Abstract— Acute hypotensive episodes (AHE) are serious clinical events in intensive care units. The prediction of occurrence of an Acute Hypotension Episode (AHE) up to an 1.5 hours in advance is to be made using two groups of ICU patient records from the MIMIC II Database from the Physionet. The physionet challenge is divided into two parts. The first part is to distinguish between patients who have experienced acute hypotension episodes and patients who do not. The second part of this challenge is to predict acute hypotension episodes. The technique proposed in this paper uses time domain features along with principal components of the Arterial Blood Pressure (ABP) waveform averaged over beats lying in each non-overlapping 60s interval for 1.5 hours prior to the start of the forecast window. Classification is performed with a simple Linear Support Vector Classifier (LSVC) after feature selection using genetic algorithms.

Keywords- Hypotension Prediction, Arterial Blood Pressure, Principal Component Analysis, Feature Selection, Support Vector Machine.

I. INTRODUCTION

The occurrence of Acute Hypotension Episodes is a critical event in ICU as it can cause multiple organ failure and result in death, so timely interventions can reduce the risk. We define an AHE as incidence in which one minute averages of ABP (mean arterial pressure) falling below 60 mmHg for at least 90% during any 30 minute period within interval. Prediction of AHE can provide medical experts enough time to prevent its occurrence through proper intervention. Therefore a methodology for predicting AHE can have a significant effect in decreasing mortality rates in ICUs due to AHE.

Physionet Challenge 2009 [1] is to forecast which subjects in the ICU would experience an AHE within a predefined forecast window of one hour using biomedical signals (ECG and ABP) data along with other physiologic information prior to the start of the forecast window (at time T0) as shown in fig. 1. The subjects are divided into two groups, H (patients with an AHE in the forecast window) and C (patients without an AHE in the forecast window). The H group is subdivided into two categories: H1 (patients who received a presser medication) and H2 (patients who did not receive a presser medication). The C group is also divided into two subgroups: C1 (patients without an AHE outside the forecast window) and C2 (patients with at least one AHE outside the forecast window). Physiologic data from patients in each of the four subgroups with correct classifications are provided as the training dataset. Physiologic data from patients with partial classification information are also provided as the testing dataset [1].

II. METHODOLOGY

Different steps are included in proposed approach. These steps are as shown in figure 2.

A. Data Acquisition
ABP waveform data for each subject has been provided by Physionet. This data is a part of MIMIC II database [2]. Length of collected data should be at least 10 hours so that it would be enough for analyzing. The sampling frequency of the ABP data is 125Hz. Figure 3 shows a typical ABP waveform. ABP data of 1.5 hour prior to the start of the forecast window is used in this study.
The goal of the feature selection process is, given a dataset that describes a target concept using ‘n’ attributes, to find the minimum number ‘m’ of relevant attributes which describe the concept as well as the original set of attributes do. Feature selection plays a central role in the data analysis process. In this work we analyze the performance of feature selection using Genetic Algorithms (GA) [7]. Each individual is taken to be a bit string Z. An active bit in this chromosome indicates that the corresponding feature will be used in the classification process. For each individual Z in the population, its fitness is evaluated by calculating the classification error for leave-one-subject out cross validation using features which have their corresponding bits active in the chromosome. Cross validation is based on features extracted above from each 60s intervals of ABP data of all records in the training set.

Different parameters used for GA run are as follows:[7]

- Population size = 30
- Max. Number of Generations = 150
- Max. Number of Stall Generations = 10
- Crossover = Scattered (Probability = 0.8)
- Mutation = Uniform (Probability = 0.05)
- Number of Elite Individuals Retained = 2

E. Feature Selection

The method presented in this paper is applied to the selected records from MIMIC II database. The leave one out
cross validation is applied to training set, for H/C classifier all the cases are well classified and got the resulting accuracy of 93% on the event 1 test set.

Table 1 presents the occurrences where AHE episodes have been identified for A and B records. A correct prediction of 10 out of 10 AHE for test set A is achieved.

| Dataset A  | 1, 2, 4, 9, 10 |

Table 1. AHE Detection

This result clearly illustrates the proposed scheme in predicting AHEs gives better efficiency and this method predict occurrence of AHE up to 1.5 hours in advance.

IV. CONCLUSION AND FUTURE WORK

This paper presents an effective technique for solving the prediction problem presented in event-1 of the Physionet Challenge 2009. The proposed method uses only 5 features and allows an approximately linearly separable boundary between two classes. Using genetic algorithm, number of feature reduces which causes reduction in complexity and computations, thus accuracy increases. This information can be used to develop better medication for patients with AHE and understand medical causes of occurrence of AHE.

In future, this algorithm can be extended for event-2 of the physionet challenge and to the design of a more practical AHE prediction system which can be deployed in ICUs.

REFERENCES


