A Method Based on HMM for Early Prediction of Sepsis

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Introduction: This study aims to detect and predict sepsis precisely in ICU patients according to the data published for Physionet challenge 2019. Sepsis prediction can help in early intervention and therefore less mortality rate.

Methods: Consider the $n \times f$ data X, where n is the number of patients, f is the vector of features containing, vital signs, demographics, and lab values for each patient. Hidden Markov Model (HMM) can predict a sequence of sepsis states $s = [s_1, \cdots, s_n]$, where $s_i \in \{0, 1\}$ for a sequence of observations. In order to apply HMM on this multi-dimensional feature data, the weighted sum of features has been utilized as the observation sequence. The weights are calculated as the significance level of a paired t-test between features of sepsis and non-sepsis subjects, and only features with $p < 0.01$ are selected. The missing data are interpolated for every feature. HMM emission and transition matrices are then calculated by maximum likelihood estimation. And, the sepsis states of each patient is estimated by the Viterbi algorithm. Moreover, the posterior state probability, $P(\text{state=sepsis}|\text{Observation}_{1,\cdots,t})$, is computed at each time, t by the Forward-Backward algorithm.

Results: The algorithm is implemented for the public Physionet dataset consists of 1433 patients with hourly records. 10-fold cross-validation is used to evaluate the model. 0.84, 0.12, 0.85, and 0.09 are obtained for area under the curve(AUC) of ROC, AUC of precision, accuracy, and f-measure. A normalized utility function, created for the challenge, to evaluate the early predictions of sepsis is computed as 0.23 for the proposed method.

Conclusions and Perspectives: HMM is applied on an available clinical data with the independence assumption of features; however, to tackle this problem, Linear-chain conditional random field (CRF) is implemented in this study and the results will be compared to HMM in the final abstract.