Comparison of Inductive Modeling Method to Other Classification Methods for Holter ECG

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Abstract. *In this work we present a study which compares method based on inductive modeling called GAME with several classification algorithms. To compare these methods we will use long-time Holter ECG data. More specifically we focused on the task of classification of normal N beats and premature ventricularV beats.*

Some of the tested methods represent the state of the art in pattern analysis, while others are novel algorithms developed by us. All the algorithms were tested on the same datasets, namely the MIT-BIH and the AHA data bases. The results for all the employed methods are compared and evaluated using the measures of sensitivity and specificity.

Keywords

Inductive modeling, Holter ECG, heart beat classification, GAME

1 Introduction

Long term holter [1] monitoring is widely applied to patients with heart problems such as arrhythmias. Identification of heart beats with unusual timing or unusual electrocardiogram (ECG) morphology can be very helpful for early diagnosis of hearts with pathological electrophysiology.

Many different methods have been proposed to solve the crucial problem of long-term holter recordings evaluation which actually is transformed into the problem of discrimination between normal N and premature ventricular V beats. Solving this problem is of major importance for the identification and diagnostic of heart problems. An advanced system with automatic classification and analysis capabilities is needed in order to process the large amounts of data the holter measurement records.

Much research effort has been put till today to examine and classify data, which are usually based on beat-shape description parameters [2, 3] , shape descriptive parameters transformed with the Karhunen-Loeve coefficients [4], and hermite polynomials [5]. Some other works use frequency-based features [5] or time-frequency features [6] and features obtained from heartbeat interval measurements [7] to identify cardiac arrhythmia. Different methods which deal with this problem range from linear discriminants [5, 3], neural networks [5], and self-organized maps [8], to other methods as in [8].

In any case, for the comparison of different approaches the setup of the experiments, where the type of the training and the selection of testing sets are defined, is of high importance. There are two main setups to be considered: training based on a local learning set [8, 2] and on a global learning set [8, 9].

When the local training is used, the classifier is fitted at least partially to the data given by the measurements on the patient on which the testing will be performed. Therefore this approach requires a cardiologist to annotate part of the signal in advance before the automatic classification can be started.

On the other hand the global classification is independent of a patient and therefore it is expected to be much more robust in classifying new recordings because it does not require an annotation of a cardiologist in advance. But the drawback of this method is that it usually yields worse results in comparison with the locally trained classifiers since the morphology of N and V beats differ not only from patient to patient, but also according to the position of the ECG leads, even on the same person.

In addition to this, published works differ also in the results presentation. Some papers use accuracy measures [9] this is common for the classical AI field. Others use as measures the sensitivity and specificity [8] that are more suitable for the classification in the medical field. While the accuracy gives an overall insight of the correctness of the methods, the sensitivity and the specificity evaluate the methods from the clinical point of view; this is more suitable for decision making in the situations dealing with uneven numbers of beats for each classification group.

In this paper we attempt to provide a thorough investigation of different pattern analysis techniques using a global classifier on two different datasets. The results are then compared by the means of sensitivity and specificity.

In our work we will use two different databases with Holter ECG recordings. One of them will be MIT-BIH and the second AHA (American Heart Association) databases [10, 11]. These will be described in details in Section 5. Both data bases have undergone the same preprocessing steps, where the same features have been computed. In Section 6, the results are compared using the well established measures of sensitivity and specificity and we will discuss our results.

2 GAME Inductive Modelling Method

In many applications it is important to find optimal model of unknown system (for example in classification, prediction, approximation, etc.). Such model can be found using two different approaches – deductive and inductive. The GAME artificial neural network (ANN) is based on inductive approach. This means that parameters and also structure of the ANN are parts of a learning process (the parameters are selected and the NN is constructed from some minimal blocks during the learning process).

The GAME ANN extends the concept of GMDH network [12, 13]. The GMDH allows only one type of minimal block (neurons with one transfer function). On the other hand in GAME ANN there are neurons with many different transfer functions (linear, sigmoid, polynomial, etc...). The GAME has a feed-forward structure [14] as illustrated in figure 1.

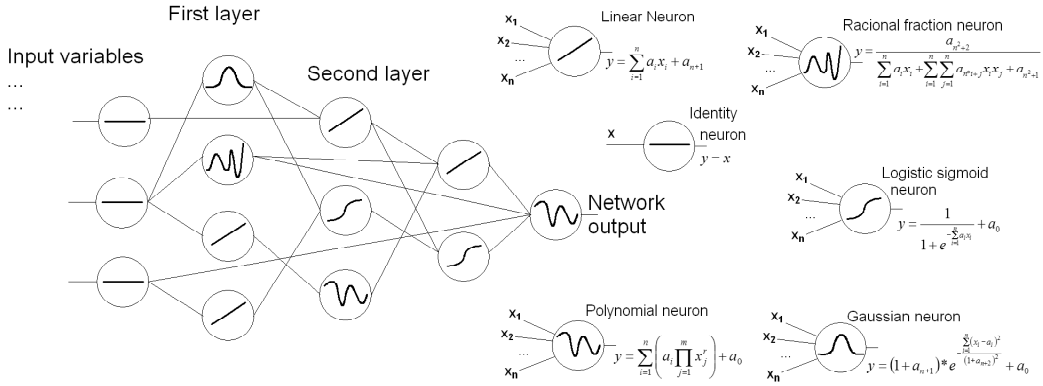

Fig. 1. Example of GAME artificial neural network with different types of neurons.

The GAME NN is built during the training phase from scratch. Each new layer is constructed in the following way: at first a large number of new neurons is generated. Neurons differ in the transfer function, the number of inputs and in the number of neurons in previous layer that the new neuron is connected to.

The next step is to find the optimal setup of internal parameters and the best connections to neurons in previous layer. To do this, GAME uses an advanced genetic algorithm. The population consists of neurons in each new layer and each neuron is coded to a genome.

Figure 2 shows example of genome coding. Coding contains information about neurons in previous layer which are connected to the neuron coded by genome, type of transfer function and some parameters of the transfer function. Parameters of transfer function consist of two parts - the first contains coefficients which are set by optimization method, the second contains structural information, these are modified by genetic algorithm.

For example on figure 2 the a_1, a_2 ... are coefficients set by optimization method, the powers of x_1, x_2 ... (in polynomial neuron) are modified by genetic algorithm.

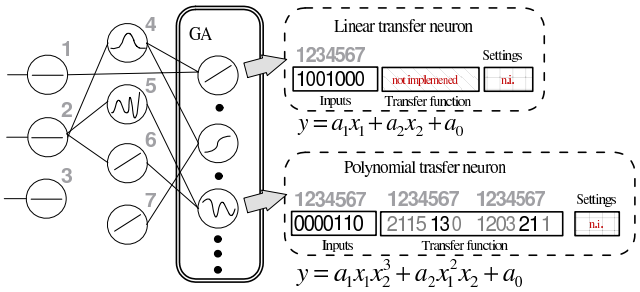

Fig. 2. Coding scheme of neurons in GAME ANN.

In the beginning of the genetic algorithm, the neurons are generated randomly (derivation of the first generation). The neurons are evaluated using a validation set and their accuracy corresponds to neuron's fitness. Then neurons are selected to cross-over according to their fitness. The cross-over primary involves only the part of genome which encodes the connections to the previous layer. If both neurons employed in cross-over have the same transfer function, their structural parameters are also "crossed-over". When the cross-over is finished all neurons optimize their transfer function using a properly assigned method. After that the genetic algorithm is repeated for a number of generations until the accuracy of the population exceeds a specified threshold.

All neurons in new layer are evaluated using separated testing set and the worst neurons are deleted from the layer. Then the layer is "frozen" and the algorithm continues with creation of a new layer. This is repeated until a neuron with a satisfactory accuracy is found and this neuron is the output of the network.

2.1 GAME method setup

The number of inputs is equal to number of features extracted from the data – 14. For the main experiment neuron with following transfer function are allowed: linear, polynomial, exponential, sigmoid, sinus, gausian.

Neurons may be connected to any neuron in previous layers or any input.

For the second experiment only neurons with following transfer functions are allowed: linear, polynomial and sigmoid.

3 Other Classification Methods

3.1 Rule-Based Decision Tree (RBDT)

In the case of the Rule-Based Decision Tree (RBDT) [15], the domain of each feature (i.e. a value measured on each ECG beat) can be divided into several intervals, which are selected by experience and knowledge of clinicians. The rules that are in each node of the decision tree have the structure illustrated below:

```
if (intQRS >= 100) & (intQRS <= 110)
pass_status.QRS = 'widening'
elseif (intQRS > 110)
        pass_status.QRS = 'wide'
elseif (intQRS < 100) & (intQRS > 50)
        pass_status.QRS = 'normal'
else
        pass_status.QRS = 'artefact'
end
goto next_rule
```

The ECG beats are then sorted to "clusters" defined by the cartesian product of the intervals. Such an approach has, at least for the clinicians, great advantage over the "black box" methods because the final decision can be easily explained. Moreover, such an approach enables to use the classification result for further classification stages without the need to recompute certain parameters.

3.2 Rule-Based Decision Tree Clustering Based on Fuzzy Intervals

The RBDT described in the previous section has a drawback when dealing with border casesv – e.g. two very similar ECG-beats can be classified differently only because their parameters are very close to the border of an interval resulting in categorizing each one of them to a different class. For this reason we propose a generalization of the RBDT and we replace the crisp intervals by fuzzy intervals.

Fuzzy sets [16] are a generalization of the classical sets. The membership function in the case of a crisp set can take the value of 1 ("belongs to") and 0 ("doesn't belong to"). The idea of fuzzy sets is to extend this set of truth values, i.e. the output of the membership function, to take values in the interval [0, 1]. This allows us to express the state of a partial belonging to a set which is useful in modeling vague values as e.g. "small", "medium", "great", etc. Interested readers may find more information e.g. in [17, 18].

The generalisation of the RBDT to fuzzy sets is in fuzzyfied intervals. This means that intervals may be overlapping.

3.3 Self organizing map ANN

The Self Organizing Map (SOM) artificial neural network (ANN) is an unsupervised clustering method [19]. The SOM consists of neurons organized on a regular low-dimensional grid. Each neuron is represented by a d-dimensional weight vector, where d is equal to the dimension of the input vectors. Each neuron is connected to adjacent neurons by a neighborhood relation, which determines the structure of the map.

The SOM is trained iteratively. For each training step, one sample is presented to the SOM input level. Distance between the sample and all the weight vectors of the SOM is calculated using selected distance measure. The closest neuron is called the Best-Matching Unit (BMU) [19]. After finding the BMU, the weights in the SOM are updated so that the BMU moves closer to the input vector in the input space. This is repeated until the stopping criterion (for example, as in our case, the number of learning steps) is reached.

In this particular case the implementation of SOM is based on MATLAB's SOMToolbox [20]. The selected SOM consists of 15x9 neurons in a hexagonal grid arrangement and we test several different sizes before choosing the 15x9 grid architecture which gives the best results.

3.4 Template matching

For clustering methods as RBDT, fuzzy RBDT and SOM we carry out the classification step separately using the template matching method. This approach has been used widely and some recent experiments are presented at [21].

The template matching method in general tries to compare the several templates (in our case representatives of the N and V classes) with the investigated part of signal. Its similarity is then usually described by some distance measure.

Median of each cluster is compared with fifty different "N" and "V" templates – twenty five for each classification group. Then, correlation coefficients are computed using the classical approach.

For the final decision on the cluster medians, the appropriate coefficients are sorted in the descending manner. Then the majority 2 out of the first 3 rule is used to assign the class to the cluster median. All the beats in the cluster represented by the median are classified according to the classification of the corresponding median.

3.5 Support Vector Machines

Support Vector Machines (SVMs) are learning systems that are trained using an algorithm based on optimization theory [22, 23]. The SVM solution finds a hyperplane in the feature space that keeps the empirical error small while maximizing the margin between the hyperplane and the instances closest to it. Every new pattern x is classified to either one of the two categories (in case of dichotomizing problems $y_i \in \{-1, 1\}$ through:

$$f(x) = sign(\sum_{i=1}^{n} y_i a_i K(x, x_i) + b)$$

where b is a threshold parameter. The coefficients are found by solving a maximization quadratic programming problem which is "controlled" by a penalty factor C and are assigned to each of the training patterns x_i. The points for which $a_i > 0$, are called Support Vectors and are the points lying closest to the hyperplane.

The kernel function K implicitly performs the mapping from the input space to the feature space. Among others, the most popular kernels are the polynomial, the radial basis function networks and the two-layer perceptrons. In our experimental procedure we employ the radial basis function machines (the width s, which is common to all kernels, is specified also a priori by the user [24])

$$K(x, x_i) = exp(-\frac{1}{2s^2}\|x - x_i\|^2), i = 1 \dots l$$

3.6 Back Propagation ANN

Back Propagation Neural Network is probably the most well-known supervised learning technique used for training artificial neural networks. It trains feed-forward networks with one or more hidden layers. The algorithm [,] was introduced in 1974.

During the recall phase, the sample is presented to the network and values are propagated from inputs to outputs of the ANN. The difference between desired and actual outputs is calculated formulating the overall network's error. This error is propagated backwards from output neurons toward inputs. For each neuron its contribution to the output error is calculated and the weights of its connections are adjusted accordingly. The weights are adjusted using the gradient descent algorithm, which has the disadvantage

of getting trapped in local minimum. To overcome this, techniques like the addition of a momentum term, or the delta-bar-delta rule are used.

The back-propagation network used in this study (selected after thorough testing of different configurations) had 7 neurons in the first hidden layer and 4 neurons in the second. For training of the ANN, the standard BP algorithm is implemented in WEKA [25] with momentum and decreasing learning rate.

3.7 Radial Basis Function ANN

Radial Basis Function (RBF) ANN is trained with a fast supervised learning algorithm which is suitable both for regression and classification. It consists of one input, one output and one hidden layers, which contain RBF neurons. Each RBF neuron is described by a transfer function

$$y = exp(-\frac{X_i - C_i}{s^2})$$

that represents a d-dimensional Gaussian "bump" (where d is the dimension of the input vectors), with the center at a point C_i and a width s. Output neurons calculate the weighted sum of RBF neurons output. Training of the network is divided into two phases. In the first phase, C_i and s are set for each RBF neuron. The second phase adjusts weights of output neurons. The details can be found in [26].

4 Specificity and Sensitivity

Specificity and Sesitivity are measures of binary classifier quality. Pripary use of this measures is in medicine where it says how successful is the method in diagnosing healthy and ill people. But nowadays they are also used in other fields.

In Specificity and Sensitivity analysis are also important terms true/false positive and true/false negative. In our work we will use there terms as follows:

- "true positives" ... correctly classified as abnormal (the group "V" in our case).
- "true negatives" ... correctly classified as normal (the group "N" in our case).
- "false positives" ... incorrectly classified as abnormal.
- "false negatives" ... incorrectly classified as normal.

From true/false positives and true/false negatives we will compute sensitivity and specificity as follows:

$$Specificity = \frac{NumberofTrueNegatives}{NumberofTrueNegatives + NumberofFalsePositives}$$

A specificity says how many people will the test correctly recognize as healty. The value of 100% means that the test recognizes all healthy people as healthy and lesser values means that also some ill people are classified as heatly.

$$Sensitivity = \frac{NumberofTruePositives}{NumberofTruePositives + NumberofFalseNegatives}$$

A specificity says how many people will the test correctly recognize as ill. The value of 100% means that the test recognizes all ill people as ill and lesser values means that also some healty people are classified as ill.

5 Data, Preprocessing and Features

5.1 Heart beat databases

For training and testing the previously described methods, the MIT-BIH arrhythmia database [10] and the AHA database [11] are used. From both databases, thirty minute long segments annotated by experts are used. Since we focus on the discrimination between ventricular and normal beats, only beats labeled as 'V' or 'N' are selected for the classification purposes.

5.1.1 MIT-BIH database

The beats annotated as right ('R') or left ('L') bundle branch blocks ('BBB') are relabeled as 'N' since the annotations 'R' or 'L' represent morphology of the beat instead of the site of beat origin, which we are interested in. Our final set contains 89724 'N' and 6895 'V' beats from MIT database.

5.1.2 AHA-database

It is important to note that the AHA database does not have the Supra Ventricular complexes labeled 'S', which are available in the MIT database but they are labeled as normal 'N' instead. The records from the AHA database are divided into eight classes of ten records each, according to the highest level of ventricular ectopy present:

- no ventricular ectopy (records 1001-1010)
- isolated unifocal PVCs (2001- 2010)
- isolated multifocal PVCs (3001- 3010)
- ventricular bi- and trigeminy (4001 -4010)
- R-on-T PVCs (5001 - 5010)
- ventricular couplets (6001 - 6010)
- ventricular tachycardia (7001 - 7010)
- ventricular flutter/fibrillation (8001 - 8010)

We select only these records from the AHA database whose final structure would be similar to that of the MIT-BIH database. Therefore, we exclude all records from last two classes (7001 through 8010) and also the difficult to measure R-on-T recordings (5000 through 5010). In total, we choose 110083 'N' and 8333 'V' beats from the AHA database.

5.2 Preprocessing of the signal

Power line interference is filtered using an adaptive filter. Low-frequency drift is filtered during the pre-processing phase using a Matlab-designed high pass filter with cut off frequency at 0.66Hz [27].

Then the preprocessed signal is analyzed and the typical points on the ECG curve are measured out using gradient methods on appropriately filtered signal. We measure out the beginning and the end of the QRS-complex, along with the maxima of the complex (the highest R peak). Toff position is determined and the P-wave existence measurement is carried out.

5.3 Features

We compute eight parameters that characterize the shape of each ECG beat as shown in Table 5.2. Our shape-descriptive features selection is based on our previous work [15]. We select only those features that are performing well. An additional reason which justifies our selection is that most of these features are widely accepted and understood by the medical community.

The amplitude features represent maxima of the amplitudes. The ratio features represent the ratios of the amplitudes of the main deflections. Two well-known intervals – width of QRS complex and corrected QT interval (using Fridericia equation [27]) are computed as well. Generally they discriminate pathological beats from the normal ones.

5.4 Training and testing sets

Since the local training needs a rather complicated a-priori annotation of the part of the signal, we choose the global training. For this global training, one of the databases plays a role of a training resp. testing set and the other one is used as a training resp. testing set. For the purposes of the ANN and SVM training, subsets with even representation of the V and N beats are randomly selected.

For the template matching technique 25 representatives of the N and V templates are selected from the training database.

6 Results

Now we will sumarize our results.

For RBDT, fuzzy RBDT, and SOM methods, which are primarily acting as clustering methods, template matching technique is used to enforce classification. In the case of ANN the algorithms are implemented in WEKA [25]. SVM classifiers are trained using different combinations of the hyperparameters C and ρ which lead to different values of sensitivity and specificity.

We will present our results in Tables 2 and 3.

First in the Table 2 we will present results for training data. As you may see almost all methods achieved great specificity and sensitivity results. Both values are often higher than 90%.

Now if you look at table 3. Now results are not so good as in previous case. In gereral the specificity parameters are still good but sensitivity is poorer. Also Table 3 shows that in general results are mutually comparable. The best classifier seems to be the SVM which achieves the best values for sensitivity although it does not ahcieve top values for specificity.

All presented methods have much better Specificity parameter, which means that all methods easily recognizes normal beats as normal, but also small number of ventricular beats is classified as normal. The other parameter – specificity – is quite poor and it means that many normal beats are classified as ventricular.

This is also problem of the GAME neural network. More it achieves very poor results. In the next part we try to find out why.

FEATURES USED FOR ECG BEAT DESCRIPTION			
Amplitude of wave peaks		Ratios of peak amplitudes	
Width of intervals		ampR	ratRT
intQRS	ampS	ratRS	intQTc
ampQ	ratQR	ampTpos	ampTneg

Tab. 1. Features extracted from the signal

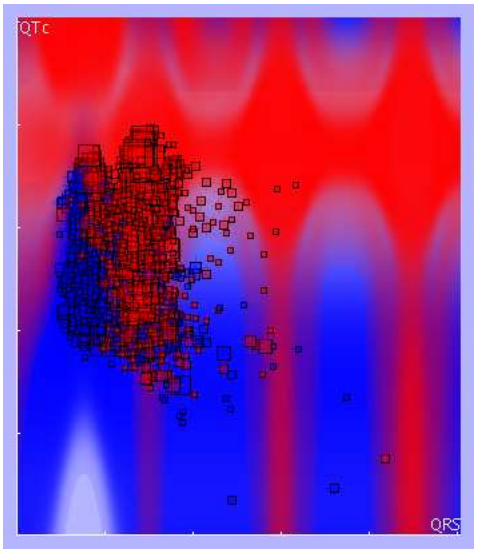

Fig. 3. Visualisation of GAME models. This figure shows model results for training data.

First, figure 3 shows situation for training data. The background represets response of trained models to changes in QRS x QTc pane, while other input attributes remain constant. These input attributes we have chosen because we determined them as the most significant. The red area represents space where ventricular beats are classified and the blue represents space where model recognizes normal beats. Each heart beat is represented by one square. Red squares represent ventricular 'V' beats and blue squares represents normal 'N' beats. The figure shows that

- there is no clean boundary between normal and ventricular beats in this pane. And some normal and ventricular beats are mixed, especialy in bottom and left part.
- the models were able to learn correct respponses.

The figure 4 shows respones for two selected testing recordings. The models are the same and therefore is the background picture. But on the left part of the figure 4 the beats are biased and all normal beats belongs to ventricular area. For other input attributes the situation is similar and therefore all beats are misclassified. This case requires an expert in cardiology who can decide if this recording is correct and correctly classified.

The right side of the figure 4 show much better image. Normal and ventricular beats are in proper places and this recording is classified with much better accuracy.

	Trained on MIT database		Trained on AHA database	
Method name	Specificity [%]	Sensitivity [%]	Specificity [%]	Sensitivity [%]
GAME	94.36	93.22	88.85	87.87
RBDT	94.68	92.40	79.17	92.33
fuzzyRBDT	98.49	95.88	77.66	91.02
BP NN	91.21	91.12	90.71	96.70
RBF	84.58	91.21	91.26	91.15
SOM	96.27	65.27	97.80	56.43
SVM	97.30	94.01	98.50	93.47

Tab. 2. Results for traing data

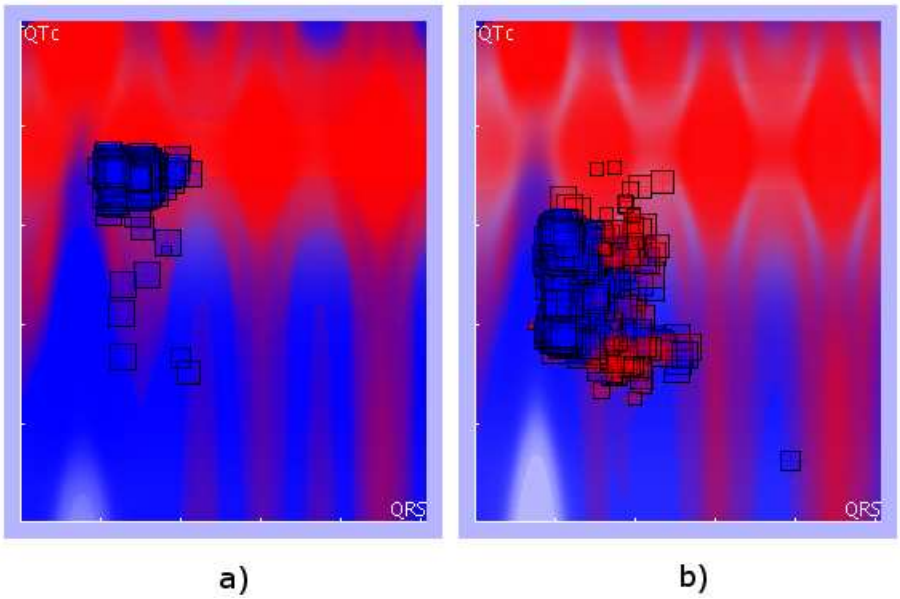

Fig. 4. Visualisation of GAME models. Figure a) shows example of completely misclassified testing dataset – almost all normal beats are classified as venricular. Figure b) shows example of testing set where classification accuracy was much better.

The relative complexity of decision boundary may suggest that created model may be overfited. To accept or reject this hypothesis we created another experiment. In this experiment we simplified the configuration of the GAME neural network. The simplier configuration means that only very basic types of neurons are available to training algorithm. This means that the decision boundary is much simplier and also that the model is harder to overfit.

The results for testing data in terms of specificity and sensitivity are summarized in table 4.

The decision boundary and the situation for training data is on the left part of figure 5. Now the decision boundary looks much simplier.

For other methods we were unable to collect figures similar to 4 or 5. This is because of limitations of software used to generate other models.

This will be subject of future work because the comparison of decision boundaries between GAME models and models generated by other methods should be the most interesting.

	Tested on AHA database (MIT Trained)		Tested on MIT database (AHA Trained)	
Method name	Specificity [%]	Sensitivity [%]	Specificity [%]	Sensitivity [%]
GAME	95.41	49.57	94.04	53.00
RBDT	64.31	77.27	64.75	72.61
fuzzyRBDT	73.60	79.43	80.50	71.61
BP NN	94.14	33.71	91.08	49.56
RBF	90.37	67.64	85.89	45.10
SOM	93.65	50.26	97.64	62.31
SVM	92.18	81.74	90.35	83.95

Tab. 3. Results for training data

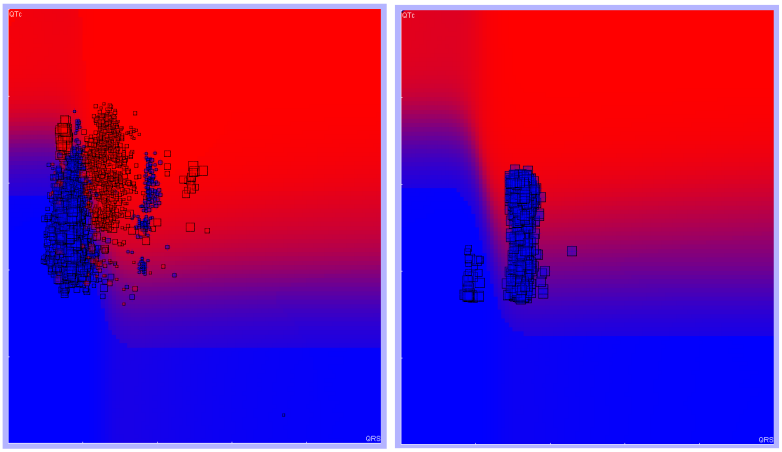

Fig. 5. Visualisation of GAME models. Experiment with simple configuration. The left part (a) shows the decision boundary and classification spaces for training data. The right part (b) shows selected testing recording and again illustrates problem with data – in the place where ventricular beats for training data, in testing data are normal beats.

6.1 Comments on Other Classification Methods

Among other methods the most usable seems to be RBDT decision tree. Its main advantage is its independence from the training set. It does not require any training for its clustering phase only for template matching. The rules are inferred from generalized knowledge and, therefore, are not affected by the structure of the database. Moreover, the decision tree algorithm is very fast and its decisions are easily to explain; this is an advantage in comparison with the ”black-box” methods.

Comparing the fuzzy RBDT to the classical RBDT, the fuzzy RBDT performs better on both databases. The reason is probably the higher number of final clusters due to much softer approach to the decisions, therefore more comparisons in the template matching phase. However, in RBDT there is only one way out from each node in case of fuzzy-RBDT there are more ways possible. The intention of fuzzy RBDT is to prepare a background for an automatic diagnosis based on fuzzy rules for a future work. Therefore, the fact that it performs better than the RBDT and its results are comparable to the global results [8] means it can be considered as a promising method.

BP, SOM and RBF ANNs are well known methods with a lot of applications in pattern analysis [24]. All the NNs exhibit high sensitivity on both testing sets. However, the specificity is low. The reason may be overtraining of the nets. RBF NN is performing very well when the AHA database features are used as the training data and the MIT database is used for testing, however the performance on the AHA database shows very low specificity.

The performance of the SVM method, even though it is not the best overall performance in any of the four measurements, is rather good and balanced on both data sets but the time cost for training is quite high.

	Tested on AHA database (MIT Trained)		Tested on MIT database (AHA Trained)	
Method name	Specificity [%]	Sensitivity [%]	Specificity [%]	Sensitivity [%]
GAME testing data	94.4	46.76	94.95	53.0

Tab. 4. Results for experiment with simple configuration

It is clear that the performance of most algorithms decreases slightly when using the AHA database. Due to the fact that the first database employed in our research is the MIT database we might have chosen rules and features according to this database. Therefore, the features extracted may be more ”tuned” towards the description of the MIT database. It turns out that the AHA database is a bit different - containing some cases that deviate from those in the MIT database. Also the variety of the features in the AHA database allows better training then the more compact MIT database. In our future work, we will try to extract features that are more insensitive to specific databases in an attempt to produce a classification scheme that will be able to generalize well under any data set condition.

7 Conclusion

The main purpose of this study is to compare and evaluate different approaches based on different principles. We choose to evaluate the examined methods using global training/testing sets that are fully independent from each other. The results shown in Table 2 and Table 3.

Examined methods achieves variable performance. The best method is SVM followed by GAME, fuzzyRBDT and SOM. From practical point of view the RBDT is also interesting becouse of medical staff which preferes methods that can easily explain its decisions.

All methods perform better when the AHA database is used as training set and MIT as testing set. The reason for this behaviour lies probably in the larger variety of records of the AHA database.

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References

[1] N. J. Holter. New method for heart studies. *Science*, 134:12141220, October 1961.

[2] P. de Chazal, O. O’Dweyr, and R. B. Reilly. Automatic classification of heartbeats using ecg morp. heartbeat intervals features. *IEEE Trans. on Biom. Eng.*, 51(7):11961206, 2004.

[3] D. Cueasta-Frau, J. C. Perez-Cortes, and G. Andreu-Garcia. Clustering of electrocardiograph signals in computer-aided holter analysis. *Computer methods and programs in Biomedicine*, 72:179196, 2003.

[4] G. Moody and R. Mark. Qrs morphology representation and noise estimation using the karhunen-loeve transform. *Computer Cardiology*, 16:269272, 1989.

[5] M. Lagerholm, C. Peterson, L. Edenbrandt, and L. Sornmo. Clustering ecg complexes using hermite functions and self-organizing maps. *IEEE Trans. on Biom. Eng.*, 47:838848, 2000.

[6] I. Christov, G. G. Herreto, V. Kraseva, I. Jekova, A. Gotchev, and K. Egiazarian. Comparative study of morphological and time-frequency ecg descriptos for heartbeat classification. *Medical Engineering & Physics*, 28:876887, 2006.

[7] M. G. Tsipouras, C. Voglis, I. E. Lagaris, and D. I. Fotiadis. Cardiac arrythmia classification using support vector machines. *The 3rd European Medical and Biological Engineering Conference*, 2005.

[8] G. Bortolan, I. Jekova, and I. Christov. Comparison of four methods for premature ventricular contraction and normal beat clustering. *Computers in Cardiology*, 32:921924, 2005.

[9] Y. H. Hu, S. Palreddy, and W. J. Tompkins. A patient-adaptable ecg beat classifier using a mixture of experts approach. *IEEE Trans. on Biom. Eng.*, 44:891900, September 1997.

[10] A. L. Goldberger, L. Amaral, L. Glass, J.M. Hausdorf, P.C. Ivanov, R.G. Mark, J. E. Mietus, G. Moody, C. K. Peng, and H. E. Stanley. Physiobank, physiotoolkit and physionet: Compnents of a new research resource for complex physiologic signals. *Circulation*, 101(23):e215e220.

[11] The American Heart Association. *AHA-Database. AHA Database Series 1*, aha database series 1 edition, 1997.

[12] J. A. Muller and F. Lemke. *Self-Organising Data Mining*. Berlin, 2000.

[13] H. Madala and A. Ivakhnenko. *Inductive Learning Algorithm for Complex System Modelling*. CRC Press, 1994.

[14] Pavel Kordk. *Fully Automated Knowledge Extraction using Group of AdaptiveModels Evolution*. PhD thesis, Czech Technical University, Prague, March 2007.

[15] V. Chudacek, L. Lhotska, C. Stylios, G. Georgoulas, and M. Staviar. Comparison of methods for premature ventricular beat detection. *ITAB Conference*, 2006.

[16] Zadeh L. Fuzzy sets. *Inform. Control*, page 338353, 1965.

[17] Klir. G. J. and Yuan B. *Fuzzy Sets and Fuzzy Logic: Theory and Applications*. Prentice Hall, 1995.

[18] Nguyen H. T. and Walker E. A. *A First Course in Fuzzy Logic*. CRC Press, 1997.

[19] Kohonen T. *Self-Organising Maps*. Springer, 1995.

[20] Vesanto J., Himberg J., Alhoniemi E., and Parhankangas J. Self-organising map in matlab: the som toolbox. *TOOLMET*, 2000.

[21] Chiu C., Lin T., and Lau B. Using correlation coefficient in ecg waveform for arrhythmia detection. *Biomedical Engineering Application, Basis and Communication*.

[22] Burges C. J. C. A tutorial on support vector machines for pattern recognition. *Data Mining and Knowledge Discovery*, vol. 2(no. 2):pp. 121167, 1998.

[23] Muller K. R., Mika S., Ratsch G., Tsuda K., and Scholkopf B. An introduction to kernel-based learning algorithms. *IEEE Trans. on Neural Networks*, vol 2(no 2):pp 181201, 2001.

[24] S. Haykin. *Neural Networks: A Comprehensive Foundation*. Prentice Hall, 1999.

[25] I. Witten and E. Frank. *Data Mining Practical Machine Learning Tools and Techniques*. Elsevier, 2005.

[26] Buhmann M. D. and Ablowitz M. J. *Radial Basis Functions: Theory and Implementations*. Cambridge University, 2003.

[27] Daskov I. K., Dotsinsky I. A., and Christov I. I. Development in ecg acquisition, preprocessing, parameter measurement and recording. *IEEE Eng Med Biol*, vol 17, 1998.