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QRS Detection using Morphological and Rhythm information

A.I. Rasiah, R. Togneri and Y. Attikiouzel
Centre for Intelligent Information Processing Systems
Department of Electrical and Electronic Engineering
University of Western Australia

Abstract

An approach has been developed using artificial neural networks to detect QRS complexes within an ambulatory ECG signal. The method employs the use of an artificial neural network classifier to recognise the morphology of a QRS complex based on amplitude and derivative features. The feature vectors are derived from a representative annotated ECG trace and are used in the formulation of the ANN's training set. The outputs, or p.d.f. estimates generated by the neural network are then used to determine if a "QRS-like spike" has occurred. These spike detections then undergo further post-processing which, biases these detections such that the spike detection "nearest" the anticipated location of the next QRS is confirmed as a QRS complex. This anticipation of the QRS complex location is based on the estimation of the next RR interval using past RR intervals of previously confirmed QRS complexes. Such post-processing has the effect of greatly reducing the number of false positive detections, particularly in noisy ECG traces.

Introduction

QRS detection is a well known problem of which many approaches to its solution have been proposed; [1][2] to name a few. It represents the first stage of ECG analysis and its use in ECG monitoring equipment is now not uncommon. In this paper, we employ a decision theoretic pattern recognition approach to QRS detection incorporating both morphological and rhythm information in the process.

Outline of Approach

The outline of the QRS detection approach investigated in this paper is functionally represented in the figure 1. This approach assumes the ECG signals acquired undergo basic signal conditioning prior to digitisation; i.e. the use of an anti-aliasing filter at least. It also encourages as much signal conditioning to be done to clean-up the ECG signal before feature extraction; some such methodologies were reviewed in [1].

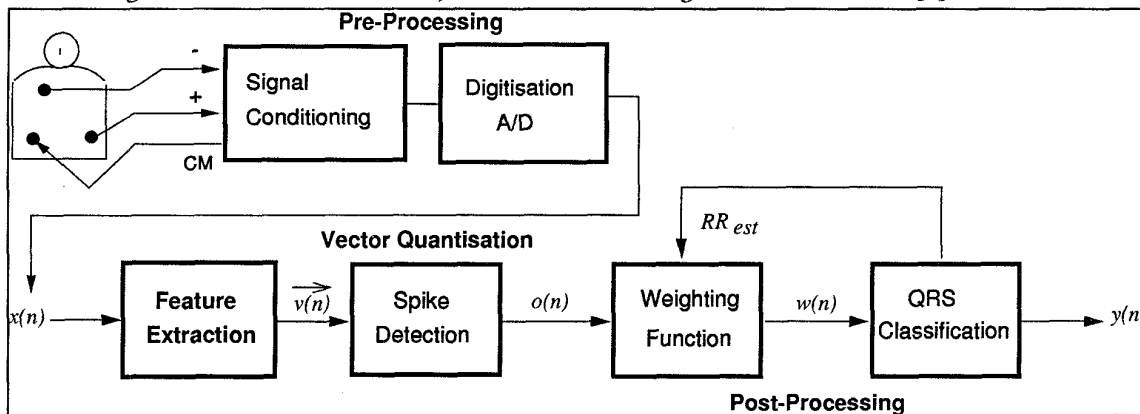


Figure 1: Functional stages of the QRS detection algorithm

The approach adopted endeavours to emulate the decision process of a human in his or her recognition of QRS complexes within an ECG signal. It begins by first detecting all spikes that have a morphological resemblance to a QRS complex. The algorithm then uses the rhythm information between QRS complexes, i.e. the "regularity" of the RR interval (interbeat value) to influence the selection of a spike as a QRS complex - see figure 1. It does this by weighting the results of the spike detector such that the spike closest to the predicted location in time of the next QRS complex has the largest value output value, $w(n)$, within the search area and is consequently selected as a QRS complex - see figure 2 and figure 3. The prediction of the location of the next QRS complex is derived from an estimate of the next RR interval, RR_{est} . To determine this estimate, knowledge of previous RR intervals computed from previous QRS classifications is required. Suffice to say, when the algorithm is initiated no prior RR interval information is available, and as such the output of the spike detector is unbiased where every spike detected which is at least RR_{min} (typically 35 samples i.e. 0.35secs) from the previous detection is assumed as a QRS complex. Therefore, if the computation of the estimated RR interval requires n prior RR interval values, it follows that the output of the spike detector will remain unbiased until $n+1$ QRS complexes have been registered. If the ECG signal is initially noisy, then there is a valid concern that

these initial detections may all be false positives. In such a scenario, the initial RR interval values may be initialised to some starting value eg. 1sec which works out to 60 bpm. Alternatively, the spike detection can be made more "strict" by using conservative p.d.f. estimates thresholds, to reduce the probability of a false positive spike detection.

In addition to estimating the RR interval, two further parameters, α_0 and α_1 are required to provide a search area in time of width $(\alpha_0 + \alpha_1) \cdot RR_{est}$ where the weighting function is given by (8)-(9) - see figure 3. Outside this search area all spikes detected are ignored. If a spike is detected and a QRS classification is made, a new estimate of RR_{est} is made using RR interval of this QRS classification to that of the previous one. If no QRS classification is made within the search area, L_0 is set to $(1 - \alpha_1)RR_{est}$, $u_1(n)$ becomes the weighting function and the search continues from the estimated QRS location - see figure 4. Once a QRS classification has been made, the weighting function reverts back to $u_0(n)$ and the estimated RR interval, RR_{est} , remains the same. Note that it is important to have these "search area" parameters because they compensate for the inaccuracies in the estimation of the RR interval. Remember, that although the electrocardiogram gives the appearance of metronomic regularity, measurements of RR intervals reveal a chaotic behaviour in time - see [3].

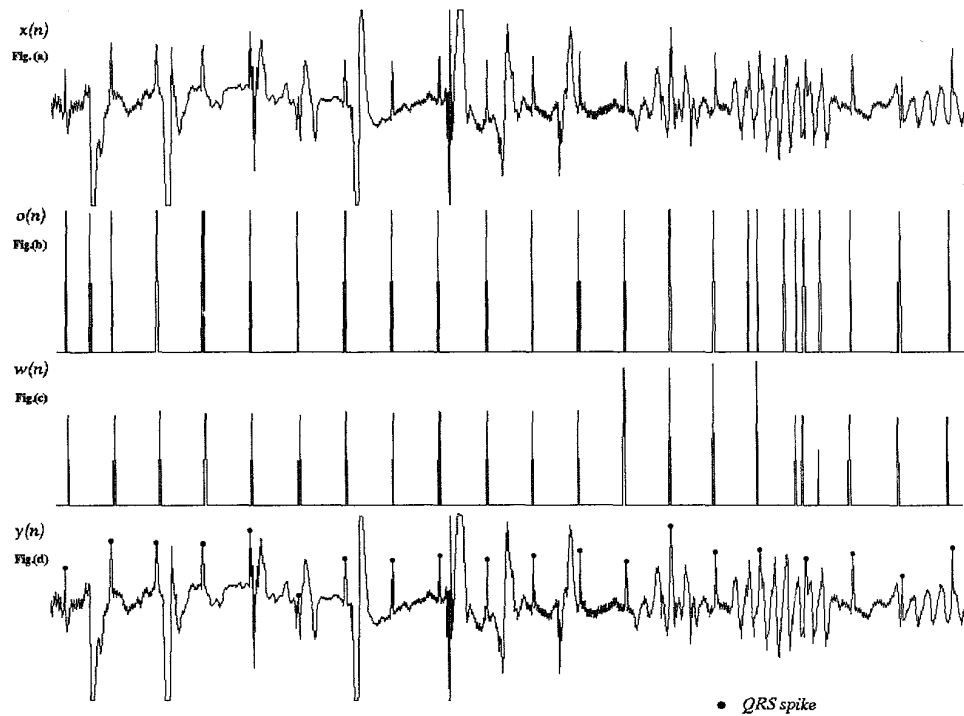


Figure 2: QRS detection algorithm. (a) Ambulatory ECG signal $x(n)$, (b) Output of spike detector $o(n)$, (c) Biased output of spike detector $w(n)$ and (d) ECG signal with QRS complexes detected $y(n)$

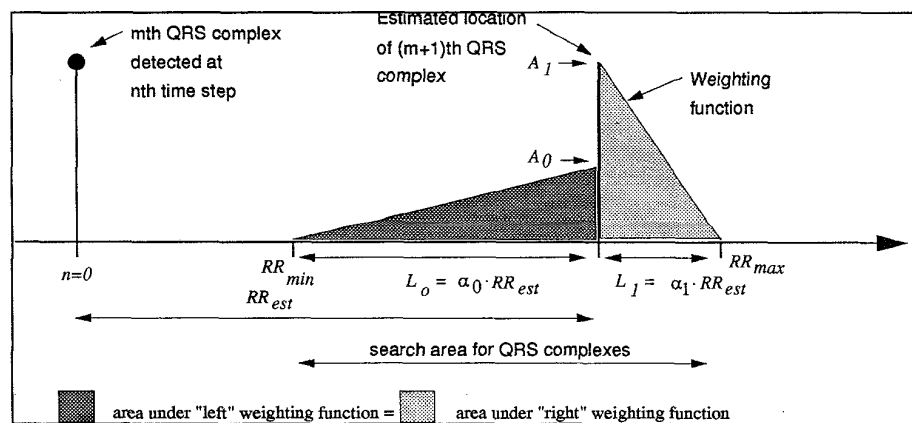


Figure 3: Triangular weighting function with search parameters α_0 and α_1 and interbeat estimate RR_{est}

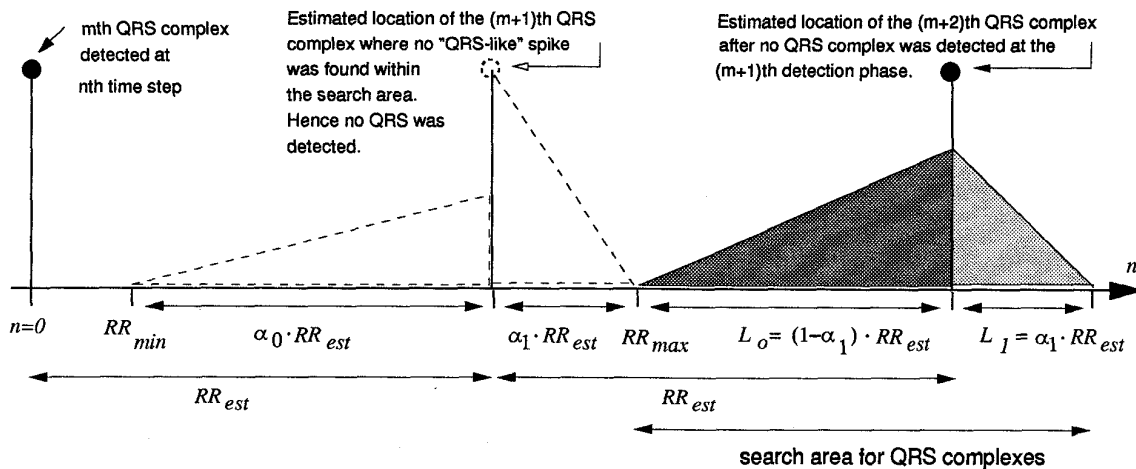


Figure 4: Weighting function when no QRS detection is made.

Feature extraction

The features selected were required to describe the morphology of a QRS complex. Given that the sampling rate was 100Hz, and that the width of QRS complexes in humans is known to vary from approx. 0.05s to 0.08s, a width of seven samples is a sufficiently large time window to contain the required QRS complex signal. Within this window, five features were derived to describe the amplitude of would be QRS complexes. From these five, an additional five features describing the first derivatives were used. Thus the feature vector at time n , $v(n)$, had 10 dimensions defined as follows.

1st derivative at n th sample,

$$\frac{dx(n)}{dn} = x(n+1) - x(n-1) \quad (1)$$

$$v_1(n) = x(n-5) - (x(n) + 5x(n-6))/6$$

$$v_2(n) = x(n-4) - (x(n) + 2x(n-6))/3$$

$$v_3(n) = x(n-3) - (x(n) + x(n-6))/2$$

$$v_4(n) = x(n-2) - (2x(n) + x(n-6))/3$$

$$v_5(n) = x(n-1) - (5x(n) + x(n-6))/6$$

$$v_6(n) = x(n-4) - x(n-6) \quad v_7(n) = x(n-3) - x(n-5)$$

$$v_8(n) = x(n-2) - x(n-4) \quad v_9(n) = x(n-1) - x(n-3)$$

$$v_{10}(n) = x(n) - x(n-2)$$

The first five features, defined as the amplitude of the samples $x(n-5)$ to $x(n-1)$ are measured from the linear line defined by samples $x(n-6)$ and $x(n)$.

This was done to remove the influence of a wandering baseline. Bearing in mind the above feature vector definitions and that power line interference can be notoriously common in ambulatory electrocardiograms even when there is adequate filtering, the sampling rate is purposely selected at twice the frequency of such an interference. This will ensure that both aliasing does not occur and that the morphology of this interference, as described by the above features, is vastly different from that of a QRS spike. Note that a sampling rate of a 100Hz would be chosen for a power line interference of 50Hz (for a 60Hz power line interference sampling is chosen at 120Hz or more conventionally 128 samples per second).

Figure 5: Derivation of features from a digitised ECG. The diagram shows a digitised ECG trace with samples $x(n-6)$ through $x(n)$ plotted against time steps $n-6$ through n . A straight line is drawn through samples $x(n-6)$ and $x(n)$. Vertical lines connect samples $x(n-5)$ through $x(n-1)$ to the baseline line. The vertical distances from the baseline to these samples are labeled $\Delta x(n-5)$ through $\Delta x(n-1)$. The diagram illustrates how the first five features v_1 through v_5 are derived from these amplitudes.

Spike Detection

As shown in figure 1, the vector quantiser stage serves to detect "QRS-like" spikes in an ECG trace. It essentially has to decide if the vector, $v(n)$, presented represents a signal that belongs of the class of "spike" signals that are QRS-like (QRS class) or not (NON-QRS class). The spike detector outputs a 1.0 when "QRS-like" spike is seen and zero otherwise, ie. its output, $o(n)$, is binary. To evaluate the use of ANNs as spike detectors, the approach was tested with the multilayer perceptron (MLP) with back-propagation [4] and probabilistic neural network (PNN) [5]. In addition to the decision rules that accompany each ANN, the spike detection algorithm includes further conditions to ensure that only one "detection" (ie. value for which $o(n)=1$) is produced by each QRS spike seen.

MLP with back-propagation

The outputs of the MLP, MLP_{QRS} and $MLP_{NON-QRS}$ are dichotomous nodes, ie. ± 1.0 . The decision rules for classification is, if $(MLP_{QRS}(n) > MLP_{NON-QRS}(n))$ then $o(n) = 1$

Probabilistic Neural Network

The outputs of the PNN, PNN_{QRS} and $PNN_{NON-QRS}$ are real-values nodes. The decision rule for classification is, if $(P(\omega_{QRS} | v(n)) > P(\omega_{NON-QRS} | v(n)))$ then $o(n) = 1$. As shown in [5] the outputs of the PNN approximate the conditional probability density function. However, for the decision rule to satisfy bayes "minimum-error rate" case, assumptions were required to be made on the apriori probabilities of the classes concerned. We investigated two such assumptions ie. (2) and (3) and found the results favoured (3).

$$P(\omega_{QRS}) = P(\omega_{NON-QRS}) \quad \text{and} \quad P(\omega_{QRS}) + P(\omega_{NON-QRS}) = 1 \quad \Rightarrow \quad P(\omega_{QRS}) = P(\omega_{NON-QRS}) = \frac{1}{2} \quad (2)$$

$$P(\omega_{QRS}) + P(\omega_{NON-QRS}) = 1 \quad \text{with} \quad P(\omega_{QRS}) = \frac{N_{QRS}}{N_{QRS} + N_{NON-QRS}} \quad (3)$$

Note that the assumption of equality among the apriori probabilities in (2) is only valid within the context of the spike detector. It is not true for the entire QRS detection process given the inclusion and influence of the weighting function on the classification outcome. Since the output of the spike detector is multiplied with $w(n)$ (see (10)), $w(n)$ is seen to produce a "biasing effect" on the posteriori estimates with n . Therefore the influence of $w(n)$ on the overall classification process negates the assumption of (2) as the entire process behaves as though $P(\omega_{QRS})$ and $P(\omega_{NON-QRS})$ vary with n .

Interbeat value estimation

The QRS detection algorithm proposed has been devised in a manner such that its parameters, RR_{est} , α_0 and α_1 , maintain an intuitive meaning and have values bounded by the prior knowledge of constraints known about the human cardiac system eg. $30 < \text{heart rate} < 200$ bpm. The parameters mentioned are estimated as follows.

- RR_{est} : This parameter is an estimation of the next interbeat value, which is used in determining the next location of a QRS complex. Contrary to the conventional dictum that a normal heartbeat is highly regular, examination of measurements of the interbeat value reveal a behaviour of the *normal sinus rhythm* which can be characterised as *chaotic*. Since the algorithm is only concerned with the estimation of the immediate interbeat value, a simple averaging estimation technique was used. Note a similar technique was suggested by [6].

$$RR_{est}(m) = \frac{RR(m) + RR(m-1)}{2} \quad \text{where if } ((RR_{est} > 1.0\text{sec}) \text{ and } (\text{random}() > 0.5)) \quad RR_{est} = \frac{RR}{2} \quad (4)$$

- α_0 and α_1 : These parameters dictate the width of the "search area", within which a QRS complex may occur. They represent the percentage of RR_{est} to search before and after the point RR_{est} , respectively - see figure.3. Therefore for large values of RR_{est} the search area is larger. This was done because fluctuations in the heart rate (bpm) for low heart rates produce changes in RR intervals that are larger in magnitude than a fluctuation of equivalent magnitude when the heart rate is high. If the prediction of the next interbeat value is reliable, then α_0 and α_1 can hold small values ie. the search area need not be large. Alternatively, if our prediction of the next interbeat value is poor, and misclassifications (false negatives) are numerous, a large value of α_0 and α_1 is required to expand the search area to cater to possible large fluctuations in the heart rate. The values of α_0 and α_1 are defined in terms of β_0 and β_1 respectively. β_0 and β_1 are themselves defined as the percentage the RR_{est} is from RR_{min} (typ. 35 samples = 0.35secs = 170bpm) and RR_{max} (typ. 200 samples = 2secs = 30bpm) respectively (5). Usually a person's heart rate will never rise or fall by an amount exceeding half his/her current heart rate. The bounding limits of α_0 and α_1 as given in (6) were determined heuristically. The lower limits were chosen on an adhoc basis bearing in mind the values of RR_{min} and RR_{max} . The upper limit was evaluated for various values between 0.2 and 0.8 with the MLP model, and the value with the lowest number of false and missed detections selected. Note that in all testing done, α_0 and α_1 were upper-bounded by this chosen value ie. 0.3. Interestingly enough this value of 0.3 corresponds to a range of bpm values between 39 and 120 which is characteristic of the range of "normal" heart rate values. Also, the magnitude of α_0 and α_1 will determine the "strength" of the weighting function, $u_0(n)$.

$$\beta_0 = \frac{RR_{est} - RR_{min}}{RR_{est}} \quad \beta_1 = \frac{RR_{max} - RR_{est}}{RR_{est}} \quad (5)$$

$$\alpha_0 = \begin{cases} 0.1 & \beta_0 < 0.1 \\ 0.3 & \beta_0 \geq 0.3 \\ \beta_0 & \text{otherwise} \end{cases} \quad \alpha_1 = \begin{cases} 0.1 & \beta_1 < 0.1 \\ 0.3 & \beta_1 \geq 0.3 \\ \beta_1 & \text{otherwise} \end{cases} \quad (6)$$

$$L_0 = \begin{cases} \alpha_0 RR_{est} & \text{if a QRS classification was made} \\ (1-\alpha_1) RR_{est} & \text{if no QRS classification was made} \end{cases} \quad \text{and} \quad L_1 = \alpha_1 RR_{est} \quad (7)$$

• weighting functions $u_0(n)$ and $u_1(n)$: The weighting function is used to determine which spike to pick as a QRS complex if there is more than one spike detection in the search area defined by L_0 and L_1 . This is done by picking the largest value of $w(n)$ within this search area where $w(n)$ is defined as follows - see figure 3 and 4.

$$u_0(n) = \begin{cases} \frac{1}{2\alpha_1} \left(1 - \frac{n-RR_{est}}{\alpha_1 RR_{est}} \right) & n \geq RR_{est} \\ \frac{1}{2\alpha_0} \left(1 + \frac{n-RR_{est}}{\alpha_0 RR_{est}} \right) & n < RR_{est} \end{cases} \quad u_1(n) = \begin{cases} 1 - \frac{n-RR_{est}}{\alpha_1 RR_{est}} & n \geq RR_{est} \\ 1 + \frac{n-RR_{est}}{(1-\alpha_1) RR_{est}} & n < RR_{est} \end{cases} \quad (8)$$

$$w(n) = \begin{cases} (u_0(n)+OFFSET) o(n) & \text{if a QRS classification was made} \\ (u_1(n)+OFFSET) o(n) & \text{if no QRS classification was made} \end{cases} \quad (9)$$

$$y(n)=1 \text{ iff } w(n)>w(i) \forall i, n \in \{RR_{est} - L_0, \dots, RR_{est}, \dots, RR_{est} + L_1\} \text{ where } i \neq n \Rightarrow \text{QRS Complex} \quad (10)$$

If one examines (8)-(10) and figure 3, one will find that a QRS complex is detected at the largest value of $w(n)$ within the search area. The function $w(n)$ is defined as a scaled form of the spike classifier's output. The *OFFSET* (eg. 10^{-6}) term is included in (10) so that $w(n)$ is non-zero at $(n-RR_{est})=\alpha_0 RR_{est}$ or $\alpha_1 RR_{est}$. The weighting function, $u_0(n)$ has three distinct modes of operation which depend on the value of RR_{est} . We called these modes *normal*, *transient* and *abnormal*. A detail investigation of these modes can be found in [7].

ANN Training

Four MLII ECG traces with approx. 32 minutes of monitoring time were used in the evaluation of the algorithm. They were acquired from healthy "active" subjects using a HP 78342A bedside monitor linked to a personal computer with an A/D board. All ECG signals were sampled at 100Hz with 12bit A/D precision. The bedside monitor provided the appropriate signal conditioning. All the traces had significant noise intentionally introduced during the acquisition procedure to evaluate the robustness of the approach proposed. Annotation of the QRS complexes within these traces were done by manual inspection of each trace.

To construct the feature set we used the noisiest of the four ECG traces acquired; the remaining three were reserved for testing. Together with the annotation of this trace, the feature vectors for the QRS class were extracted from the entire trace. Feature vectors for the NON-QRS class were generated by picking random locations in time along this ECG trace and checking each location to make sure a QRS complex did not exist there and that this location had not already been picked before. The number of NON-QRS class feature vectors to pick was decided in the following manner. First let us assume a minimum RR interval of 30 samples (ie 0.3 secs at 100Hz), and a tap length of six samples. Then for each pair of QRS's, there are five (ie. RR/TAP_LENGTH) tap length's that make up the RR interval. Hence for each QRS feature vector we pick five NON-QRS feature vectors. In other words, if N QRS class feature vectors were extracted then $5N$ NON-QRS class feature vectors are generated. Note all feature vectors were generated from the digitised signal $x(n)$, scaled to values between ± 1.0 . There was a total for {16555, 3111} vectors extracted from the training ECG trace for the NON-QRS and QRS class respectively. This full set was then divided equally into three sets ie. the training set, evaluation set and testing set.

In training the MLP, backpropagation was used with the full set. The number of epochs used in training the MLP was estimated from a two pass procedure; where in the first pass the mean square error is plotted against the no. of epochs. By then inspecting this plot, an appropriate point is chosen such that no significant improvement in the mean square error is seen, and the training repeated up to this chosen point. A network with

one hidden layer of five nodes was used ie. (10:5:2).

In training the PNN, a clustering algorithm described in [7] was used reduce the training set to a size of {48, 25} vectors. The evaluation set was then used to determine the smoothing factor such that the percentage of correct classification against this set was maximised. Performance is quoted from the results returned by the testing set.

Results and Conclusion

The results on the approach tested on the four 32min. ECG MLII trace records (which had a total of 11984 QRS complexes) are tabulated in tables 1 and 2. Also, tabulated are results of nine rule based algorithms as reviewed in [1]. The time trials quoted, are the processing times of all the records on a SPARC2.

Table 1: Results without the post-processing stage.

Detection Scheme	Amplitude & 1st deriv			1st derivative		1st&2nd deriv.		Digital filters		ANN	
	AF1	AF2	AF3	FD1	FD2	FS1	FS2	DF1	DF2	MLP	PNN
Algorithm Type											
Time Trials (secs)	1	6	1	1	1	8	8	6	14	140	1760
No. of detections	12649	12669	13494	12996	14017	13545	12839	11322	12325	12644	12757
True detections	11626	11487	11763	11746	11779	11848	11826	10693	11003	11923	11927
False detections	1023	1182	1731	1250	2234	1697	1013	629	1322	721	830
Missed detections	358	497	221	238	205	136	158	1291	981	61	57

Table 2: Results with the post-processing stage.

+ post processing	AF1	AF2	AF3	FD1	FD2	FS1	FS2	DF1	DF2	MLP	PNN
No. of detections	11723	11655	11896	11846	11913	11963	11887	10813	11157	11955	11966
True detections	11539	11416	11679	11681	11639	11742	11761	10629	10898	11894	11884
False detections	184	239	217	165	274	215	126	178	259	57	82
Missed detections	445	568	305	303	345	242	223	1355	1086	89	100

The best approach is picked as the one with the lowest cost ie. (false detections+missed detections). Also, the post-processing stage reduces the total cost in all but one of the algorithms and always significantly lowers the number of false detections. To conclude, the results demonstrate significant improvements of the decision theoretic approach over rule-based schemes. Also, the time trials suggests that this approach can be realised in realtime.

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