Myocardial Ischemia Event Detection based on Support Vector Machine Model using QRS and ST Segment Features

Rudys Magrans[1,2], Pedro Gomis[1,2], Pere Caminal[1,2]

[1] ESAII Dept, EEBE, CREB, Universitat Politècnica de Catalunya, Barcelona, Spain
[2] CIBER – BBN (Bioenginering, Biomedicine and Nanomedicine), Spain

Abstract

This study aimed to develop a nonlinear support vector machine (SVM) model to detect ischemic events based on a dataset of QRS-derived and ST indices from non-ischemic and acute ischemic episodes.

The study included 67 patients undergoing elective percutaneous coronary intervention (PCI) with 12-lead continuous and signal-averaged ECG recordings before and during PCI. Fifty-four indices were initially considered from each episode. The dataset was randomly divided into training (80%) and testing (20%) subsets. The training subset was used to optimize the SVM parameters algorithm and for determining the most important statistically significant indices, by using repeated k-fold cross-validation (with N=25 repetitions and k=5). The described procedure was run on 25 randomized training/testing subsets to assess the average performance.

On average, the most important indices were the QRS-vector difference and the ST segment level at J-point + 60 ms computed from the synthesized vector magnitude, and the summed high-frequency QRS components of all 12 leads at 150 – 250 Hz band. The performance of testing was: classification error = 12.5(8.3 - 16.7)%, sensibility = 83.3(75.0 - 91.7)%, specificity = 91.7(83.3 - 91.7)%, positive predictive value = 90.9(83.0 - 92.3)% and negative predictive value = 85.7(80.0 - 91.7)%. The method used to construct the SVM model is robust enough and looks promising in detecting acute myocardial ischemia and myocardial infarction risk.

1. Introduction

Detection of acute myocardial ischemia is habitually analysed by the predictive power of ST-segment deviation in the standard 12-lead ECG [1]. However, other indices associated with the ventricular depolarization have also been considered to improve the diagnosis of ischemia. These QRS-derived features include the R-wave amplitude change [2], QRS area, QRS-vector difference [3] and high-frequency QRS (HFQRS) [4], computed on 12-lead ECG, the vectorcardiogram (VCG) or signal-averaged ECG (SAECG). Most of them have been individually studied, thus it is not clear what the relationship among them are. It has been found that several parameters are closely interrelated, providing in consequence little different value than others that have proven to be most significant in identifying patients with myocardial ischemia at risk of suffering heart attack.

Machine learning techniques have been used as statistical models for classification in many areas. Among these techniques, support vector machines (SVM) have been proved as an efficient classifier in diverse fields, including medicine [5]. SVM models can include individual depolarization and repolarization indices to take decisions about normal and ischemic events. The amount of QRS-derived recently studied and the traditional ST-segment deviation as markers of myocardial ischemia can be integrated in a SVM model used to detect these events. The aim of this study was developing a nonlinear (Gaussian kernel) support vector machine model to detect ischemic events based on a dataset of QRS-derived and ST indices from non-ischemic and acute ischemic episodes.

2. Methods

2.1. Population and data acquisition

Sixty-seven patients from the STAFF III database [6] were included in the study. The database comprises a set of records from 104 patients with stable angina pectoris who underwent elective percutaneous coronary interventions (PCI) at the Charleston Area Medical Center, WV. The occlusion periods were considerably longer than those in usual coronary angioplasty procedures due to the treatment protocol that included a single prolonged occlusion instead of a series of brief occlusions in each artery, a method used before coronary stents were widely available. The recordings at the end of the occlusions are a very good model of hyper acute of

transmural ischemia. Inclusion criterion was occlusion duration of at least 3-min and strict criteria concerning the noise level in each of 12 leads of the ECG signal [7]. Balloon inflation periods ranged from 2.1 to 9.9 minutes (mean 4.7 min).

Continuous 9-leads ECG's (I, II, III (Mason-Likar electrode positions) and V1-V6) were recorded at 1 kHz, with 0.6μV of amplitude resolution with equipment provided by Siemens-Elena (Solna-Sweden). The three augmented aVL, -aVR and aVF were computed from the limb leads. For each patient, two ECG epochs were analysed for posterior signal averaging: (i) a pre-inflation ECG that was acquired during 5 minute before any catheter insertion, and (ii) the occlusion ECG recording which commenced about 1 minute before balloon inflation and continued during the inflation period and ended at least 3 minutes after deflation.

2.2. Signal averaging and data selection

Continuous ECG signals were averaged to ensure low noise level using two methods. For pre-inflation (control) ECGs conventional ensemble averaging was applied, whereas, for the occlusion ECG epoch an exponential averaging recursive technique was employed to track changes in QRS morphology [4]. Noise level was estimated in each lead of the bandpass filtered signal-averaged beat as the RMS value during 100 ms, starting 100 ms after QRS end [8]. The inclusion noise criteria were a noise level 0.75 μV of lower for each of the 12 individual leads and similarity of noise level, within 0.35 μV, between the control beat and the end of the occlusion (PCI) beat.

For each patient two SAECG beats were selected to assess the effect of acute myocardial ischemia provoked at the end of the occlusion period respect to baseline. The baseline beat (control) was selected from the pre-inflation ECG recording within the noise criteria. As occlusion-ischemic (PCI) ECG beat, the averaged beat at the end of balloon inflation was selected, since maximal myocardial ischemia could be expected to occur in the last part of the PCI procedure. However, if the noise criterion was not fulfilled then the previous averaged beat up to 20 sec backwards was chosen.

2.3. Set of ECG indices

The database is composed of 67 patients. For each patient, there is a total of p = 54 non-invasive measures from the SAECG for each episode (control and PCI period). Therefore, the dataset is composed of a total of N = 134 p-dimensional observations, belonging to one of two classes (control or PCI) balanced on the number of observations is concerned. The SAECG measures are described in Table 1. ST60 was calculated in each leads at ST-J point + 60 ms and ST60VM was computed from the vector magnitude. R-wave amplitude (ampR) for each lead, as ST60, was measured using the PR segment as the isoelectric level. QRSVD was computed from difference between the PCI and control QRS complexes areas in the VCG [3]. The QRS was band-pass filtering at the band of 150 to 250 Hz, using a Butterworth filter in a forward-backward fashion; then, HFQRS indices were obtained from the RMS value of the filtered QRS [4].

Table 1. SAECG-derived indices from each episode.

Index	n =12 indices, 1 *per* lead
ST60	ST-segment deviation J+60 ms
QRSA	QRS-complex area
ampR	R-wave amplitude
HFQRS	RMS of high-frequency QRS
	1 index, sum of 12-leads
Sum_ST60	ST60 sum, $\sum_{i=1}^{n} ST60_i$
Sum_QRSA	QRS area sum, $\sum_{i=1}^{n} QRSA_i$
Sum_ampR	ampR sum, $\sum_{i=1}^{n} ampR_i$
Sum_HFQRS	HFQRS sum, $\sum_{i=1}^{n} HFQRS_i$
	1 index, from vector magnitude, VCG
QRSVD	QRS-vector difference
STVM60	ST60 vector magnitude

2.4. SVM model

A support vector machine with a Gaussian radial basis function (RBF) kernel was used to build the prediction model, based on the recommendations of several studies [5,9]. Among several options, a strategy for efficient selection of the most important statistically significant variables was chosen.

Feature selection

Pre-processing of the set of variables firstly include a z-score transformation in order to normalize the data with mean equal to zero and standard deviation equal to one. This transformation facilitates the training algorithm to give the same weight to each variable. Secondly, the Wilcoxon signed-rank test was applied to compare if related variables between the episodes are different. A p-value < 0.05 was considered statistically significant. Out of the 54 variables used, 34 (63%) obtained p <0.05 and 21 (38.9%) p <0.001.

Then, the statistically significant variables were sorted according to their discriminatory power (high to low). The selection of the final subset of variables to construct the model was performed by forward stepwise selection algorithm. This procedure allows considering the

interaction between each of the variables and their effect on model performance. Here, the training set is used to select the variables and adjust the SVM model. This action of variable selection is incorporated within the cross-validation procedure for SVM parameters optimization algorithm described below.

Optimization of the model parameters

The grid search method with repeated k-fold cross-validation was used to optimize SVM algorithm parameters and generate the final prediction model. Briefly, the training observed subset D (about 80%) is randomly subdivided in *k* partitions for cross-validation. Each partition includes a training (L) and a validation (T) subset and predictive model f is generated for each value of the selected variables. Then, the model is applied to T and the procedure is repeated k-folds with k = 5. The procedure is repeated Nrep = 25 times, with a random subdivision of D in *k* different partitions each time and the errors are averaged. The model parameters were adjusted minimizing the misclassification rate function.

3. Results and discussion

Figure 1 (a) shows the evaluation results of the quality of training and how they are affected by having different sets of training/validation. Variability in the cross-validation error for the set of models generated with the best combination of parameters was low and also similar in the different training subsets tested (about 1% standard deviation). This shows the robustness of cross-validation methodology against different training/validation partitions of the training subset. Furthermore, the fact that variability is similar between different subsets of training indicates good parameter setting quality performed.

The assessment of the prediction model in terms of misclassification was done from the subset of independent testing data. Figure 1 (b) presents a description of the error distribution in cross validation and testing with independent data, evaluated on 25 different training/testing partitions. On average, the misclassification with independent data (in testing) was 12.5%, slightly higher than the error average obtained in the cross-validation (11.7%), as expected. However, the variability of the error was higher (20% range) than that observed in cross validation. This high relative variability may due to the low resolution in the error function due to the small number of observations included in the subset of testing (24 in total, 12 controls and 12 PCI). Note that each wrongly classified observation represents a variation in error testing with independent data of 4.16%. Anyhow, we have used other more appropriate measures than the classification error to characterize the ability of generalization of a model.

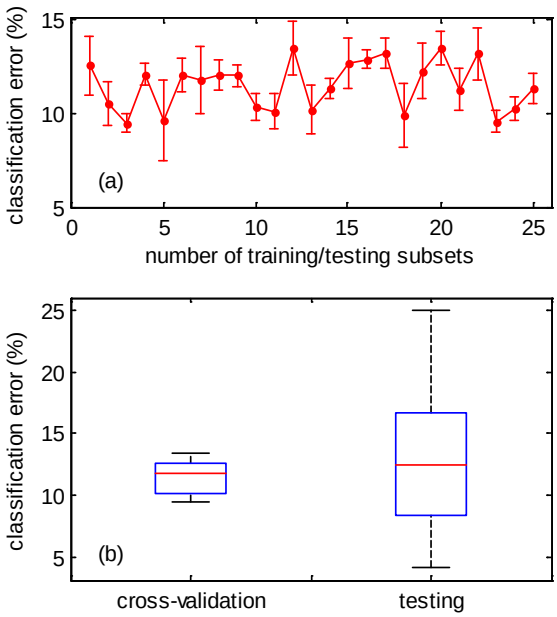

Figure 1: (a) Classification error (mean, SD) computed on the 25 repetitions of the cross-validation for each randomized training/testing subsets. (b) Distribution of the mean error in cross-validation and the classification error for testing on all the 25 training/testing partitions.

On average, the most important statistically significant variables were QRSVD, STVM60 and Sum_HFQRS, in that order. The QRSVD variable was selected in all tested partitions, STVM60 in 19 partitions (76% of the time) and Sum_HFQRS 12 times (48%). Figure 2 summarizes the maximum number of selected variables in each tested partition.

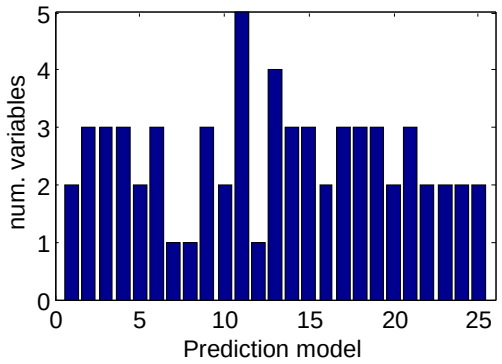

Figure 2. Number of statistically significant variables selected as the most important in different partitions.

Table 2 summarizes the sensitivity (SE), specificity (SP), positive predictive value (PPV) and negative predictive value (NPV) for the tested partitions. These four measures are more appropriate to characterize the final performance of the models that the classification error. The values of the quantities are quite good,

considering the small number of observations of the validation set, since that this limitation penalizes more those four measures than the classification errors. In this case, the resolution is lower, around 8%, because these measures are calculated on each class of the data subset. Therefore, the fact that the values of SE, SP, PPV and NPV reported in the table are not optimistic may be due to the small number of observations that make up the validation subset rather that the ability of models to separate observations of different classes.

Table 2. Percentiles 50 (25, 75) in (%) calculated on the 25 partitions training/validation tested.

Statistical measures	SVM classification
SE	83.3 (75.0, 91.7)
SP	91.7 (83.3, 91.7)
PPV	90.9 (83.0, 92.3)
NPV	85.7 (80.0, 91.7)

On average, the models generated following this strategy had a probability of about 91% in predicting ischemia and a probability of 86% in the no ischemic observations. We also believe that these values are highly reliable, due to the robustness of the procedure to adjust the algorithm parameters and determine the most important variables.

4. Conclusion

In this work the power of support vector machines have been used for predicting myocardial ischemia in a group of patients with occlusion of coronary arteries due to a PCI procedure. The feature selection was done using a univariate statistical test and an algorithm for selecting the most important variables sequentially, with SVM and cross-validation. The task of feature selection to identify the most important variables has been crucial because the presence of noise or redundant variables, and to avoid the known problem of high dimensionality. The values of SE, SP, PPV and NPV obtained are quite promise, and reliable, considering the values reported in previous studies. Finally, we believe that support vector machine models, with the strategy of including the most important statistically significant variables, could have clinical interest to identify patients in risk of myocardial infarction.

Acknowledgements

This work was supported by TEC2014-60337-R grant from the Ministerio de Economía y Competitividad (MINECO).

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Address for correspondence.

Pedro Gomis.
Universitat Politècnica de Catalunya,
Pau Gargallo, 5, ESAII, 08028 Barcelona, Spain.
pedro.gomis@upc.edu