Fuzzy Signatures for BiDirectional Neural Network Classification

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Abstract. The multi-class classification in medical diagnosis problem requires extracting important features from patient readings to produce a prediction. Our dataset contains 1000 entries from SARS-CoV-1, high blood pressure, pneumonia patients and normal symptoms. We use a single hidden layer bidirectional neural network model, which has shown success in classifying data with noisy and missing attributes, to test a series of fuzzy signatures. Fuzzy signatures are vectorized representations of underlying relationships between fuzzy values of the SARS-CoV-1 dataset such as "slight", "moderate", and "high" for temperature readings. We aim to find the least amount of input features needed to train a perfect classifier. Previous work has investigated the importance of aggregation methods using fuzzy signature structures. Our method starts with the entire set of features and first applies aggregation methods and then removal to reach the minimal set of features. We find basic aggregation methods and removal of irrelevant features can achieve 100% classification accuracy using a fuzzy signature structure with five input features; "High" nausea, "yes" abdominal pain, "high" temperature aggregation, and "high" blood pressure aggregation, including one of the following: "slight" nausea, "medium" nausea, or "no" abdominal pain. We also find that more complex approaches and models are needed to handle highly dimensional datasets. Future research on the SARS-CoV-1 dataset could use pre-training techniques on a similar dataset.

Keywords: machine learning, neural networks, multi-class classification, fuzzy signatures

1 Introduction

Multi-class classification has a wide range of applications such as object recognition, medical diagnosis, speech recognition, and text recognition. In these problems the goal is to take a number of features and predict the class which the features belong to. Neural networks can be used to extract features that may be difficult for humans to recognise easily. This gives neural networks their potential on multi-class classification problems. When solving these problems with many features there is the potential of noisy attributes to exist especially in real world data. These attributes are ones that do not contribute to the class for the classification problem and hence can cause issues with the neural network accuracy. There are several methods that can be used to overcome noisy attributes but, in this work, we have explored the use of fuzzy logic. Fuzzy logic allows the degree of membership rather than "true" or "false" from Boolean logic. Hence using the knowledge of the features in the dataset, we attempt to find aggregations based on a fuzzy signature [2]. We can then use the aggregations as input to the BDNN (BiDirectional Neural Network) [1].

BDNNs [1] have been shown to be useful for some real-world problems, and have potential for use in artificial data sets, with missing and noisy attributes. When features are missing, this neural network can use its reverse pass with back-propagation techniques to generate the missing features given an input. The neural network can also introduce bias in both forward and reverse directions to reduce the impact of noisy attributes on the model. We have used fuzzy signatures and BDNNs to predict and classify medical conditions from four datasets containing diagnostic symptoms of temperature at various times, blood pressure, conditions of nausea, and abdominal pains. For symptoms of temperature the data has been collected at the 4-hour intervals of 8am, 12pm, 4pm, and 8pm due to the nature of fevers [2]. The blood pressure symptoms are split into systolic and diastolic categories which represent the distinct readings of two different measurements. In the datasets, temperatures, blood pressures and nausea are divided into fuzzy sets of "slight", "moderate/medium", "high", and "yes" and "no" for abdominal pain. Overall, there are 23 features present in each dataset entry and each dataset contains 1000 entries of data relating to patients with high blood pressure, pneumonia, SARS (SARS-CoV-1), and normal condition, respectively.

In general, highly dimensional data requires a higher complexity of algorithms or neural network architecture [3], [4]. Otherwise, the time basic approaches take to produce meaningful results could be days or months. In this dataset, there are 23 input features which may be able to be reduced or removed to produce better results. Therefore, we have chosen a fuzzy signature approach to aggregation of multiple input features. This way we can use our knowledge of the dataset to improve the performance of our classification model. We use a BDNN to classify the aggregated attributes and to determine the effectiveness of the approach. This work aims to determine the usefulness of applying fuzzy logic to a multi-class classification problem.

2 Method

2.1 Data Analysis and Pre-processing

This work involves combining the four datasets of high blood pressure, pneumonia, SARS (SARS-CoV-1), and normal condition into a single dataset. Each dataset contains 1000 entries with the same 23 features mentioned above. Therefore, the classification problem is across 4000 rows and 23 columns. Intuitively, there are several columns in the dataset that are less important to classification and can therefore be seen as noisy attributes. This work aims to use fuzzy signatures to aggregate the columns of the dataset such that more useful columns remain. The multi-class classification problem we have outlined can be represented in many ways. However, our approach uses a single target column with integer values representing which original dataset the entry came from. In this case, the values for the four classes are: $\{$High Blood Pressure class $= 0$, Normal class $= 1$, Pneumonia class $= 2$, SARS class $= 3\}$. Therefore, the output of the classification model should be a number closest to the whole number representing the target class. Once the target label is assigned, the entire dataset is then shuffled to a randomised order.

Upon analysis of the SARS dataset, we can gather important understanding into how certain features are related to others. For example, high systolic and high diastolic blood pressures seem highly correlated in Figure 1. They form one tight cluster with zeros and another larger cluster greater than 0.5. However, there is a dense section of values above 0.8 in the second cluster. Whereas medium systolic and medium diastolic blood pressures create three clusters. A relatively tight cluster around and below 0.2, a moderate cluster greater than 0.2 and less than 0.5, and a loose cluster above. In this case when the values increase the clusters grow and become sparser. Finally, there are two clusters for the slight blood pressures. One like the dense section in high blood pressures where values are above 0.8, and another along the axis of diastolic values but remaining at zero for systolic. From these findings, we may decide to naively aggregate blood pressure into “slight”, “medium”, and “high” but findings suggest the most important component is the systolic blood pressure reading [8]. Therefore, future work could research the influence of these findings in the SARS dataset.

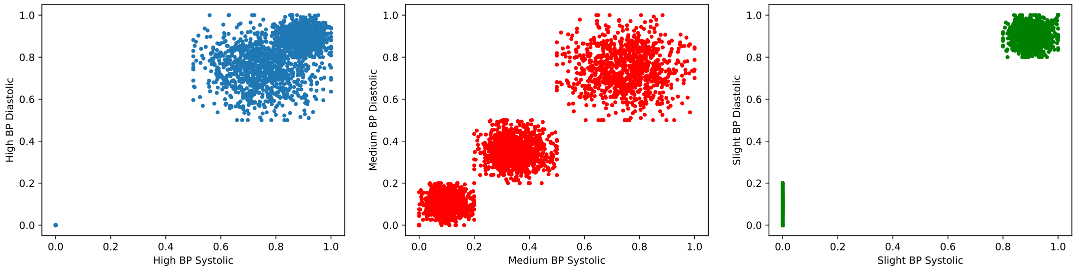

Fig. 1. Fuzzy values of high, medium, and slight for systolic against diastolic blood pressure attributes.

In addition to the analysis of the blood pressure attributes, the temperature attributes may be another avenue for reducing dimensionality. The dataset contains temperature at four different times of the day which reflects fluctuation throughout the day. Hence, taking the maximum of the fuzzy value of slight, moderate, and high across all time periods is one method of aggregating these series. Although, it is still unclear how the three fuzzy values relate to each other. Therefore, similarly to the blood pressure analysis, we take the maximum aggregation across the day and plot the fuzzy sets against each other in Figure 2. Interestingly, both the combinations of slight and moderate temperature, and slight and high temperature have an inverse relationship. Whereas moderate and high temperature have a positive correlation. Therefore, we can use this analysis of correlation to improve our fuzzy signature aggregation technique.

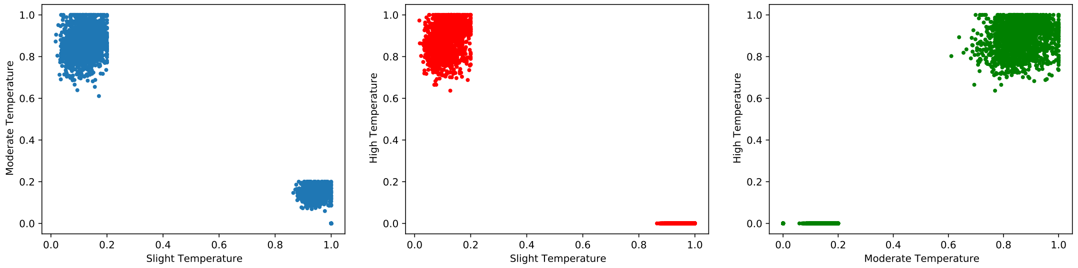

Fig. 2. Maximum aggregated fuzzy values of slight, moderate, and high for temperature attributes.

2.2 Fuzzy Signature

We would like to apply our knowledge of the dataset through aggregation of features to reduce the number of noisy attributes. This paper uses the idea of vectorized fuzzy signatures [2] to define the order to implement aggregation. One method for visualising the fuzzy signature is in a tree which shows the hierarchical structure. For our dataset, the general fuzzy signature shown in figure 3 has a depth of 3. Hence, we are treating each column in the dataset as a leaf or element in a vector. The parent node or vector represents the grouping of properties.

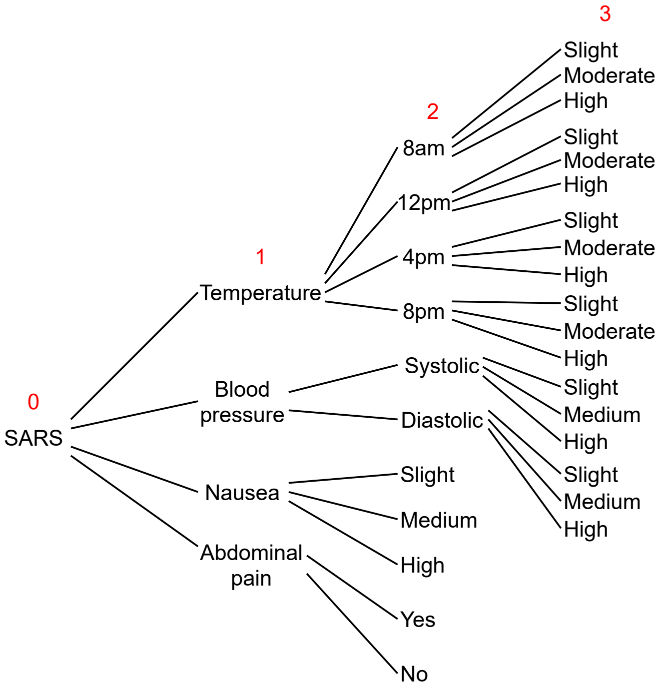

Fig. 3. General Fuzzy Signature of SARS entry with depth (red).

2.3 Testing Environment

To use of the properties discovered in the general fuzzy signature, we can choose a method of aggregation. In this paper we use four methods of aggregation; maximum, mean, minimum and mean maximum (see [2]). Hence, our aim is to find combinations of aggregation methods that finds the least number of input features needed to maintain a 100% training and testing classification accuracy. The computer hardware that was used in testing was an Intel i5-4690K CPU in the Pytorch version 1.8.1 environment.

Our work uses a BDNN model where forward and reverse passes are done in alternate steps each pass. Output is a classification value that corresponds to a target class. This can be rounded to the nearest whole number. The accuracy of the classification model is $number\ of\ correct\ predictions/number\ of\ targets * 100 = \%accuracy$. For each test, the train-test split is 80-20 which represents a reasonable amount of training data for this small dataset and a smaller test set for evaluating the performance of the aggregation method. We used the number of epochs of 500 which was adequate for most aggregation methods to begin converging on final loss. More specifically, this involves 250 forward steps and 250 backward steps using the BDNN method described.

The details of the BDNN are as follows and are illustrated in figure 4 (without hidden bias neurons). The model contains an input layer of varying number of neurons, a hidden layer with 23 neurons, and a single output neuron. The input layer varies as the aggregation method reduces the number of columns. The choice of hidden layer nodes was selected based on a validation set across several aggregation methods and is equal to the maximum number of columns in the non-aggregated test. Each layer is fully connected with bias included. Forward and reverse direction error back-propagation updates the weights using the Sigmoid activation function. The weight updates are based on the Mean Squared Error loss function as this is a multi-class problem. This loss is a sum of forward and reverse losses. The optimiser used is AdamW with a learning rate of 0.01 as a parameter because of the speed of convergence using weight decay.

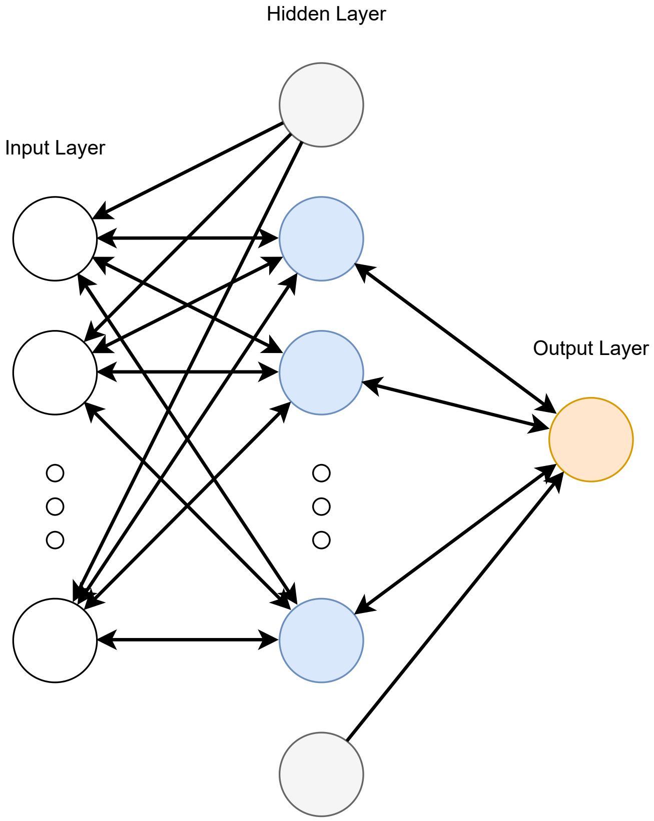

Fig. 4. BDNN model with input neurons (white), bias neurons (grey), hidden neurons (blue), and output neuron (orange).

3 Results

We have implemented a BDNN for the SARS dataset with the addition of seven columns for target and aggregated series. The index values for each feature can be found in figure 5. Hence, we can use these indices to define the features used for classification tests. To begin the testing process, we only reduced the features by a small number of features, which allowed the hyper-parameters mentioned above to be found. The use of various aggregation methods for temperature across the day and all other features resulted in 100% train and test accuracy. The aggregation methods used were maximum, mean, minimum, and mean maximum for: columns [12,13,14,15,16,17,18,19,20,21,22,24,25,26,23]. Note that every test uses column 23, the target class column.

Temp 8am			Temp 12pm			Temp 4pm			Temp 8pm		
Slight	Mod	High	Slight	Mod	High	Slight	Mod	High	Slight	Mod	High
0	1	2	3	4	5	6	7	8	9	10	11

BP Systolic			BP Diastolic			Nausea			Abdominal Pain	
Slight	Med	High	Slight	Med	High	Slight	Med	High	No	Yes
12	13	14	15	16	17	18	19	20	21	22

Target class	Slight temp. agg.	Mod temp. agg.	High temp. agg.	Slight BP agg.	Med BP agg.	High BP agg.
23	24	25	26	27	28	29

Fig. 5. Tables of index values of SARS dataset and additional columns.

Next, using the same aggregation methods on the systolic and diastolic blood pressures and all other feature we achieved a 100% accuracy once again. Hence, the columns were: [1,2,3,4,5,6,7,8,9,10,11,18,19,20,21,22,27,28,29,23]. In this test, the temperature columns were not aggregated. Therefore, the next test was using both the temperature and blood pressure aggregations. To save time, the mean maximum aggregation method was used for this test on: [18,19,20,21,22,24,25,26,27,28,29,23]. Again, the classification accuracy was 100% for both train and test sets.

At this point in the testing, we only have 11 features and are still able to achieve perfect accuracy. However, there are still fuzzy sets for nausea and abdominal pain. Therefore, we introduced the technique of removing less relevant columns. The next test has only the positive column for abdominal pain, or in other words removes "no": [18,19,20,22,24,25,26,27,28,29,23]. This removal resulted in a perfect accuracy. Also removing the "slight" and "medium" values for nausea had similar success, or: [20,21,22,24,25,26,27,28,29,23]. Combining the last two removals of columns gave us: [20,22,24,25,26,27,28,29,23]. Hence, with eight features we achieve perfect classification.

Finally, if we apply the same removal technique to the aggregated columns, then we are left with 4 input features: [20,22,26,29,23]. The features remaining are "high" mean maximum temperature and BP aggregation, "yes" abdominal pain, and "high" nausea. The training accuracy for was 99.6916% and testing 99.8679%. Changing the aggregation method for the same features results in similar accuracy with plus or minus 0.3%. Adding back any one of the following features: 18, 19, 21, with any aggregation method was enough to achieve perfect classification. Consequently, the number of input features for the testing environment used in this paper that the SARS dataset can be represented by is 5.

4 Discussion

The results of the tests we created in this paper suggest that the classification of SARS, high blood pressure, and pneumonia from the datasets involves a small number of features. Using a single hidden layer with the raw dataset is enough to train a classifier on this dataset. Since the dataset is 4000 entries and the training data is around 3200 entries, we may want to use a pre-training strategy to maximise the training process. We describe more techniques to consider in the 'Future Work' section. However, by reducing the number of features using the general fuzzy signature for the SARS dataset, we can demonstrate that the information of both features remains and shares a relationship.

The classification problem defined by a single multi-class target represents one technique. Alternatively, we could use an encoding of k bits, where k is the number of bits needed to represent the number of classes in the problem [3]. This approach makes use of the neural network topology but requires different methods for calculating accuracy. The single multi-class target approach is limited by the defuzzification of the result. In other words, the use of numbers 0-3 representing four distinct classes introduces underlying ambiguity. For example, the ordering of the classes may change the accuracy of the classifier and could lead to overfitting, always predicting less than zero or greater than 3, if the initial weights are not carefully set. Hence, for these reasons the single multi-class approach can be improved.

Our use of a forward and backward passes, where backward pass is essentially a reversed forward pass, introduces a difference in loss each forward and backward pass. Hence, we use the sum of these two losses and alternate the forward and backward passes. This is due to the breaking of learning weights and bias each backward pass, as shown in figure 6. Another solution would be to use normal forward pass until some threshold is reached or x number of passes are completed and then switch to a backward pass. In this scenario, used in [1], the loss function would be based on the direction the pass was completed. This method creates less variability after each consecutive forward pass and could converge faster.

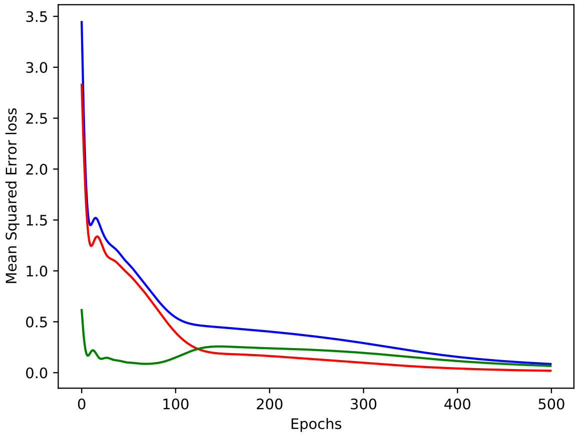

Fig. 6. Plot of Mean Square Error for total (blue), forward (red), backward (green).

In this paper, the fuzzy signature-based aggregation method demonstrated the importance of the choice of which features could be removed or aggregated for accuracy in classification. Previous work into the same dataset also concludes that the accuracy of their aggregation method was high [2]. This paper found a drop-off in accuracy after reduction to 5 features using aggregation methods and removal. Hence, these fuzzy signatures have a limit for the aggregation methods and removal that were tried. The limitation of the technique used is that these features are manually extracted. Therefore, for high dimensional data, the time it would take to find these fuzzy signatures manually is outweighed by the current state of the art deep neural network models [7].

5 Conclusion

The outcome of this paper is that the use of fuzzy signature-based aggregation can be applied to reduce the dimensionality of the SARS-CoV-1 classification problem. The signature with the least number of features was “high” nausea, “yes” abdominal pain, “high” temperature aggregation, and “high” blood pressure aggregation, including one of the following: “slight” nausea, “medium” nausea, or “no” abdominal pain. From this result, we can use five features and maintain 100% classification on training and testing sets. The considered aggregation techniques were maximum, mean, minimum and mean maximum.

6 Future Work

Current works into SARS-CoV-2 classification give insight into the potential for the multi-class problems in real world situations [5] Although, more powerful neural network techniques are used today, such as Convolutional Neural Networks. These methods offer better feature extraction and classification capability than BDNNs. More computational power has also allowed complex, deeper neural network structures to be used over simple ones. The size of the dataset is small, therefore, we could pre-train on a similar dataset and freeze the weights of some neurons. This would use the current research of transfer learning or CNNs and potentially build a powerful medical diagnosis model. Also, the use of multi-class performance scores [6] provide an opening for future work into complex multi-class classification problems using some of these more powerful neural networks. Using a fuzzier logic approach to classification problems would not round to the nearest whole number, but instead have a degree of certainty for each classification. The work in this paper would only need slight changes to accommodate for this approach which could include a different accuracy function or a criterion, encoding of classes and extra neuron method [1].

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