Detection of Hypertension Through Features from Heart Rate Variability and Machine Learning Analysis

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Aims: Hypertension (HT) is a major factor leading to all-cause mortality. Strong connection between HT and autonomic modulation has brought heart-rate variability (HRV) to the forefront of HT analysis. Nevertheless, little is known on whether HRV is still efficient in HT detection under the coexistence of severe pathologies. The present study aims to define the best set of features to optimize the HT detection using machine- learning (ML) techniques.

Methods: 202 5-minute ECG recordings from the MIMIC-II database were extracted and resampled to 500 Hz. Recordings were classified by blood pressure (BP) into normotensive (NT), prehypertensive (PHT) and hypertensive (HT) with a cut-off BP of $< 120/80$ mm Hg, $\leq 139/89$ mm Hg and $\geq 140/90$ mm Hg, respectively. Time-, frequency-domain and Poincaré HRV features were utilized. Multi-class and between-class comparison was performed with non-parametric tests and SVM, kNN, AdaBoost and trees classifiers with 10-fold cross-validation and a 20% test set. 1-vs-all analysis was also performed.

Results: Statistically significant differences ($p \leq 0.022$) were found in PHT-HT, NT-HT and NT-vs-all and HT-vs-all comparison for most HRV features. Differences were more prominent in HT group ($p \leq 0.0003$). The best multi-group classification accuracy was 95% using median normal-to-normal (NN) interval, SD of NN (SDNN), variance of NN (VARNN), root-mean-square of SD of NN (RMSSD), pnn50 and very low frequency (VLF) features. 1-vs-all analysis showed HT detection accuracy of 87.5% using SDNN, VARNN, pnn50, low frequency (LF), high frequency (HF) and SD1 of Poincaré plot and NT detection accuracy of 95% using VARNN, LF, HF and SD1.

Conclusions: HRV can be used to monitor BP in critically-ill patients. The suggested models can be easily implemented and achieve high classification accuracy. The results suggest the use of the proposed models in order to detect HT or HT-prone patients in diseased population.