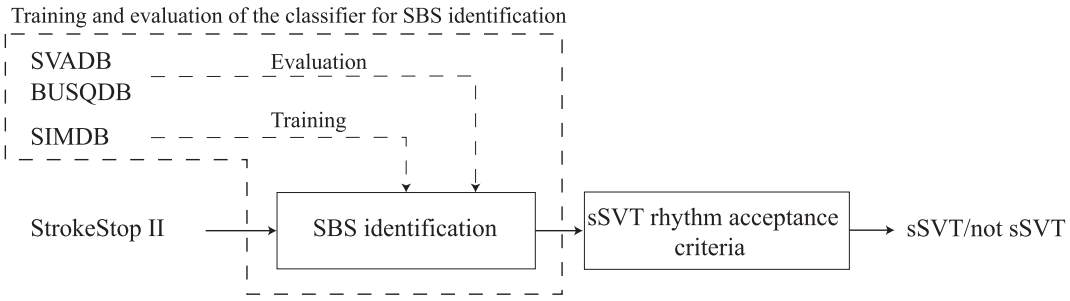

FIGURE 2. Structure of the proposed nsSVT detector, and usage of the databases for training and evaluation.

in 9,449 segments with SBSs and 6,868 segments with non-SBSs.

Since ventricular ectopic beats were not introduced in the simulator, such beats were imported from the MIT–BIH Supraventricular Arrhythmia Database (SVADB), see below, replacing one detection in 2,581 randomly selected SBSs in order to balance the simulated database. A segment with a ventricular ectopic beats was annotated as a non-SBS.

B. MIT-BIH SUPRAVENTRICULAR ARRHYTHMIA DATABASE

The SVADB contains 78 half-hour, two-lead ECG recordings, annotated on a beat-to-beat basis. Twenty-seven out of the 78 recordings[1] contain supraventricular tachycardia (SVT) of at least 5-beat length.

C. BRNO UNIVERSITY ECG SIGNAL QUALITY DATABASE

The Brno University ECG Signal Quality Database (BUSQDB) contains 18 single-lead, 24-h ECGs recorded during everyday activities, annotated with respect to three levels of signal quality, either allowing a complete wave analysis, QRS detection only, or no analysis at all. Three out of 18 signals were fully annotated in terms of signal quality, while the remaining 15 signals were annotated in two 20-min segments [27].

In the present study, segments annotated as 'no analysis' are used to evaluate the performance of SBS identification with regard to rejection of noisy segments.

D. StrokeStop II DATABASE

The StrokeStop II Database (SSIIDB) contains 186,697 30-s screening ECGs from 6,315 75- and 76-year old participants. The ECGs were recorded using the handheld Zenicor device (Zenicor Medical System AB, Sweden). Based on the N-terminal B-type natriuretic peptide level, participants went through either index screening or intermittent screening. Index screening involves only one single recording, while intermittent screening involves four recordings per day during two weeks. In total, 280 recordings were annotated as containing nsSVT.

Written informed consent was obtained from each patient before inclusion in the StrokeStop II Database. The study protocol conforms to the ethical guidelines of the 1975 Declaration of Helsinki and was approved by the regional ethics committee (DNR 2015/2079-31 and 2020-01436).

In the present study, SSIIDB is used to evaluate the performance of the nsSVT detector.

[1]Recording numbers: 801, 806, 807, 808, 809, 810, 812, 826, 840, 844, 846, 847, 849, 851, 854, 855, 856, 857, 859, 860, 862, 864, 865, 870, 885.

III. METHODS

The two-step structure of the proposed nsSVT detector is illustrated by the block diagram in Fig. 2. The first step is to find beat sequences with similar morphology, irrespective of prevailing rhythm and absolute beat morphology. This means that not only is nsSVT identified as an SBS, but so are normal sinus rhythm, sinus tachycardia, ventricular tachycardia, and AF. Rhythms excluded by the first step include isolated ventricular ectopic beats, ventricular bi- and trigeminy, and noise/artifacts.

The second step excludes SBSs whose rhythm does not fulfill certain criteria related to changes in heart rate relative to that of the surrounding rhythms and to RR interval irregularity, avoiding that atrial bigeminy, supraventricular beats (isolated and couplets), and interpolated atrial beats not accompanied by a compensatory pause, are identified as SBSs. Non-sustained sinus tachycardia, although relatively rare, will be identified as an SBS.

The ECG signals were preprocessed using a zero-phase, Butterworth bandpass filter with cut-off frequencies at 1 Hz and 40 Hz to suppress baseline wander and high-frequency noise. Since the ECGs of the above-mentioned databases were recorded with different sampling rates, all recordings were resampled to 1000 Hz. The built-in QRS detector of a commercial software (Cardiolund AB, Lund, Sweden) was used.

A. SIMILAR BEAT SEQUENCE IDENTIFICATION

Using a sliding window approach, SBSs are identified using information of the residuals, determined by subtracting a template beat from the other beats of the window. The W beats contained in the k:th sliding window form the columns of the matrix

$$\mathbf{X}_k = \left[\mathbf{x}_k \ \cdots \ \mathbf{x}_{k+W-1}\right],$$

where each column vector $\mathbf{x}_l$, $l = k, \ldots, k + W - 1$, contains N samples of a 300-ms interval centered around the

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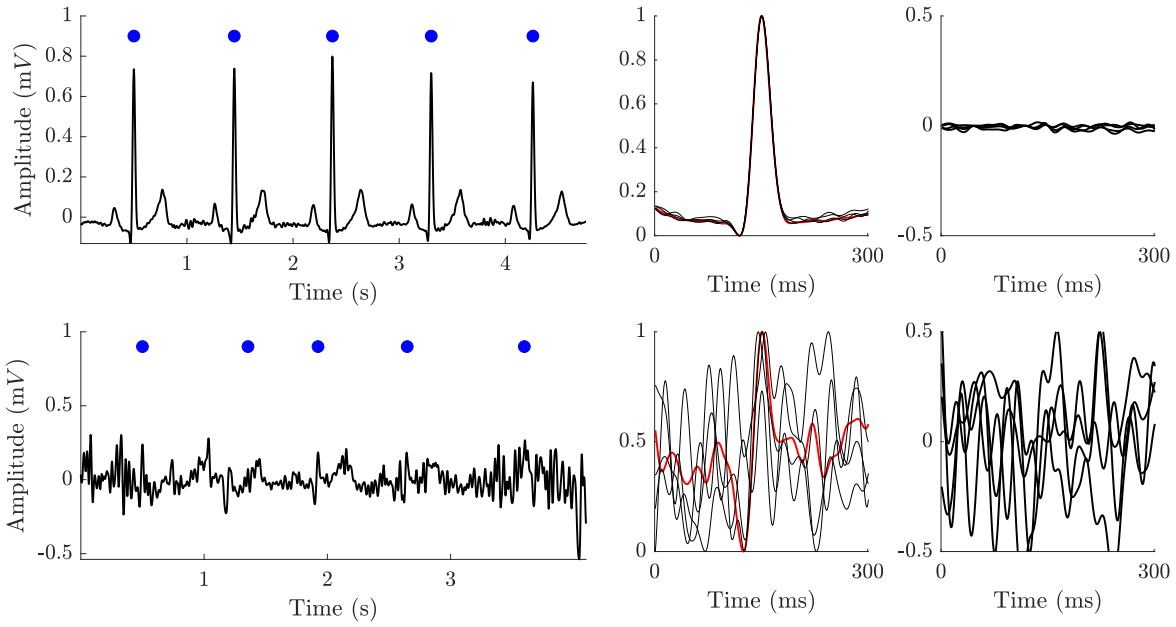

FIGURE 3. Illustration of an SBS (top) and a non-SBS (bottom). The left column shows two ECGs and the detected beats (blue dots). The middle column shows the superimposed beats and the template beat (in red) following min-max normalization. The right column shows the superimposed residuals obtained by subtracting the template beat from the detected beats.

l:th beat. Since the shortest possible nsSVT episode is here taken to be 5, the window length W is set to 5. To facilitate the analysis of different databases, $\mathbf{x}_l$ is subject to min–max normalization, resulting in the normalized matrix $\bar{\mathbf{X}}_k$ which is used to compute the residuals.

In each window, the template beat is taken as the beat yielding the lowest mean absolute value of the residuals when subtracted from each of the other $W-1$ beats in $\bar{\mathbf{X}}_k$, resulting in the matrix

$$\mathbf{E}_k = \left[\mathbf{e}_k \ \cdots \ \mathbf{e}_{k+W-2}\right],$$

where the columns contain the residuals related to the non-template beats. Clearly, the amplitude of the residuals in these vectors is close to 0 whenever the beats $\mathbf{x}_k, \ldots, \mathbf{x}_{k+W-1}$ exhibit similar morphology, and vice versa. Note that the order of columns of $\mathbf{E}_k$ may differ from that of $\mathbf{X}_k$. The normalized matrix $\bar{\mathbf{X}}_k$ and the residual matrix $\mathbf{E}_k$, obtained from an SBS and a non-SBS episode, are illustrated in Fig. 3.

Using $\mathbf{E}_k$, the following three statistical features are proposed as a first set: 1. the median absolute deviation of all elements of $\mathbf{E}_k$, 2. the difference between the 99:th percentile and the 1:st percentile of all elements of $\mathbf{E}_k$, and 3. the total number of outlier samples of $\mathbf{E}_k$ (defined below).

The number of outliers is typically much larger for beats with non-similar morphology than for beats with similar morphology, and, therefore, the total number of outliers is used as a feature. An outlier sample $e_{n,j}$ in $\mathbf{e}_j$ is identified when the following criterion is fulfilled:

$$\left|\frac{e_{n,j}-m_j}{\alpha_j\,\sigma_{\mathrm{MAD},j}}\right| > 1, \quad n=1,\ldots,N;\ j=k,\ldots,k+W-2, \tag{1}$$

where m_j and $\sigma_{\mathrm{MAD},j}$ denote the median and the mean absolute deviation of $\mathbf{e}_j$, respectively, N is the number of samples of a beat, and α_j is the 75% percentile of the samples in $\mathbf{e}_j$. The number of outliers is identical to the number of $e_{n,j}$ that fulfills the criterion in (1).

Inspired by the work in [28], [29], and [30], a second feature set is considered for comparison which builds on principal component analysis (PCA) of the beat matrix $\bar{\mathbf{X}}_k$. The following three features are proposed: 1. the mean cross-correlation resulting from correlation of the largest principal component, i.e., the eigenvector corresponding to the largest eigenvalue, to each of the W beats, computed in a 100-ms interval centered around the beat, 2. the lowest crosscorrelation instead of the mean, and 3. the percentage of variance explained by the largest principal component. The features derived from $\mathbf{E}_k$ and $\bar{\mathbf{X}}_k$ are listed in Table 1.

A support vector machine (SVM) classifier with a radial basis function kernel is used for SBS identification. An advantage of an SVM over other classifiers is that the computation of model parameters corresponds to a convex optimization problem. Therefore, given a data set and a set of hyperparameters, an SVM converges to the same solution [31]. In addition, an SVM with a radial basis function kernel has only two hyperparameters, the penalty parameter C and γ, which simplifies the optimization; for details on SVMs and their properties, see [31].

The hyperparameters C and γ are selected using five-fold cross-validation performed on SIMDB. When C and γ are selected, the final models, based on either $\mathbf{E}_k$ or $\bar{\mathbf{X}}_k$, are trained using the entire SIMDB. The performance of the SBS identification is evaluated using SVADB and BUSQDB. The former database is used to assess the capability of the SVM

TABLE 1. features extracted from the residual matrix $\mathbf{E}_k$ and features extracted from the normalized beat matrix $\bar{\mathbf{X}}_k$ using principal component analysis. PC stands for principal component.

	Features
$\mathbf{E}_k$	Median absolute deviation of all elements Percentile range (0.99–0.01) of all elements Number of outliers computed from $\mathbf{e}_j$
$\bar{\mathbf{X}}_k$	Mean crosscorrelation of the beats with largest PC Lowest crosscorrelation of the beats with the largest PC Percentage of variance explained by the largest PC

TABLE 2. database usage and number of segments.

Databases		Number of segments	
		Similar	Non-similar
SBS training	SIMDB	9,449	9,449
SBS evaluation	SVADB	2,532	37,270
	BUSQDB	–	9,244

to identify SBSs in the presence of ventricular ectopic beats, while the latter is used to assess the capability to identify non-SBSs caused by noise and artifacts.

The number of segments used for training and evaluating the classifier for SBS identification are presented in Table 2. The number of segments refers to episodes with 5 detections, irrespective of episode length. Note that only one segment per recording is selected from each of the ECGs in SIMDB.

B. RHYTHM CRITERIA for nsSVT DETECTION

The nsSVT detector supplements the SBS identification with two rhythm criteria to sharpen the detection of nsSVT. To accomplish this, the following two RR interval sets are defined:

- The vector $\mathbf{r}_m$ ($m = 1, \ldots, M-3$) contains 4 consecutive RR intervals, starting at the m:th RR interval, whose total duration does not exceed 2400 ms are identified as an SBS, where M is the number of identified SBSs.
- The vector $\mathbf{r}'$ contains the RR intervals of the 30-s recording, excluding those of $\mathbf{r}_m$.

Given that an nsSVT does not exceed 30 s and exhibits a considerably faster heart rate compared to the other parts of the 30-s recording, the following criterion is introduced:

$$\frac{\text{median}(\mathbf{r}_m)}{\text{median}(\mathbf{r}')} \leq \delta, \tag{2}$$

where δ is a user-defined constant.

To avoid detection of atrial bigeminy, supraventricular beats (isolated or couplets), and interpolated atrial beats not accompanied by compensatory pause, the following criterion is introduced:

$$\frac{r_m^s(3) - r_m^s(2)}{\text{median}(\mathbf{r}')} \leq \eta, \tag{3}$$

where η is a user-defined constant. The scalars $r_m^s(2)$ and $r_m^s(3)$ correspond to the second shortest and second longest RR intervals within the ascendingly sorted vector $\mathbf{r}_m^s$, respectively.

An nsSVT is detected whenever $\mathbf{r}_m^s$ satisfies both (2) and (3).

C. PERFORMANCE EVALUATION

Sensitivity (Se), specificity (Sp), and positive predictive value (PPV), defined by

$$\text{Se} = \frac{N_{\text{TP}}}{N_{\text{TP}} + N_{\text{FN}}}, \tag{4}$$

$$\text{Sp} = \frac{N_{\text{TN}}}{N_{\text{TN}} + N_{\text{FP}}}, \tag{5}$$

$$\text{PPV} = \frac{N_{\text{TP}}}{N_{\text{TP}} + N_{\text{FP}}}, \tag{6}$$

respectively, are used as performance measures. N_{TP} is the number of true positives, N_{TN} is the number of true negatives, N_{FP} is the number of false positives, and N_{FN} is the number of false negatives.

The application of the above-mentioned performance measures depends on whether SBS identification or nsSVT detection is investigated. The following definitions apply:

1) PERFORMANCE OF SBS IDENTIFICATION

N_{TP} is the number of correctly identified SBSs, N_{TN} is the number of correctly identified sequences with non-similar beats, N_{FP} is the number of falsely identified SBSs, and N_{FN} is the number of falsely identified episodes with similar beats.

2) PERFORMANCE OF NSSVT DETECTION

N_{TP} is the number of correctly identified ECGs with nsSVT, N_{TN} is the number of correctly identified ECGs without nsSVT, N_{FP} the number of falsely detected ECGs without nsSVT, and N_{FN} is the number of falsely detected ECGs with nsSVT.

IV. RESULTS

A. PERFORMANCE of SBS IDENTIFICATION

The results of the performance evaluation are presented in Table 3, where Se and Sp are first computed for each subject in SVADB and BUSQDB, and then the medians are presented together with the 25 and 75 percentiles. Using the $\mathbf{E}_k$-based features on SVADB, the resulting Se and Sp are 100% and 98.0%, respectively, for lead 1, and 100% and 94.5%, respectively, for lead 2. Note that the segments selected from BUSQDB only contain detections of non-similar morphology due to noise and artifacts (cf. Sec. II-C), and therefore only Sp is applicable, found to be 97.6%.

Using the $\bar{\mathbf{X}}_K$-based features, the resulting Se and Sp are 100% and 91.9%, respectively, for lead 1, and 100% and 77.0%, respectively, for lead 2 on SVADB. The measure Sp on BUSQDB is 93.5%. Thus, $\mathbf{E}_k$-based SBS identification is found to be superior to $\bar{\mathbf{X}}_K$-based SBS identification.

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TABLE 3. Subject-wise performance of SBS identification. Since BUSQDB only contains non-similar beats, Se is not applicable. Values are expressed as medians (25–75 percentiles).

	SVADB				BUSQDB
	Lead 1 Se (%)	Lead 1 Sp (%)	Lead 2 Se (%)	Lead 2 Sp (%)	Sp (%)
$\mathbf{E}_k$-based	100 (93.2–100)	98.0 (89.2–100)	100 (100–100)	94.5 (73.0–100)	98.0 (91.9–100)
$\bar{\mathbf{X}}_k$-based	100 (100–100)	91.9 (87.9–99.5)	100 (91.7–100)	77.0 (30.5–92.1)	93.5 (76.7–100)

TABLE 4. Performance of nsSVT detection.

	Se (%)	PPV (%)	Sp (%)
$\mathbf{E}_k$-based	84.6	18.5	99.4
$\bar{\mathbf{X}}_k$-based	86.4	4.6	98.6

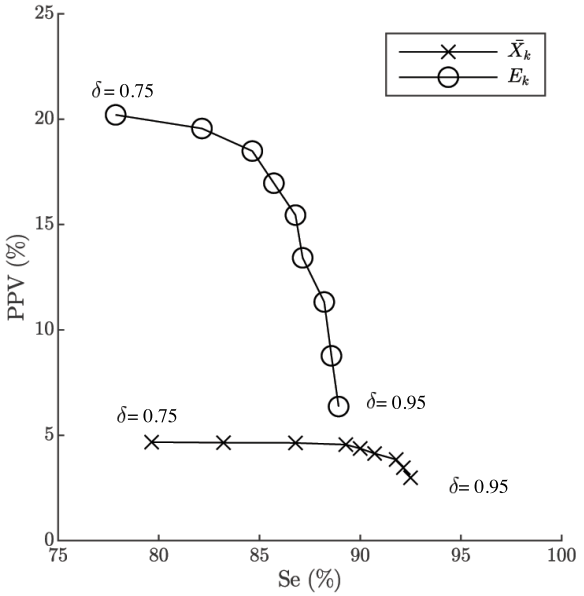

FIGURE 4. Performance of nsSVT detection when δ is varied from 0.75 to 0.95 in steps of 0.05. η is set to 0.25.

B. PERFORMANCE of nsSVT DETECTION

The detection performance is evaluated using SSIIDB. The influence of the rhythm parameters δ and η on performance is shown in Fig. 4. The results presented in Table 4 are based on using $\delta = 0.8$ and $\eta = 0.25$.

The measures Se, Sp, and PPV of the $\mathbf{E}_k$-based detector are 84.6%, 99.4%, and 18.5%, respectively. The corresponding results for the $\bar{\mathbf{X}}_k$-based detector are 86.4%, 98.6%, and 4.6%, respectively. Comparing the $\bar{\mathbf{X}}_k$-based detector with the $\mathbf{E}_k$-based, a 1.8% increase in sensitivity is obtained at the cost of a significant reduction in PPV. When expressed in terms of the number of false positives, the reduction in PPV leads to an increase from 1, 045 recordings to 4, 997 recordings. Thus, the performance of the $\mathbf{E}_k$-based nsSVT detector is superior to that of the $\bar{\mathbf{X}}_k$-based detector. The significance of this result is discussed below in terms of reduction in expert review burden, notably a reduction by a factor of 6.

Since multiple ECG recordings are available for most subjects in SSIIDB, a subject-based performance evaluation is applicable as well. For the $\mathbf{E}_k$-based detector, Se, Sp, and PPV of 89.8%, 92.0%, and 27.7% are achieved, respectively, on the subject-level. For the $\bar{\mathbf{X}}_k$-based detector, the corresponding numbers are 93.7%, 73.3%, and 10.6%, respectively.

V. DISCUSSION

A. nsSVT DETECTION in AF SCREENING

The feasibility of AF screening is highly dependent on the performance of automated approaches as manual review of screening databases is time-consuming and very costly. Ideally, all patients with AF should be identified, while the number of false positives should be kept as low as possible. This performance requirement was addressed in [25], where the objective was to reduce the number of false positives without introducing false negatives. In the present study, such a requirement is relaxed as subjects with nsSVT may not be referred to as patients from a clinical perspective, but rather they are susceptible to develop AF, and therefore subject to extended screening.

In the present study, Se and PPV of 84.6% and 18.5%, respectively, were achieved. It should be noted that PPV depends on the prevalence of nsSVT, and therefore can be used as an indicator of the reduced need for expert review. Without nsSVT detection, the StrokeStop II database requires expert review of 667 ECG recordings (i.e. 186,697/280) in order to find one ECG recording with nsSVT. In [17], this number was reduced to about 31 recordings, but then accepting that 7.9% of all cases of nsSVT remained undetected. In the present study, the number of recordings needed to be reviewed to find one single nsSVT is further reduced by a factor of 6, but at the expense of a decrease in Se from 92.1% to 84.6% compared to [17]. The performance measure Se can be increased with another choice of δ and η, however, this comes at the expense of a lower PPV, i.e., additional ECG recordings calling for expert review, see Fig 4. The decrease in sensitivity is due to that some of the annotated nsSVT episodes were not SBSs or did not satisfy both rhythm criteria.

Due to the lack of annotated, public databases, it is difficult to determine an optimal value for the nsSVT rhythm criteria in (2) and (3). The database SSIIDB is highly imbalanced which complicates the use of subject-wise cross-validation.

To improve the sensitivity without decreasing the PPV calls for a structural change of the detector, for example, by using deep learning to identify SBSs directly from the raw ECG. Another possibility could be to use another database better suited for training, either created by the more advanced, recently developed ECG simulator described in [33] or composed of real ECGs; however, as already noted, annotated

public databases are unfortunately lacking. To improve the PPV without decreasing the sensitivity, the approach presented in [32] may be used to differentiate nsSVT from PACs.

The proposed approach to nsSVT detection is based on the assumption that the variability in beat-to-beat morphology within such episodes is subtle. To the best of our knowledge, the publicly available ECG recordings with the most occurrences of nsSVTs are found in SVADB. However, nsSVTs are limited in number: only 26 recordings contain runs with at least 5 supraventricular beats, where only one single recording contains two SVT episodes with duration of about 5 and 8 minutes, thus accounting for a considerable number of the SBS episodes in SVADB (cf. Sec. 2). Therefore, this database alone is not large enough for training of machine learning techniques.

The decision to use 5 beats as the minimum duration of SVT episodes is partly motivated by the difficulty to judge rhythm irregularity based on fewer beats. To detect shorter episodes calls for P wave information, however, such information is often difficult to rely on when analyzing screening ECGs recorded using a handheld device. Another reason is that the StrokeStop II database was annotated using the 5-beat definition.

The nsSVT detection problem may alternatively be addressed as a problem of signal quality assessment, followed by a supraventricular/premature atrial beat detector. However, the majority of detectors for supraventricular/premature atrial beats are, in fact, beat classifiers known to provide low sensitivity [12], [15]. The detector proposed for premature atrial beats in [13], which yielded a high sensitivity in SVADB, uses two-lead ECG signals. In the present study, the proposed method solves both quality control and ectopic beat handling in one single step, achieved by a design which is independent of beat morphology and lead selection.

B. TRAINING CONSIDERATIONS

The first step of the nsSVT detector is to identify episodes with similar morphology. The motivation to use the SVM was the convex optimization problem and the few hyperparameters, facilitating model optimization. Other machine learning models, including decision trees and random forests, were found to yield similar results.

The purpose of using SVADB and BUQDB was to highlight the performance of the SBS identification on relevant and publicly available databases with beat annotations. However, using these two databases along with SIMDB to train the final model, the nsSVT detection performance did not improve. One explanation is that SVADB and BUQDB introduce a large imbalance of the training data, which needs to be handled by, e.g., data under/oversampling, weighted loss function, or use of classifiers with intrinsic capacity to deal with data imbalance, see, e.g. [34].

Other explanations are that the considerable number of beat sequences in SVADB, expert annotated as normal, ventricular, or supraventricular beats, display significant variability in morphology due to the presence of noise and artifacts, together with the fact that the information in both leads were used for beat annotation, see Fig. 5. The same explanations apply to the beat sequences with at least one aberrant beat annotation, where the beats may display a similar morphology in one of the leads, but not in the other. Hence, in the present study, SBS identification training is done using only SIMDB, where training data with reliable annotations are generated.

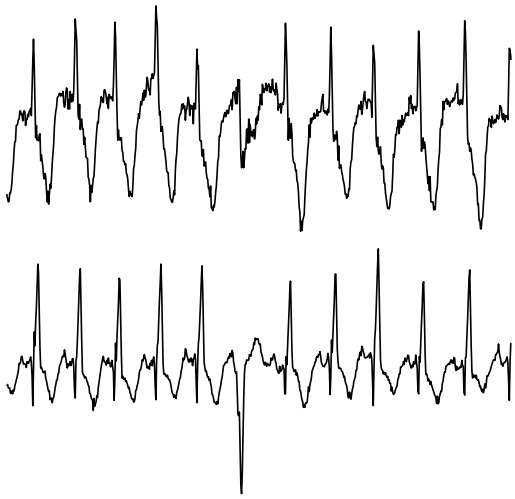

FIGURE 5. A run of supraventricular ectopic beats in SVADB. All the beats are annotated as supraventricular beats ('S'), while the morphology of one beat is significantly different from the other beats. For training of SBS identification, such beat sequences should be annotated as non-SBSs.

The presence of ventricular ectopic beats is a major source of false positives in nsSVT detection. The features extracted for SBS identification are defined in a way so that non-SBSs, caused by ventricular ectopic beats and false detections, can be distinguished from SBSs. The features are independent of the location of ventricular ectopic beats and false detections within $\bar{\mathbf{X}}_k$.

C. LIMITATIONS

The noise added to the ECGs in SIMDB was recorded during exercise stress testing, cf. Sec. II-A. This is a limitation of the study since such noise is less representative of ECGs recorded by a handheld device, where poor hand contact, hand motion, and device displacement deteriorate signal quality.

The SVM for SBS identification is trained using simulated ECG signals with normal sinus rhythm and AF. While the proposed strategy is independent of rhythm and PQRST morphology, other approaches to nsSVT detection, including end-to-end deep learning-based, would be applicable provided a simulation model for nsSVT would be available.

A comparison of performance involving some other nsSVT detector is desirable. However, since the proposed detector is the first of its kind, such a comparison could not be done. To some extent the nsSVT detector builds on the same idea as that of novelty detection, namely to model the stable mode of operation while a deviation (''novelty'') from that model can be identified using, e.g., an SVM [35]; such identification is also referred to as one-class classification. In terms of nsSVT

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detection, novelty is identified whenever an episode with beats of deviating morphology is present. However, novelty detection has typically been considered in applications where data change only once from a stable to an "unstable" mode, whereas nsSVT detection has to handle repeated changes between two modes, suggesting that two-class classification is more suitable.

D. FUTURE WORK

Future work should focus on nsSVT simulation models as these are expected to facilitate the development of better-performing nsSVT detectors. Such simulation models should be complemented with models for noise and artifacts typical of handheld recorded ECGs.

VI. CONCLUSION

This paper presents an approach to nsSVT detection in single-lead, 30-s screening ECGs, based on morphological beat similarity. The results show that a significant reduction in the expert review burden can be achieved using the proposed detector. The lower number of recordings for expert review facilitates the identification of subjects at risk of developing AF.

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