SEIZURE CLASSIFICATION USING PARALLEL GENETIC NAIVE BAYES CLASSIFIERS

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ABSTRACT

Epilepsy affects 50 million people worldwide and is one of the most common serious brain disorders. Seizure detection and classification is a valuable tool for maintaining the condition. An automated detection algorithm will allow for accurate diagnosis. This study proposes a method using unique features with a novel parallel classifier trained using a genetic algorithm. Ictal states from the EEG are segmented into 1.8 s windows, where the epochs are then further decomposed into 13 different features from the first IMF. All of the features are fed into a genetic algorithm (Binary Grey Wolf Optimisation Option 1) with a Naive Bayes classifier. Combining the simple-partial and complex-partial seizures provides the highest accuracy of all the models tested.

1. INTRODUCTION

Epilepsy is one of the most common neurological disorders in the world [1], roughly affecting 50 million people worldwide [2]. Epileptic seizures occur when millions of neurons are synchronously excited, resulting in a wave of electrical activity in the cerebral cortex [3]. Electroencephalography (EEG) is a noninvasive tool that measures cortical activity with millisecond temporal resolution. EEGs record the electrical potentials generated by the cerebral cortex nerve cells [4]. As a result this tool is commonly used for the analysis and detection of seizures [5]. Epilepsy causes many difficulties in relation to the quality of life for the patient. The International League Against Epilepsy (ILAE) have outlined a list of different seizures [6]. There are two responses on the individual, categorized as a motor or a non-motor response. Motor seizures cause involuntary spasms. Non-motor seizures affect the consciousness of the patient reducing their ability to pay attention.

The novelty of these models is the use of a genetic algorithm in a parallel multi-class seizure detection system. The use of the genetic algorithm allows for dynamic feature selection and a reduction in the feature matrix that is feed into the classifier. Additionally another novelty is the combination of the simple partial seizure and the complex partial seizure being feed into a genetic parallel multi-class classifier. This highlights the improvements for all of the other classes in the model.

Kukker et al. [7] used a fuzzy Q-learning genetic classifier to improve their original features. The signal is converted using empirical mode decomposition (EMD), the intrinsic mode functions (IMFs) are converted using the Hilbert Huang Transform (HHT). Nineteen features are extracted from the conversion with a distinct set of annotations created for each of the IMFs generated. The CHB-MIT dataset was used achieving a classification accuracy of 96.79%.

Ammar et al. [8] used a particle swarm genetic algorithm for a patient specific seizure classification system, this classification model used seizure and non-seizure as their annotations. The features extracted where Kurtosis, skewness and standard deviation achieving an accuracy of 98.89%. A smaller dataset (Bonn) was used with a support vector machine (SVM) classifier.

This paper proposes a methodology to classify seizures using parallel genetic Naive Bayes classifiers. The algorithm will firstly model a set of features that are taken from the first IMF of the EMD. After the feature extraction is performed a genetic algorithm is used to optimise the chosen features.

This paper is organized as follows: Section 2 explains the dataset that was used in this research; Section 3 describes the proposed feature selection algorithm used for seizure classification; Section 4 presents and discusses the results obtained; and Section 5 provides some conclusions.

2. DATASET

The dataset from the Temple University Hospital (TUH) Seizure Corpus v1.5.3 was used in this study. This dataset is a subset of a much larger dataset offered by the same university called the EEG corpus [9][10]. The dataset is divided by the TUH into two sets, defined as training and testing with demographics being made equal across both sets. The dataset was annotated by a team established by the university based on the signals and the neurologists’ report.
3. FEATURE SELECTION

3.1. Preprocessing

To maintain consistency in the dataset, only the 19 channels common to all the seizures defined by the International 10–20 System were used [11]. By doing so, we were able to remove the unwanted channels such as the electrocardiogram (ECG), electromyography (EMG), as well as photo stimulus channels. The signals were resampled to 250 Hz as this is the lowest frequency common to all seizures. The 60 Hz line noise was removed with a bandstop infinite impulse response (IIR) filter. The EMD was then performed and the first IMF was taken for the analysis of the signals. The signals were then divided into 1.8 s windows, which was chosen because it reflects on the shortest ictal window of all the different seizure types. Each feature was calculated for each channel of the windowed signals.

3.2. Time Domain Features

3.2.1. Standard Deviation

Ictal episodes have a higher energy compared to the non-ictal episodes. However, some seizures have a lower energy response such as absence, complex-partial, and simple-partial [12, 13, 14]. The standard deviation $\sigma$ measures how much energy is created away from the mean, where a higher energy level would naturally produce a higher $\sigma$. The formulation for $\sigma$ can be written using

$$\sigma = \sqrt{\frac{1}{N-1} \sum_{i=1}^{N} (x_i - \bar{x})^2},$$

where $x_i$ is the preprocessed EEG time series described in Section 3.1, $\bar{x}$ the mean of $x_i$, and $N$ the number of samples.

3.2.2. Shannon Entropy

The Shannon entropy method can be used to measure the chaotic nature of EEGs, and it can be defined using

$$H(X) = -\sum_{i=1}^{n} p(x_i) \log_2(p(x_i)),$$

where $X = \{x_1, x_2, \ldots, x_n\}$ is a set of finite discrete random variables, and $p(x_i)$ the probability of $x_i \in X$ such that $\sum_{i=1}^{n} p(x_i) = 1$ [15].

3.2.3. Kurtosis

Kurtosis $\gamma_2$ is the degree of “peakedness” of a real valued random variable, which is used to determine if $\sigma$ is created from small constant deviations or if large inconsistent deviations are present in the signal [16]. The formulation for $\gamma_2$ can be written using

$$\gamma_2 = \frac{\mu_4}{\sigma^4},$$

where $\mu_4$ is the fourth central moment.

3.2.4. Hjorth Criteria

Hjorth parameters measure a signal via three criteria: activity, mobility, and complexity. Activity uses variance as its basis and is therefore not used as a feature. However, mobility $h_m$ and complexity $h_c$ can be used to measure the mean frequency of a signal and deviation from a pure sine wave, respectively [17]. Both parameters can be expressed using [4–5].

$$h_m = \frac{\text{var}(\frac{dx}{dt})}{\text{var}(x_i)}, \tag{4}$$

$$h_c = \frac{h_m(\frac{dx}{dt})}{h_m(x_i)}, \tag{5}$$

where $\text{var}(x_i)$ represents the variance of the EEG time series data $x_i$.

3.2.5. Skewness

Skewness measures the symmetry of the time series data, where it can be written using

$$\tilde{\mu} = \frac{\sum_{i=1}^{N} (x_i - \bar{x})^3}{(N-1)\sigma^3}. \tag{6}$$

3.3. Fractal Analysis

Fractals are used to measure the self-similarity of the given time series value. Absence, tonic, and tonic-clonic seizures have rhythms generating self similar waveforms [14, 18].

3.3.1. Higuchi Fractal Dimension

The time series data have to be firstly decomposed into a set of subseries in the format shown in [19], which can be defined using

$$X_{km} : x(i), x(i + k), x(i + 2k), \ldots, x(1 + mk), \tag{7}$$

where $k$ is the fractal dimension, $X_{km}$ is the subtime series, and $m$ is the length of the fractal series. Equation [7] denotes that a higher value of $k$ leads to more subseries created in the fractal dimension calculation. To measure the similarity of the subseries a curve is created. The length of the curve can be found using

$$L_m = \frac{1}{k} \left[ \sum_{i=1}^{r} |x(m + ik) - x(m + (i - 1)k)| \frac{N-1}{rk} \right], \tag{8}$$

where $r = \left\lceil \frac{N-m}{k} \right\rceil$ computes the nearest integer for $r$ and $x(i)$ is the subseries given in (7).
3.3.2. Katz Fractal Dimension

Katz utilizes the same subseries defined in (7). It is another fractal estimation algorithm where the successive points are measured to compute the self-similarity such that the fractal dimension of the subseries $X_{km}$ can be written using

$$D = \frac{\log(L/a)}{\log(d/a)}, \quad (9)$$

where $d$ is the Euclidean distance of each point in the new time series found in (8) and $L$ and $a$ are the sum and average of the Euclidean distances of the sample point $d$, respectively. And since it is established that $n = L/a$, (9) can also be expressed using

$$D = \frac{\log(n)}{\log(n) + \log(d/L)}, \quad (10)$$

where $d$ is the Euclidean distance of each point in the new time series found in (8) and $L$ and $a$ are the sum and average of the Euclidean distances of the sample point $d$, respectively.

3.4. Energy and Nonlinear Energy

The total energy of the time series data can be computed using

$$E = \sum_{i=0}^{N} x_i \quad (11)$$

Also, the mean nonlinear energy can be found using

$$\sum_{i=2}^{N-1} C(i-1) = x_i^2 - x_{i-1}x_{i+1}, \quad (12)$$

where $C$ is the nonlinear energy.

3.4.1. Spectral Entropy

To calculate the spectral entropy of a time series data, it was initially converted to the frequency domain using fast Fourier transform, which was then further converted into power by writing

$$S(x_i) = |\text{FFT}(x_i)|^2, \quad (13)$$

where FFT$(x_i)$ is the fast Fourier transform of the time series $x_i$. The entropy was then calculated using Shannon entropy as shown in (2). The mean, maximum, and minimum were then taken as the features to be fed into the classifier.

To balance the dataset an upsampling method was used where the least represented labels were repeated by the nearest integer factor of the largest label. In the first model, the largest label is the complex-partial seizure. In the second model, the largest is the complex-partial seizure. In the third model, the largest label is the focal-onset label.

3.5. Genetic Algorithms

Genetic algorithms are optimisation methods that mimic Darwin theory. They are exploratory procedures that are try to find the near optimal solutions to complex problems. Emary et al. [22] studied a wild grey wolf pack. This lead them to provide 3 different genetic algorithms. In this paper Algorithm 1 is used because it provides the shortest compilation time.

3.6. Classification

The classifier chosen is the Naive Bayes (NB) classifier. It is a probabilistic classifier based on the Bayes theorem under the assumption that any feature of a particular class is independent of any other feature. Error estimation is computed based on the maximum likelihood [23]. To compare the features and their ability to detect the individual seizures a parallel classification system is needed. Each one of the classifiers is trained in a one vs all set up. To remove the need for six different confusion matrices a heatmap was generated for each of the classifiers with the False Positive (FP) and the False Negative (FN) placed at the bottom of the heatmap. The True Positive (TP) is placed with the corresponding name of the classifier and the predicted name (these are the same). This makes comparison between each of the individual classifiers easier.

4. RESULTS AND DISCUSSION

The first model chosen is the baseline model. This model does not use the genetic algorithm and does not combine the complex partial seizure and simple partial seizure into one label. This model is a single multiclass classifier. The second model uses the genetic algorithm to find the features that provide the most optimum F1-score, with the labels provided by the TUH. This is a parallel classifier and contains six different NB classifiers. The third model uses the genetic algorithm to find the features that provide the most optimum F1-score with the combined label. This is a parallel classifier and contains 5 different NB classifiers. The initial NB classifiers’ confusion matrix is shown in Figure 1. At least one seizure in each seizure type was detected by the classifier. There are a lot of wrong classifications predominately the complex-partial seizure as simple-partial seizures. The simple-partial and the complex-partial seizure are very similar, both being of a focal nature. It is unexpected that the simple-partial and the complex-partial are being misdiagnosed as tonic-clonic seizure. A tonic-clonic seizure can have a focal onset, where its focal onset can propagate into a bilateral tonic-clonic seizure [6]. The first heatmap is shown in Figure 2. The tonic-clonic had the highest F1-score with 0.96 followed by the absence seizure with 0.93. The tonic-clonic and simple-partial seizure performed poorly by having higher FPs and FNs than TPs in the system. The heatmap does highlight a large reduction in FP. Myoclonic seizures also had a notable
In comparison with Kukker et al. [7] the models did not achieve the same accuracy of 96.79%. This model is used for multiclass seizure detection and not just detecting if it is seizure and non-seizure. Comparing seizures is more difficult because the signals have more similarity than the non-seizure and seizure components. This explains the reduction in accuracy.

Depending on the chosen classifier an implementation of a genetic algorithm should be considered for two reasons; firstly to increase the accuracy, and secondly to reduce the size of the feature array.

Using parallel classifiers for multiclass seizure detection increases the storage space required on the final implementation, in comparison with having a single classifier performing multiclass detection. The processing power is also increased because of the multiple iterations performed.

5. CONCLUSION

Implementation of a genetic algorithm is a new standard that should be used when building a machine learning platform for seizure classification. It requires more training time but further investigations highlight which features are comparative. The value of spending increased time at the training stage will ensure that the model increases in accuracy along with combining focal seizures to further increase the classification rate.

To further improve the models accuracy a new set of features that are more tailored to each of the individual seizures. Individual pre-processing stages would improve the training and testing but again increase the memory requirement on the system.

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