Prediction of Intracranial Pressure Values of Traumatic Brain Injured Patients Using Hierarchical Temporal Memory Network

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Abstract. *The goal of this pilot study is to analyze intracranial pressure (ICP) data from a group of 42 patients and to build a Hierarchical temporal memory (HTM) model that will try to predict future ICP values. As a references, Support Vector Regression (SVR) with RBF kernel was used. To better compare the practical performance of the models, a binary alarm with threshold set to a value when a medical intervention is needed was used. The results show better recall and MSE for HTM while better false omission rate for SVR.*

Keywords: Intracranial pressure, Time series prediction, HTM – Cortical learning algorithms, Support vector regression

1. Introduction

Patients with severe traumatic brain injury (TBI) have a significant risk of hypotension, hypoxaemia, and brain swelling. Neurological damage invoked by these dangerous conditions may not occur immediately at the moment of primary injury at an accident scene, but evolves over time as a secondary injury. The secondary brain injury is the leading cause of in-hospital deaths after brain trauma and it is directly associated with the increase of intracranial pressure (ICP) and subsequent decrease in cerebral perfusion that brings about brain tissue ischaemia. As described in [1], organized emergency services can improve outcome for patients with severe TBI, provided the patients are immediately transported to an Intensive Care Unit (ICU) which has possibilities to monitor the ICP values permanently.

ICP is measured in millimeters of mercury (mm Hg) and, at rest, normally varies between 7–15 mm Hg for adults [2]. 30–40 mm Hg is the upper limit of ICP normality, and the values above this limit serve as an alarm for the initiation of special treatment [1]. Although, several neurological indicators are useful for the decision to trigger additional life-saving interventions in TBI cases, periodical (or continuous) measuring the ICP values represents the crucial indicator. Several papers were published ([3, 4]) in which attempts to analyze/evaluate inner structure of the ICP waveforms as functions of time have been described.

In our paper we treat the discretized (with the one-hour time step) ICP records as time series and investigate whether predicted ICP values can provide additional information important for making medical decisions on special TBI treatment initiation. Assuming similar causes of changes in ICP for various patients we propose to use a predictive model capable of learning from multiple independent time series. In order to allow for using the model for online analysis of the live ICP measurements at ICU we furthermore propose to use a model that provides online learning and inference. Currently, to our knowledge such criteria meet only Hierarchical Temporal Memory (HTM) with its up-to-date learning algorithms called *Cortical Learning Algorithms* (CLA) [5]. As a reference we used Support Vector Regression (SVR) model in a simulated online mode.

2. Subjects and Methods

Dataset

For our pilot study a set of clinical records of ICP for 42 TBI patients in the period of maximally 10 days were available. Within these data 30 records belonged to those patients who had survived and had been discharged from ICU in a stabilized state. 12 patients have deceased. Due to the various clinical limitations, the ICP recording was performed as non-overlapping one-hour intervals characterized by maximum values within those intervals. These maxima represented a discretized version of an ICP record (sequence). The starting time of the ICP records varied for individual patients, and for the survived patients the maximal duration of the ICP measurement was set to 10 days (240 time instants). The clinical protocol also lead to occasional discontinuity in the ICP recording caused by necessity to disconnect a patient for the time of examination at another clinical department. The remedy for all of such missing values has been made by linear interpolation of data. For each patient, there is a label of his/her state (lethal or vital) assessed at the time he/she left the ICU, however, this information was not used during learning.

Hierarchical Temporal Memory

Hierarchical temporal memory (HTM) is a large-scale computational model of the algorithmic and structural properties of the neocortex developed by Hawkins, George, and their colleagues at Numenta Inc. [6]. The reference implementation is distributed in the NuPIC[1] package.

Recently, the initial HTM learning algorithms (Zeta1), have been replaced by a new generation, called Cortical Learning Algorithms (CLAs) [5]. The main change is that CLAs work with data encoded in binary representations where only small percentage of the bits are "on" at one time and each bit only partly captures the original data. This is called a *sparse distributed representations* (SDRs). SDRs enables HTM to become an online learning system that models complex time-varying data and makes continuous predictions about future inputs. The proper function of HTM required that input data are first encoded into SDRs in such a way that similar inputs map into similar representations, i.e., a small change in the SDR should not greatly change the semantics of the data after decoding. In terms of structure, HTM is a hierarchical memory model comprised of neurons, called *cells*, organized into a grid of columns which form an HTM region. Multiple regions may be connected to form a more complex hierarchy. Each column in a region is connected to a unique subset of the input bits. Due to local inhibition among columns, the activations of the columns in a region form a SDR as well. A very important feature is that activation of a column is context-dependent, thus HTM can learn to represent the same pattern in different temporal contexts. In a column, one or multi-step prediction is implemented by creating lateral connections between an active cell with a subset of previously active nearby cells. The formation speed of these connections can by adjusted by a learning rate parameter.

3. Prediction of ICP

The basic idea of how to utilize these data for making reliable clinical decisions in every moment of the development of patients' health conditions is to explore a possibility of ICP values prediction, which can be used, together with apriori setting of a critical ICP threshold, for alarm triggering. We argue that a prediction of future ICP values could help to indicate future states of a patient, and thereby to make the earlier decision on initiation of the special treatment protocol. Thus we propose a binary alarm indicator implemented as a threshold set to 35 mm Hg. The alarm indicator from the predicted ICP sequences should match the alarm indicator from

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[1]Numenta Platform for Intelligent Computing

original ICP sequences. There are 18 original ICP records (no. 2, 6, 7, 9, 11, 14, 15, 19, 20, 26, 27, 28, 33, 34, 35, 37, 38, and 39) for which all the ICP values are below the given threshold.

We have accomplished the "leave-one-out" cross-validation scheme, namely, for 42 sequences, one sequence was always selected as a test sample, while all 41 remaining sequences entered the learning procedure of the HTM network. These contain patterns common for both classes which can be helpful for the ICP values prediction. For the current ICP dataset we used one-step prediction. For a dataset or live measurements with shorter time scale (e.g., in order of minutes), a multi-step prediction might be necessary to better account of future trend. After the training phase, ICP data of the testing patient were put into the HTM network one by one, while a one-step prediction value was read out. With this procedure, HTM can calculate informative prediction immediately after seeing the first ICP value measured, and simultaneously it continues learning from incoming actual data.

As a prediction method for reference we selected the well-known SVR model with RBF kernel applied to the same one-step prediction task. SVR was trained to predict next value from k previous values, i.e., ICP at time $t+1$ was predicted based on values at times $t-k+1,...,t$. For each test sequence, a training dataset from all other sequences was generated at first. Then, as the prediction for the test sequence progressed starting from the $(k+1)$-th value, this dataset was augmented with new training data from the test sequence and SVR was retrained, i.e., simulating online learning.

4. Results

We used a public NuPIC implementation of HTM in the version 0.2.1. The HTM network consisted of one region with 2048 columns and 32 cells per column. The learning rate parameter was set to 0.036. These and other learning and inference hyperparameters (described in [5]) were optimized using a cross-validation procedure with Mean Absolute Percent Error metric, which is a part of NuPIC. SVR used RBF kernel with parameter C set to 1000 and parameter γ set to 0.003. The window size k was set to 8. These parameters were found using a leave-one-out cross-validation scheme.

For the evaluation of the model predictions for each patient we used the mean square error (MSE) metric. Predicted binary alarms were evaluated using the recall and false omission rate (FOR) characteristics. Recall is defined as the proportion of number of true positives to the number of all ground-truth positives (all original alarms). FOR is defined as the proportion of the number of false negatives w.r.t. number of all predicted negatives. The rationale is that false negatives should be treated with more care due to higher associated health risk compared to false positives. Results for each patient and prediction method are shown in Fig. 1. In overall, averaged over all patients, the SVR model yields lower FOR (0.038 vs 0.031), however, the HTM model yields lower MSE (53.474 vs 62.522) and higher recall (0.265 vs 0.211).

5. Conclusions

The goal of this pilot study was to explore the usefulness of prediction of ICP for making earlier decisions on triggering a special treatment protocol. We considered the set of acquired ICP sequences as retrospective time series for which a task of prediction can be of value. We proposed to apply an HTM intelligent network, that can learn from all ICP sequences and generate one-step prediction. The prediction results achieved have been compared to the prediction results generated by a reference method of Support Vector Regression model with RBF kernel on the basis of recall, FOR, and MSE statistics. We can conclude that the HTM network manifested encouraging results that deserve to be extended further in the ongoing research. Future research
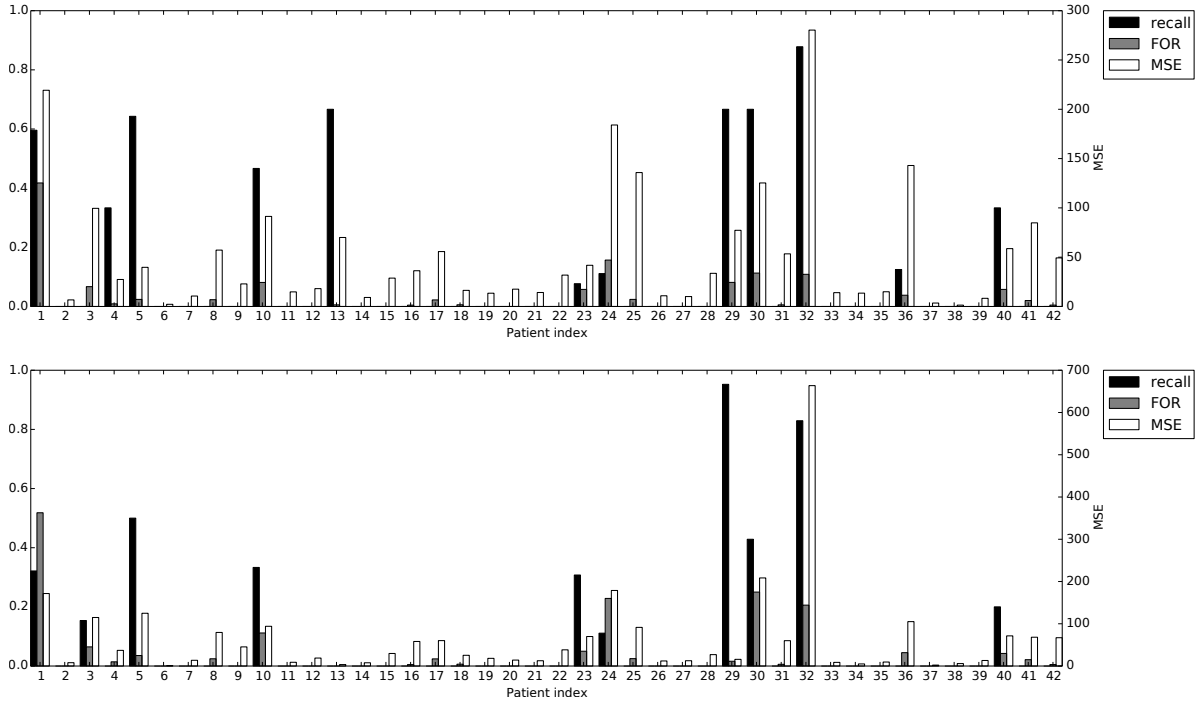
Fig. 1: Recall, false omission rate (FOR), and mean square error (MSE) for all patients for HTM (top) and SVR (bottom) predictors. Note that MSE has different scale, located on the right.

could also include combining these or similar models that have complementary performance.

Due to a lack of detailed information on medical conditions of patients with TBI at the time ICP starts, the analysis we proposed could not be complete. For more comprehensive exploration of retrospective data mining form ICP records complementary medical information will be needed.

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