Prediction of Sepsis from Clinical Data Using Long Short-Term Memory and eXtreme Gradient Boosting

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Abstract

Developing an objective and efficient computer-aided tool for early detection of sepsis has become a promising research topic. In this paper, we present two methods for early prediction of sepsis from clinical data. One is neural network-based method and the other is eXtreme Gradient Boosting (XGBoost) based method. Considering the temporal relationship between clinical data from sepsis patients in the ICU, we built a Long Short-Term Memory (LSTM) network to extract the intrinsic relation between different indicators in clinical data and meanwhile model the temporal dependencies, which only uses the previous information not future information to predict the results. Neural networks have made great achievements in unstructured data, such as image processing and speech processing, while traditional machine learning methods are better at processing structured data than neural networks. Thus, we trained an XGBoost model on the pre-processed data for improving the prediction accuracy. In official phase, we only used the first seven vital signs in our network, on test set A, the LSTM-based method has the utility score is 0.267 and the score of XGBoost-based method is 0.392. We submit the latter method as the final entry and the official final test utility score is 0.313. Our team name is CQUP’T Just Try, and the ranking is 15th.

1. Introduction

Since the concept of sepsis (i.e. Sepsis 1.0) [1] was proposed by the American College of Chest Physicians (ACCP) and the Society of Critical Care (SCCM) in 1991, research on sepsis has increased in recent years. In 2001, SCCM, ACCP, and the European Society for Critical Care Medicine (ESICM) held a joint meeting in Washington to revise Sepsis1.0, developed guidelines for medical treatment, and proposed a new diagnostic standard, Sepsis 2.0 [2]. But Sepsis 2.0 is too complicated, so it is rarely used clinically. In 2016, top scholars from the United States, Europe and Australia made a special group and proposed Sepsis 3.0 [3] based on big data analysis. Sepsis 3.0 is defined as a life-threatening organ failure caused by the body’s uncontrolled response to infection. Sepsis 3.0 uses SOFA definition organ failure and propose the concept of Quick SOFA (qSOFA) for quickly and easily to assess risk of suspected infection or clinical deterioration.

In recent years, despite the significant advances in antimicrobial treatment and organ function support technology, the mortality rate of sepsis is as high as 30%-70%. Moreover, the cost of treatment for sepsis is high and the medical resources are expensive.

The mortality rate of sepsis is positively correlated with the time of treatment delay [4]. Therefore, early diagnosis of sepsis is of great significance, not only can control the disease earlier, but also reduce unnecessary expenses for patients. In order to use the clinical data to early predict sepsis, we propose two methods, one is neural network-based method using LSTM algorithm, and the other is XGBoost [5] that is a traditional machine learning-based method.

2. Challenge Data analysis

The open training data published in challenge came from ICU patients in two independent hospitals [6]. The data for each patient will be contained within a single pipe-delimited text file. Each file has the same header and each row represents a single hour’s worth of data. Available 40 features consist of Demographics, Vital Signs, and Laboratory values. Statistically speaking, there are a total of 40,336 patient measurement records in the training set, and each row of records contains a single hour’s indicator data for the patient. The statistics show that there are 1,552,210 rows of data in the training set, and the imbalance of samples in the datasets is very serious. As shown in Figure 1, only 2932 of the 40336 subjects had sepsis, accounting for 7.27%, and the data
collected from patients with sepsis was only 27,916 rows, just only 1.8% of all data.

In summary, the three characteristics of the database increase the difficulty of finally prediction of sepsis.

3. Data processing

Based on the characteristics of the database, we perform two data pre-processing strategies: missing value filling and feature expansion.

3.1. Missing value filling

Due to the large amount of data missing and the inability to use post-time data when predicting whether there is sepsis at current time, the filling strategy we performed was as follows:

1) Along the timeline, when a data missing was encountered, the currently missing data was filled with the last non-missing data of previous data.
2) In LSTM-based method, the missing data remaining after step 1 was filled with value 0. Since XGBoost allows the existence of missing values, this pre-processing step is not performed in XGBoost-based method.

3.2. Feature expansion

We implemented two feature expansion methods. Considering that the early diagnosis of sepsis is not only beneficial to the treatment of patients, but also reduces the economic burden of patients. The challenge encourages the prediction of sepsis with 6 hours early in advance.

The training data is physiological and biochemical measurement data for each hour. The changes in physiological and biochemical indicators can reflect the health of the human body. This is an important basement for judging whether the human body is suffering from sepsis. In order to extract changes in physiological and biochemical indicators, the difference before 6 hours was calculated from the seventh hour. And not all of the features given by the training data are suitable for calculating the difference. We carefully selected 34 features for the extension of the feature difference.

Sepsis 3.0 emphasizes that Sepsis is the host's uncontrolled response to infection and life-threatening organ dysfunction. According to the Sepsis 3.0 standard, sepsis satisfies the following formula:

\[
\text{sepsis} = \text{infection} + (\text{SOFA} > 2) \tag{1}
\]

In 1994, ESICM presented the sequential organ failure assessment (SOFA) score in Paris [7]. The SOFA score can dynamically assess the condition of organ failure using limited routine measurements. According to some physiological indicators, the functional scores of 6 organ systems were estimated which to range from 0 (no organ dysfunction) to 4 (severe organ dysfunction), and the individual organ scores are then summed to a total score.
4.1. LSTM

Because most of the features have the characteristic of very serious values missing, it is not easy for training the LSTM. Moreover, considering the difficulty of data collection, here, we just use all the vital signs except EtCO2 to train the LSTM model.

LSTM is a neural network designed to process time series data, and the training data in the sepsis database includes hourly physiological and biochemical indicators. Therefore, considering the time dimension, it is very reasonable to use LSTM to treat sepsis data.

\[ X^T = X^t \quad t \in [1, T] \]  

\[ X^t = [x_1^t, x_2^t, \ldots, x_i^t, \ldots, x_j^t] \quad i \in [1, 7] \]  

Where suppose \( X^T \) is the data of a patient, \( T \) is the number of rows in a pipe-delimited text file, and each person is different. \( X^t \in \mathbb{R}^7 \) is a vector represents a row of data, and \( i \) denotes the \( i \)-th feature for training the LSTM.

![Figure 3: 5-layer LSTM network.](image)

In summary, we got 82 features, 40 are given by training data, and 42 (34+5+3) are obtained by expansion.

4. Method

Our proposed scheme includes two methods that are LSTM-based and XGBoost-based. The former can automatically extract features, the latter rely on artificial features design. We attempted to compare these two methods to find out which one is more suitable for predicting sepsis form clinical data.

4.1. LSTM

As show in Figure 3, we built a 5-layer LSTM network and the number of hidden neurons is 14, 28, 56, 112, and 224, respectively. LSTM accepts a sequence and processes it through internal neurons to output another sequence. For example, suppose \( X^t = [x_1^t, x_2^t, \ldots, x_i^t] \) is the first row of data record by a patient. A new sequence \( L^1 \in \mathbb{R}^{14} \) is output after the first layer of LSTM (i.e. LSTM_1) processing.

\[ L^1 = \hat{c}(H(X^t)) \]  

Where \( H() \) stands for processing of LSTM network, and \( \hat{c}() \) stands for relu activation function.

In a similar fashion, LSTM_5 output a vector \( L^5 \in \mathbb{R}^{224} \).

\[ L^5 = \hat{c}(H(L^4)) \]  

When the LSTM processes the data after the first line, the recurrent connections allow a memory which comes from previous inputs to influence the final network output. In order to get the final prediction, a fully connected layer with two neural units was built after LSTM. And a weighted cross-entropy function was adopted, learning rate was set to 0.01.

Due to the sample imbalance is too serious, and in order to increase the probability that one sample was predicted to sepsis, the final prediction probability of disease is the network prediction probability plus a constant 0.00024079.

4.2. XGBoost

Table 1: Conversion table for SOFA related features.

<table>
<thead>
<tr>
<th>Feature</th>
<th>Score 0</th>
<th>Score 1</th>
<th>Score 2</th>
<th>Score 3</th>
<th>Score 4</th>
</tr>
</thead>
<tbody>
<tr>
<td>Platelets</td>
<td>0.001</td>
<td>0.0005</td>
<td>0.0001</td>
<td>0.00005</td>
<td>0.00001</td>
</tr>
<tr>
<td>Bilirubin (mg/dL)</td>
<td>&lt;=0.1</td>
<td>&gt;0.1</td>
<td>&gt;0.2</td>
<td>&gt;0.3</td>
<td>&gt;0.4</td>
</tr>
<tr>
<td>Creatinine (mg/dL)</td>
<td>&lt;=0.2</td>
<td>&gt;0.2</td>
<td>&gt;0.3</td>
<td>&gt;0.4</td>
<td>&gt;0.5</td>
</tr>
<tr>
<td>Mean arterial pressure (mm Hg)</td>
<td>&gt;=70</td>
<td>&lt;70</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
</tbody>
</table>

The qSOFA uses three of the most effective indicators for predicting poor prognosis in patients with Sepsis: respiratory rate (RR), Glasgow Coma Scale (GCS), and systolic blood pressure (SBP). Since the latest definition of septic shock focuses on lactate levels, we calculated three differences in this paper, and Table 2 shows the indicator and threshold.

Table 2: Selected indicators and corresponding thresholds

<table>
<thead>
<tr>
<th>Indicator</th>
<th>Threshold</th>
</tr>
</thead>
<tbody>
<tr>
<td>SBP (mm Hg)</td>
<td>100</td>
</tr>
<tr>
<td>RR (beats per minute)</td>
<td>22</td>
</tr>
<tr>
<td>Lactate (mmol/L)</td>
<td>2</td>
</tr>
</tbody>
</table>
XGBoost is a boosting algorithm, and works very well for dealing with structured data classification problems. The idea of the boost algorithm is to integrate a series of weak classifiers into a strong classifier and XGBoost builds many CART regression trees based on sample features and integrates them for final prediction. Specifically speaking, XGBoost randomly selects features based on the pre-set parameters and automatically selects the appropriate threshold to build a CART tree. Then iteratively repeats the tree-building operation until the number of trees reaches maximum depth which pre-set. Meanwhile, the early stopping technique can also be used to stop training when the increase in the number of trees is no longer bringing gain. According to the structure of the CART tree and the sample eigenvalues, each tree assigns each sample to the leaf node, and XGBoost calculates the final prediction result based on the predicted values of the leaf nodes of all the CART trees.

We use all 82 features to train XGBoost, in our model, the number of trees in the XGBoost is 16, the maximum depth of the tree is 10, learning rate is 0.01, minimum leaf node weight is 1, subsample rate is 0.8, column sample by tree is 0.8, column sample by level is 0.9, “reg_alpha” is 1, “reg_lambda” is 0.5, and “scale_pos_weight” is 5.5. We empirically select the threshold as 0.24, and the sample was predicted to sepsis when the prediction probability of the model is greater than the threshold.

5. Result

Our team name is CQUPT_Just_Try, in official phase, the method based on LSTM achieves utility score 0.267 on test set A, meanwhile the method based on XGBoost is 0.392. Thus we submit the method based on XGBoost as the final entry and get official final test utility scores of 0.313, 0.381, and -0.174 on full test set, test set B, and test set C, respectively. Our final ranking is 15th.

6. Conclusion

In this article, two methods that LSTM-based and XGBoost-based for predicting sepsis are proposed. By comparison, the second method has a higher utility score. We think the reason is that a large number of values in the training data are missing and a serious sample imbalance, which makes the neural network-based method very difficult to train. Since XGBoost is better at handling structured data and has a missing value processing mechanism, XGBoost achieves better results after feature filling and feature expansion.

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