

Research Article

ZleepNet: A Deep Convolutional Neural Network Model for Predicting Sleep Apnea Using SpO₂ Signal

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Sleep apnea is one of the most common sleep disorders in the world. It is a common problem for patients to suffer from sleep disturbances. In this paper, we propose a deep convolutional neural network (CNN) model based on the oxygen saturation (SpO₂) signal from a smart sensor. This is the reason why we called ZleepNet a network for sleep apnea detection. The proposed model includes three convolutional layers, which include ReLu activation function, 2 dense layers, and one dropout layer for predicting sleep apnea. In this proposed model, the use of signals for detecting the sleep apnea can be reduced from 25 sensors to 1 sensor. We conducted experiments to evaluate the performance of the proposed CNN using real patient data and compared them with traditional machine learning methods such as least discriminant analysis (LDA) and support vector machine (SVM), baggy representation tree, and artificial neural network (ANN) on publicly available sleep datasets using the same parameter setting. The results show that the proposed model outperformed the other methods with the accuracy of 91.30% with the split rate of 0.2% in which the training data are 20% and testing data are 80%. The accuracy of the proposed CNN is 90.33% when compared with the LDA which achieved 86.5% accuracy with the split rate of 0.5% in which training data are 50% and testing data are 50%. It achieved 91.56% accuracy when compared with the support vector machine (SVM) in which training data are 70% and testing data are 30%. The achieved accuracy of the proposed CNN is 91.89% when compared with bagging representation tree in which training data are 90% and testing data are 10%. The accuracy of the proposed CNN is 91.30% in which training data are 83% and testing data are 17% when compared with artificial neural networks (ANN).

1. Introduction

Deep convolutional neural networks predict and analyze various health-related problems by collecting data from numerous biological sensors [1]. It will be used for sleep apnea detection. Sleep apnea is defined as the complete breathing disturbance in which those breathing pauses can last for seconds to minutes [2–4]. Therefore, it has the potential to get sleep apnea during sleep. Patients suffering from sleep apnea require many sensors, tools, and appliances, which make the patients very uncomfortable and difficult to sleep during sleep monitoring. It is of great significance to identify sleep apnea as soon as possible.

According to the American Academy of Sleep Medicine (AASM), the breathing pauses more than ten seconds can be identified as sleep apnea [5, 6]. The AASM guidelines have an impact not only on the healthcare professionals but also on the patients and the quality of the healthcare [5, 7]. It happens more than thirty times within an hour. In full-night polysomnography, there will be more than 25 sensors to identify sleep-related diseases. The detection of sleep apnea in most research studies relies too much on the experts, and there are some errors in the medical tools' detection, which will later be updated and repaired by experts. It is very time consuming to repair errors manually. However, smart phones with a SpO₂ sensor and heart rate sensor will be good

candidates for sleep monitoring. During these days, most people own one phone with more than one sensor that provides collecting data for a detail analysis. According to healthcare professionals and physicians, there are four types of sleep apnea: type 1 polysomnography, which is a benchmarking standard, type 2 sleep studies, type 3 sleep studies, and type 4 sleep studies [8, 9].

The type of studies that is used in our system is type 4 sleep studies, which are also referred to as continuous single bioparameter or dual bioparameter recording. The minimum number of signals that can be used in this type 4 study is one or two channels such as oxygen saturation and airflow [10]. However, one of the critical tools for detection of sleep apnea is the type 1 full-night polysomnography. It is very expensive when it comes to time, energy, cost, space, and portability. This study presents the real-world implementation of the convolutional neural network in type 4 sleep studies using the SpO₂ signal, which focuses more on portability, space reduction, cost savings, and less time consuming [6, 11–20]. However, type 4 sleep monitoring is not possible for sleep scoring because it does not contain electroencephalogram (EEG) and electromyography (EMG) signals, which will also be useful for identifying respiratory sleep disorder. There are several alternatives for combining different biological signals due to the researchers' and healthcare professionals' preferences. It means that there are different kinds of type 4 sleep studies [17, 21]. It is also possible to combine the use of an oxygen saturation sensor and tracheal sound by acoustic as an alternative to type 4 sleep studies.

The main objective of this paper is how to design and implement the convolutional neural network model for biological signals when it comes to the detection of sleep apnea. We compare the classification performance from different methods, including traditional machine learning methods such as least discriminant analysis (LDA) and support vector machine (SVM), bagging representation tree, and artificial neural network on publicly available sleep datasets using the same parameter setting. The contributions of this research can be summarized as follows:

- (1) We propose CNN architectures, which include three convolutional layers, including ReLu activation function and 2 dense layers for predicting sleep apnea from raw SpO₂ data captured from smart sensors. This is the ZleepNet CNN model, a network for sleep apnea detection.
- (2) We conducted experiments to evaluate the performance of the proposed CNNs and compared them with traditional machine learning algorithms on three datasets.

The outline of this paper is organized as follows: the background and related work are presented in Section 2. Section 3 introduces the explanation of deep learning design and implementation illustrated in detail. Moreover, Section 4 is the result of the experiment of the proposed deep convolutional neural network model and comparison with other models. Furthermore, Section 6 provides the

limitation and future work. Finally, we conclude the work of this paper and highlight the potential of future research for sleep apnea detection.

2. Related Work

Sleep is essential for the physiological activity of the human body and can affect our health. It is important to understand the relationship between our health and sleep quality. The poor sleep quality is an accomplice associated with anxiety, physical activity, and stress. There are different types of sleep disorders, such as insomnia, narcolepsy, and sleep apnea [2]. In recent years, there has been widespread attention of using the deep convolutional neural network in the field of speech recognition, image processing, and medical application due to enormous success, especially for accuracy result and performance [10]. The respiratory signals, which are used for the detection of sleep apnea, are SpO₂ signals, thermistor signals, nasal pressure signals, thoracic signals, and abdomen signals. SpO₂ signals are oximetry signals, which show the oxygen saturation in the blood [22–28]. The combination of SpO₂ and RR interval obtained from the electrocardiogram (ECG) achieved the global score for clinically significant apnea of 87% accuracy, 73% sensitivity, and 92% specificity [26]. A single lead ECG can also be used for the detection of sleep apnea using the Hermite basis function [12, 29–32]. Vector-valued Gaussian processes (GP) are used for the detection of sleep apnea, and the wearable sensor provides the collection of cardiorespiratory data. The oximetry is specific for the presence of OSA, which is beneficial for the detection of sleep apnea [27, 30]. The detection of sleep apnea is made by empirical mode decomposition based on the oxygen desaturation achieving sensitivity of 83% [28]. The highest accuracy, more than 90%, is achieved using an artificial neural network with a genetic algorithm for classification in which SpO₂ sensors are used for detection [33, 34].

Nasal pressure signals measure changes in the pressure of the inhalation and exhalation of the nasal airway [35]. Thoracic and abdomen signal measures the movement of the thoracic and abdomen [1, 36]. The combination of a nasal pressure and a thermistor sensor is used to analyze the respiration analysis for the detection of sleep apnea [37, 38]. A recent study has shown that it is possible to detect sleep analysis using respiratory parameters such as heart rate interpretation and SpO₂ due to the specific pattern in the respiratory parameter [39]. The link between sleep apnea and respiratory parameter is that oxygen saturation decreases when sleep apnea occurs and at the same time heart rate increases [40]. Machine learning algorithms have strong predictive power in order to draw interpretation between the biological parameter signals [8]. There is a significant relationship between snoring and obstructive sleep apnea using a simple signal processing technique in short time energy [23–25, 29, 41, 42]. Snoring can be found as an audible sound because of cessation in breathing that lasts more than a minute [16, 25, 36, 43–45]. There are several treatments for curing obstructive sleep apnea, such as ear, nose, and throat

(ENT) surgery, nasal surgery, radiowave surgery, laser surgery, circuitous surgery; positive pressure respirator (CPAP); snoring; and dental braces [14, 16, 20, 46–48].

2.1. Traditional Pattern Recognition Methods Applied to Sleep Apnea Detection. Different researchers use different combinations of characteristic signals and a classifier to detect sleep apnea. Support vector machine, bagging representation tree, and artificial neural network can also be used for sleep apnea detection as traditional pattern recognition methods [26, 33, 34].

2.2. Deep Learning Methods Applied to Sleep Apnea Detection. There has been an increasing amount of the literature on the recognition of sleep apnea using deep learning methods [1, 2, 10, 22, 24, 37, 38, 40]. Training deep learning models learn feature extractions autonomously. Deep learning models have superior performance. However, it requires abundant computing and memory resources. Due to the increase in the application of mobiles and wearable devices, most of the devices have not enough memory and computing resources for training deep neural networks.

3. Deep Learning Step

Deep learning is the expansion of the classical neural network, and the complex pattern existing in the dataset can be explored. Deep learning algorithm such as multilayer perceptron, convolutional neural network, and recurrent neural network can also perform complex computation easily in order to solve the challenging task such as image recognition, medical imaging, and speech recognition. The biological neural network of the human brain decision-making inspires the proposed deep learning model using the convolutional neural network. It is based on a single stimulus in which a number of neurons carry messages through an electrochemical process that is required for decision-making. In the real world, the identification and prediction of sleep apnea using the deep learning method would facilitate the patient with sleep apnea disease [2]. The deep learning model allows learning from the feature to represent the nature of the data and its patterns. There are two types of deep learning which are supervised learning, in which training data include both input and desired output, and unsupervised learning, in which training data contain input but not the desired output. The deep learning process includes data collection, data preparation and segmentation, and deep learning model design such as deep convolutional neural network, training, testing, hyperparameter tuning, and prediction.

3.1. Data Collection. In this study, SpO₂ sensors collect data at the rate of 16 Hz sampling. However, we can explore different sampling rates for SpO₂ sensors for different research studies. Figure 1 portrays the collection of SpO₂ sensors at 16 Hz sampling rate. In Figure 1, X₁₆ denotes that the SpO₂ data at time T₁ and X₄₈₄ denote the SpO₂ data at

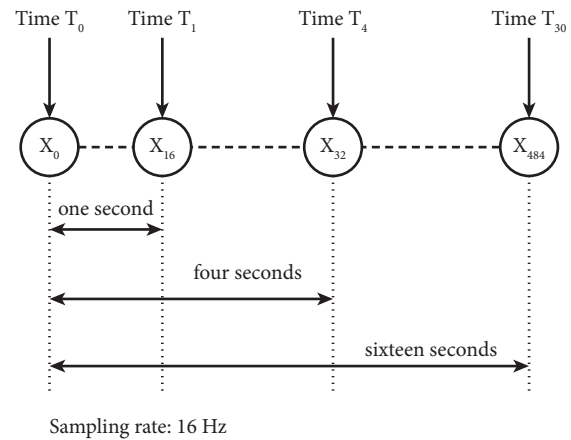


FIGURE 1: Collection of the SpO₂ sensor at 16 Hz sampling rate.

time T₃₀. In addition, it collects 16 data in one second with 4 data digit overlap. It means the duration of each feature input is according to the medical experts' advice and suggestion which is a 30 second time segment. However, it is memory consuming and resource consuming and it would not be suitable for wearable devices and mobile phones. In type 1 polysomnography sleep recording, every 30 second time segment will be allocated to a healthcare professional for a sleep analysis practicing the reference nomenclature from the American Academy of Sleep Medicine (AASM) [15, 49].

The accessibility for sleep measurement devices has drastically increased in recent years not only for the consumer grade but also for medical grades [2]. For wearable devices and mobile phones, the consideration of data and the rate of collection of data should be at a lower dimension and it would focus on more portability and lightweight computing. The mobile device has limited memory, for example, when we collect 1 Hz for each second of the SpO₂ sensor, there will be 60 data for 1 minute, and at the same time, when we collect 16 Hz for each second, there will be 360 raw data for 1 minute. The fact is that it requires around 1 GB for one night sleep recording. The data sampling rate that will be suitable for mobile devices is 1 Hz, as shown in Figure 2.

According to Figure 2, it illustrates the collection of the SpO₂ sensor at 1 Hz sampling rate. In this figure, X₁ denotes the raw SpO₂ data at time T₁, that is, at the beginning of the 16 second segment and X₁₆ denotes the raw SpO₂ data at time T₁₆, that is, at the end of the 16 second time segment at the sampling rate of 1 Hz.

3.2. Data Segmentation. This section will focus on how the original raw biological signals are transformed into a feature vector. Each epoch of the single sleep study contains 30 seconds, and the sensor gets 16 SpO₂ digit data every second. It means that there will be 16 × 30 = 480 data in 30 seconds. In this study, the consideration is that the single feature includes 484 data = 22 × 22 SpO₂ data. Each feature in the SpO₂ dataset is collecting raw data with the 16 Hz sampling rate, which will be flattened each 22 × 22 into a 484 dimensional vector. That feature vector will be used as an input to our ZleepNet CNN, and the output will be one of

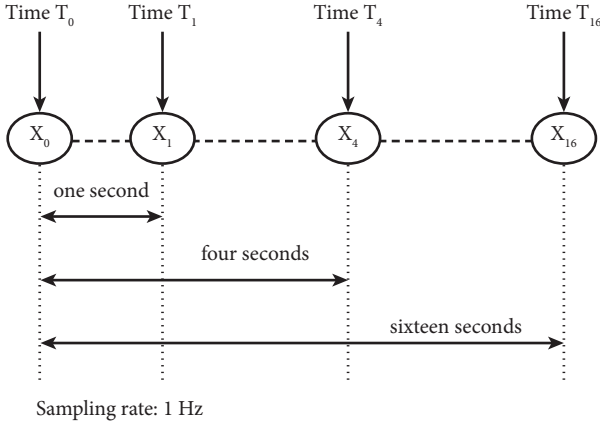


FIGURE 2: Collection of SpO2 sensor at 1 Hz sampling rate.

two possible classes: apnea, which represents as “1,” and not apnea, which represents as “0,” in the SpO₂ dataset. In Figure 3, we will discuss about how raw data are transformed into a feature dataset, which is ready to do computation for the CNN. A feature contains a number of data, which can be seen as an input to the deep learning models. Several feature records are known as a collection of feature sets. The illustrated figures are based on the sleep apnea detection, which includes more than 25 sensors. The one-dimensional feature vector and three-dimensional feature vector are shown in Figures 3 and 4, respectively. Moreover, when we have one sensor for our model, we could assume this as we have one dimension. When we use two sensor signals for the project, we could assume that we can view those data having two dimensions. When we have 25 signals, we could say that we can view the data from 25 dimensions. We could stack those 25 different kinds of vectors for one feature input. One scenario is that we could use two sensors such as SpO₂ and heart rate, or SpO₂ and thoracic signal, for deep neural networks not only for detection but also for recognition and classification.

The scenario in Figure 3 is that it will be one exact sensor, for example, SpO₂ signals or heart rate signal or thoracic signal or abdomen signal. This scenario will be dedicated to type 4 sleep studies, which contain one or two biological signals. It is up to the researcher to select which signal to choose for detection. Figure 3 illustrates simple one-dimensional feature of one sensor evolve which is suitable and ready for training, in which Figure 3(a) represents the simple logical one-dimensional feature. In addition, Figure 3(b) shows how simple input feature evolves into mathematical representation; however, it will not be considered about the label representation, and Figure 3(c) portrays the one-dimensional feature with mathematical representation of data and numeric label format. Moreover, Figure 1(d) shows the one-dimensional feature with mathematical representation of data and one hot encoding label. It depends on the researcher to decide how many raw data will be in one input vector. There will be 16 raw data in one input vector, or there will be 484 raw data in one input vector. One recommendation is that a single vector that can change to a square matrix is easy for

matrix multiplication. However, we need to consider about the row and column for the matrix multiplication of the outcomes when we use matrices that are not square. It relies upon the researcher and advice of the domain expert. The following equation reflects Figures 1 and 3 in mathematical formula, which we consider to be all of the data collected from one sensor data as X .

$$\mathbf{X} = \{\mathbf{x}_1, \mathbf{x}_2, \dots, \mathbf{x}_n\}, \quad (1)$$

$$\mathbf{F} = \{\mathbf{f}_1, \mathbf{f}_2, \dots, \mathbf{f}_n\}, \quad (2)$$

$$\mathbf{C} = \{\mathbf{c}_1, \mathbf{c}_2, \dots, \mathbf{c}_n\}, \quad (3)$$

$$\mathbf{f}_j = \{\mathbf{x}_1, \dots, \mathbf{x}_i, \mathbf{c}_i\}. \quad (4)$$

The above mentioned mathematical equations apply to our proposed research. The raw data $\{\mathbf{x}_1, \mathbf{x}_2, \dots, \mathbf{x}_n\}$ belong to the dataset \mathbf{X} in equation (1). In our proposed study, the completely raw SpO₂ data are represented in terms of \mathbf{X} . A feature or an input sample encoded with the class label is represented as \mathbf{F} . It includes several features $\{\mathbf{f}_1, \mathbf{f}_2, \dots, \mathbf{f}_n\}$ in equation (2). In each feature \mathbf{f}_i , it contains segmented raw input data together with the class and label which contains \mathbf{c}_i in class \mathbf{C} . The class \mathbf{C} consists of $\{\mathbf{c}_1, \mathbf{c}_2, \dots, \mathbf{c}_n\}$ in equation (3). In other words, the feature \mathbf{f}_j in \mathbf{F} consists of $\{\mathbf{x}_1, \dots, \mathbf{x}_i, \mathbf{c}_i\}$ in equation (3). The scenario in Figure 4 is that it will be the combination of three sensors (for example, SpO₂ signal, heart rate signal, and EEG signal or thoracic signal, abdomen signal, and heart rate signal or SpO₂, tracheal sound sensor, and EMG signal). This scenario is called the type 2 sleep studies. One of the challenges when using two or more biological signals is that the sampling rate of the data collection. It means that one signal is collected with 16 Hz sampling rate and the other signal is collected with 32 Hz sampling rate. The dimension reduction functions or dimension increasing functions need to be used for this challenge. The other challenge is that the selection of biological signals will be used for the classification. Figure 4 shows simple three-dimensional feature of the combination of different biological sensors' evolution which is suitable for training via the deep learning network. Figure 4(a) presents a simple two-dimensional logical feature. In addition, Figure 4(b) shows the three-dimensional input feature in mathematical representation of data without considering about the label representation. Figure 4(c) illustrates the three-dimensional feature with mathematical representation of data and numeric label format. Moreover, Figure 4(d) shows the three-dimensional feature with mathematical representation of data and one hot encoding label. It is important to decide how many raw data will be in one input vector. It will be the combination of three vectors, which include 16 raw data in each input vector, or it will be 484 raw data in each input vector. It relies upon the researcher and advice of the domain expert.

Figure 4 scenario is the combination of any different kinds of sensors. This scenario is for the type 1 polysomnography sleep monitoring and type 2 sleep recording.

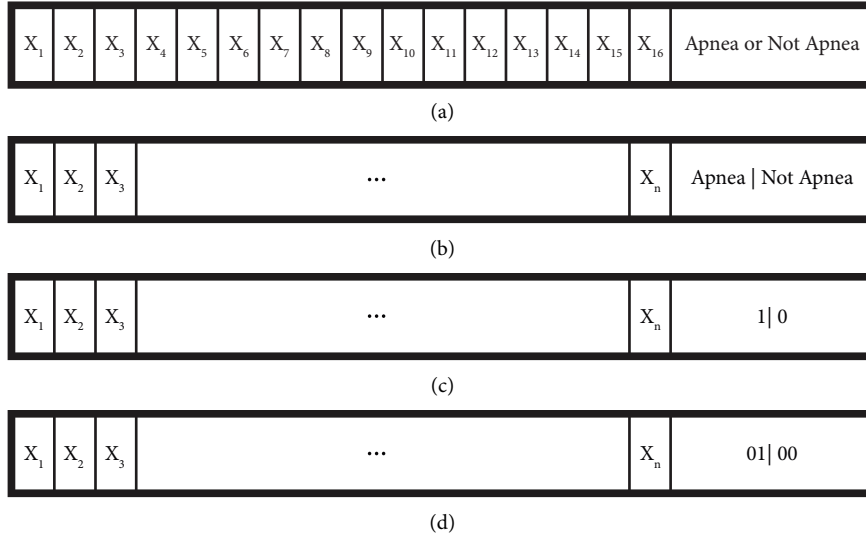


FIGURE 3: One-dimensional feature of SpO₂ sensor: (a) simple 1D feature, (b) 1D feature in mathematical representation, (c) 1D feature with mathematical representation of data and numeric label format, and (d) 1D feature with mathematical representation of data and one hot encoding.

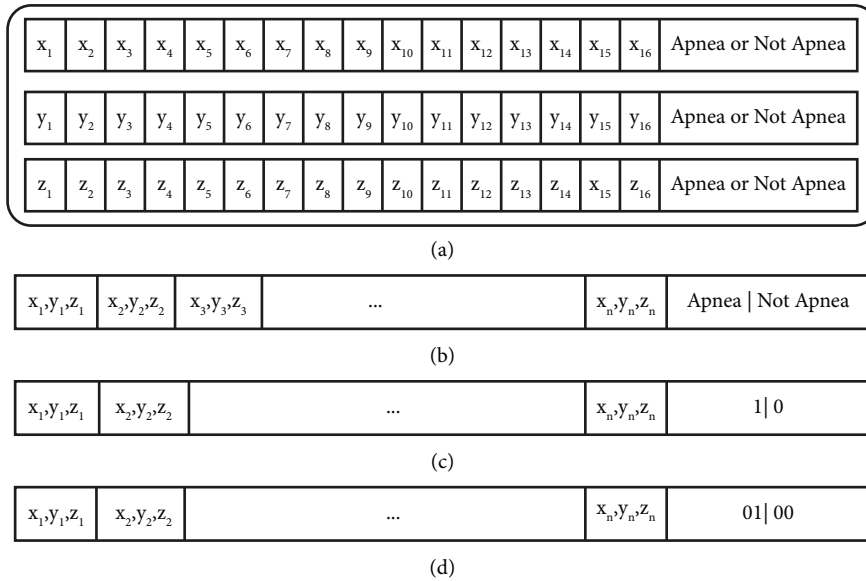


FIGURE 4: Three-dimensional characteristics of the combination of different sensors: (a) simple 3D feature, (b) 3D feature in mathematical representation, (c) 3D characteristic with mathematical representation of data and numeric label format, and (d) 3D characteristic with mathematical representation of one hot encoding.

The selection of biological signals is crucially important for the deep learning neural network and for the detection of sleep apnea. Figure 4 illustrates the combination of multiple features of biological sensors that is plausible for training and learning through the deep neural network. Figure 4(a) shows the simple logical multidimensional feature. In addition, Figure 4(b) shows multidimensional input feature in mathematical representation of data without considering the label representation. Figure 4(c) illustrates multidimensional feature with mathematical representation of data and numeric label format. Moreover, Figure 4(d) shows the two-dimensional feature with mathematical representation of the

data and one hot encoding label. It relies upon the researcher and advice of the domain expert. The following equation reflects Figure 4 in a mathematical formula, which we consider to be all of the data collected from three sensors as X, Y, and Z. It reflects our previous experiments and experiments using two or more sensors [37, 40].

$$\mathbf{X} = \{x_1, x_2, \dots, x_n\}, \quad (5)$$

$$\mathbf{Y} = \{y_1, y_2, \dots, y_n\}, \quad (6)$$

$$\mathbf{Z} = \{z_1, z_2, \dots, z_n\}, \quad (7)$$

$$\mathbf{S} = \{\mathbf{X}, \mathbf{Y}, \mathbf{Z}, \dots, \mathbf{N}_n\}, \quad (8)$$

$$\mathbf{F} = \{\mathbf{f}_1, \mathbf{f}_2, \dots, \mathbf{f}_n\}, \quad (9)$$

$$\mathbf{C} = \{\mathbf{c}_1, \mathbf{c}_2, \dots, \mathbf{c}_n\}, \quad (10)$$

$$\mathbf{f}_j = \{\mathbf{x}_1, \dots, \mathbf{x}_i, \mathbf{y}_1, \dots, \mathbf{y}_i, \mathbf{z}_1, \dots, \mathbf{z}_i, \mathbf{c}_i\}. \quad (11)$$

The raw data from three sensors $\{\mathbf{x}_1, \mathbf{x}_2, \dots, \mathbf{x}_n\}$, $\{\mathbf{y}_1, \mathbf{y}_2, \dots, \mathbf{y}_n\}$, and $\{\mathbf{z}_1, \mathbf{z}_2, \dots, \mathbf{z}_n\}$ belong to equations (5), (6), and (7). The research, which includes more than one sensor, is explained in equation (8). This means that we can add more sensors in future research studies. In other words, the number of sensors $\{\mathbf{X}, \mathbf{Y}, \mathbf{Z}, \dots, \mathbf{N}_n\}$ is in \mathbf{S} , which is a set of sensors in equation (6). The number of features or samples $\{\mathbf{f}_1, \mathbf{f}_2, \dots, \mathbf{f}_n\}$ belongs to \mathbf{F} in equation (9). The class \mathbf{C} for labelling the segmented data consists of $\{\mathbf{c}_1, \mathbf{c}_2, \dots, \mathbf{c}_n\}$ in equation (10). The feature \mathbf{f}_j consists of the appropriate data from the dataset \mathbf{X}, \mathbf{Y} and \mathbf{Z} appropriately labelled with the class $\{\mathbf{x}_1, \dots, \mathbf{x}_i, \mathbf{y}_1, \dots, \mathbf{y}_i, \mathbf{z}_1, \dots, \mathbf{z}_i, \mathbf{c}_i\}$ in equation (11).

3.3. Events of Obstructive Sleep Apnea. When the apnea event occurs, breathing stops. Then, the thermistor and nasal pressure become flat with the presence of a thoracic and abdominal signal. This is known as event 1, as shown in Figure 5. After event 1, the oxygen desaturation event occurs. It means that oxygen drops 3% or more for at least 10 seconds. It can be seen in the SpO₂ sensor signals.

After the oxygen desaturation event, there will be an arousal event in the brain wave. It means the brain sends signal to muscles in order to do breathing when oxygen drops for more than 10 seconds. Event 2 and event 3 can overlap sometime. Figure 6 shows the increase in heart rate in event 4 of Figure 5. It shows that the increase in heart rate can occur at the time of decrease in oxygen desaturation.

Each sleep dataset is divided into training and testing sets using different parameter settings in order to show that the model is consistent after data collection and segmentation process. Data normalization is performed on the data to facilitate the training process. As a result of breathing cessation, the occurrences of oxygen desaturation can be seen in event 2 in Figure 5. One of the findings is that the heart rate began to increase after the oxygen desaturation event in SpO₂ and the arousal event in the brain occurred in events 2 and 3, consecutively. It can be seen in Figure 6, where the blue line represents the heart rate signal and the gray line illustrates the SpO₂ signal. The heart rate increased sharply from 66 to 120, at the same time, the SpO₂ decreased from 95 to 89.55. The oxygen desaturation is 5.45% according to Figure 6.

3.4. Convolutional Neural Network Design for Apnea/Hypopnea Event Detection. The design and all the details in each layer of the deep convolutional neural network for the SpO₂ signal are shown in Figure 7. In this model, it includes three two-dimensional convolutional neural network layers with

the use of ReLu activation functions, three max pooling layers, one flatten and dropout layer, and two dense layers with the input size of 484 data in one input feature. The sigmoid classifier is used in the final output layer. The signal is segmented into 484 signal points in one epoch which means a 30 second segment. According to AASM guidelines, there will be 30 seconds in one epoch. In one sample, there will be 484 signal points, and it can also transform into $22 * 22 * 1$ which becomes square shaped three-dimensional data that are suitable for the deep convolutional neural network. The $22 * 22 * 1$ can change to 484 according to matrix multiplication when it comes to data input. Then, the input values of the hidden layer are reduced to half in the next two layers. For example, the $22 * 22 * 1$ input in the previous layer becomes $10 * 10 * 1$ in the output layer. The details of the layer name, input size, output size, and the number of kernels are shown in Table 1.

The input size of the deep convolutional neural network is $22 * 22 = 484$ data in each sample in combination with one label predicted by healthcare professionals. After the deep neural network, weights and biases are calculated, in which the input values are first multiplied by the weights. Then, the losses are calculated by using the categorical cross entropy in which the target distribution is compared to the predicted distribution. Third, the weights and biases are adjusted for every layer of the ZleepNet CNN during the forward pass. Every combination of weights and biases has the influence upon the loss reduction; however, loss functions are calculated from the model output which does not contain weight and bias for calculation.

There are infinite combinations of weights and biases to obtain optimal loss and accuracy. Loss reduction is called the optimization of the neural network by finding the local minimum of the loss. Adjusting weights and bias to reduce loss is one of the main challenges in neural networks. After finding the significant loss reduction, accuracy will be raised significantly. However, the loss decreases slightly; there will be a significant change in accuracy. Updating weights and biases within a number of iterations is called training the network by searching and adjusting the weight and bias to yield better accuracy and loss reduction. The data complexity is not irrelevant in deep learning when we have better CPU. However, it was quite a challenge during past few decades. Finding and adjusting the loss is called finding the local minimum of loss. The main issue at this point is that how many times we need to train the network model. However, there is no specific answer to these issues. It is up to how many iterations are needed to get the local minimum of loss.

3.5. Hyperparameter Tuning. Hyperparameter are adjustable parameters that are crucial and is not learned directly from the training process. They are fixed before the actual training begins. The most common metric to measure the best combination of hyperparameter in order to get the optimal result is accuracy, especially for the classification problem. This process is called hyperparameter optimization for the configuration of the CNN model. Hyperparameter are set in order to help and guide the learning process for getting the

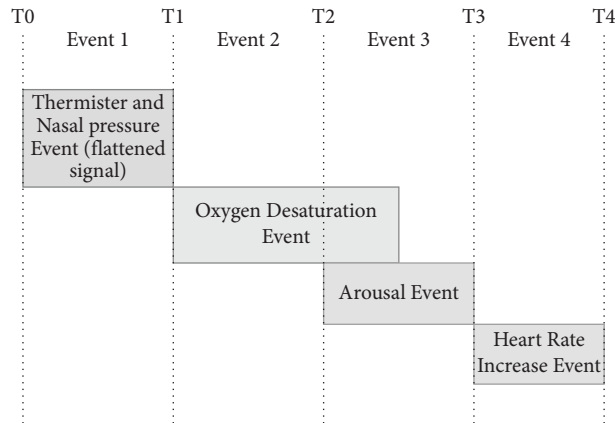


FIGURE 5: Four consecutive sleep apnea events.

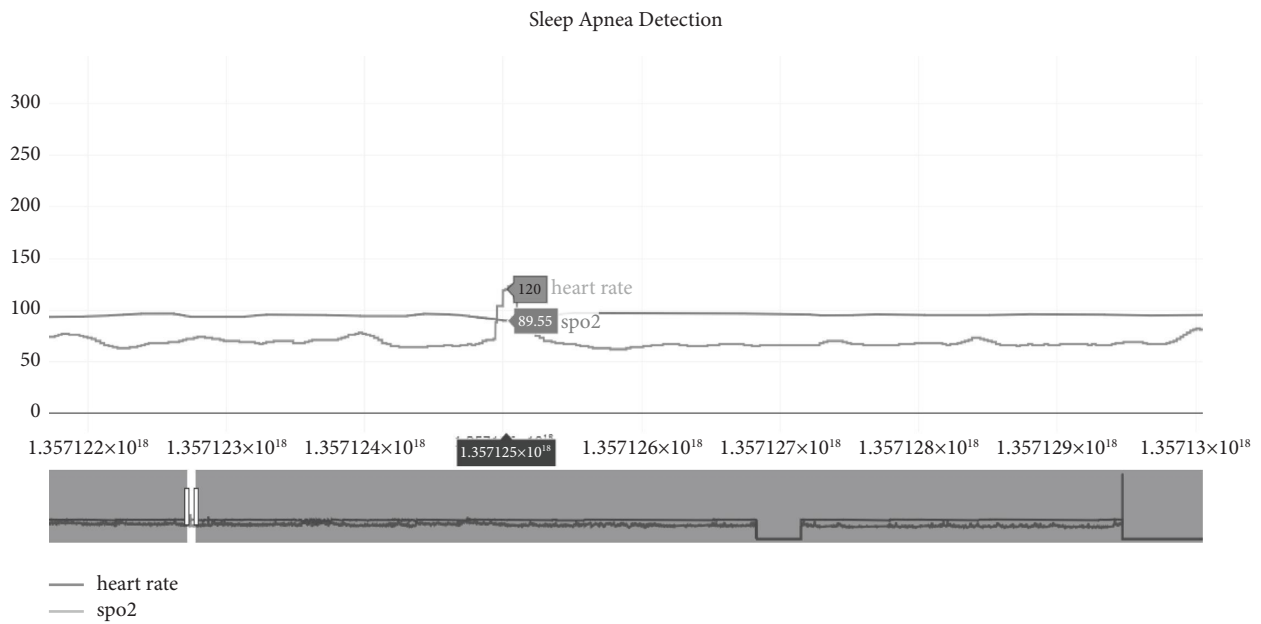


FIGURE 6: Heart rate increases after the oxygen desaturation event occurs in SpO₂.

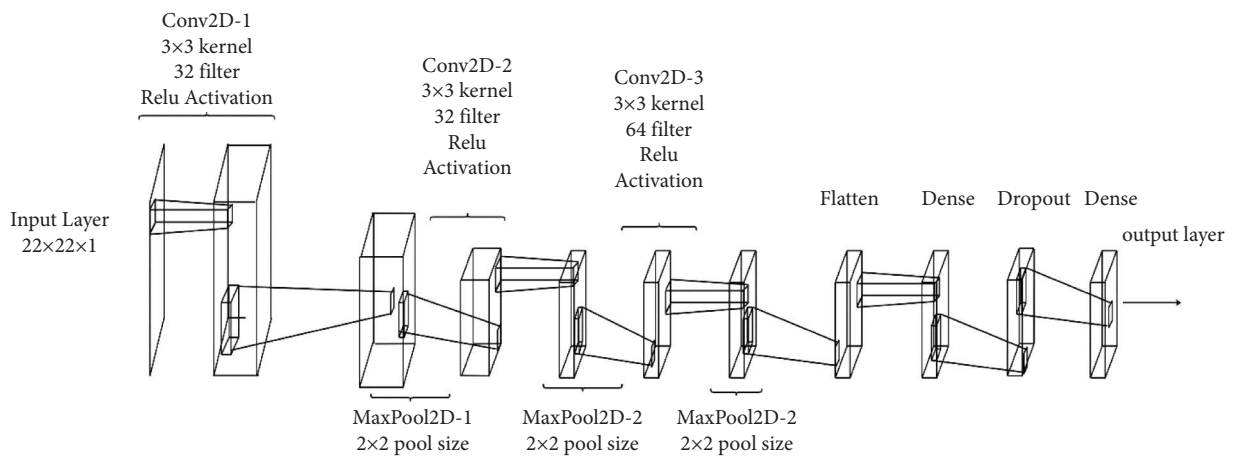


FIGURE 7: The architecture of the deep convolutional neural network model.

TABLE 1: Details of the ZleepNet CNN model.

Layer name	Input size	Output size	Number of kernels
InputLayer	$22 \times 22 \times 1$	$22 \times 22 \times 1$	1
Conv2D-1	$22 \times 22 \times 1$	$20 \times 20 \times 32$	32
MaxPool-1	$20 \times 20 \times 32$	$10 \times 10 \times 32$	32
Conv2D-2	$10 \times 10 \times 32$	$8 \times 8 \times 32$	32
MaxPool-2	$8 \times 8 \times 32$	$4 \times 4 \times 32$	32
Conv2D-3	$4 \times 4 \times 32$	$2 \times 2 \times 64$	64
MaxPool-3	$2 \times 2 \times 64$	$1 \times 1 \times 64$	64
Flatten	$1 \times 1 \times 64$	64	1
Dense	64	64	1
Dropout	64	64	1
Dense	64	2	1

most out of the model. For the regression problem, the common metric for hyperparameter optimization is the negative mean absolute error. The hyperparameters for the deep convolutional neural network model are learning rate, dropout rate, number of neurons, initializer for different weight values, and the number of epochs required for the training process. We need to adjust the hyperparameter for the optimization of our model. The hyperparameter tuning for the epoch size, batch size, optimizer, learning rate, momentum, network weight initializer, activation function, dropout rate, and the number of neurons in hidden layers is shown in Table 2.

Due to Table 2, batch size 100 and epoch size 100 should be used when we build our CNN model because of the highest accuracy achieved (0.8380). The accuracy and standard deviation achieved are 0.6080, 0.8380, and 0.6467 and 0.0331, 0.2289, and 0.1873 with respect to the epoch size 50, 1000, and 100 and batch size 80, 100, and 60, respectively. This shows hyperparameter optimization for the CNN model, which includes stochastic gradient descent, RMSProp, Adagrad, Adadelata, Adam, AdamMax, and Nadam. The best optimizer for hyperparameter tuning is the Adam optimizer. The accuracy achieved for the learning rate and momentum is as follows: (0.001 and 0.2), (0.01 and 0.2), and (0.2 and 0.4) are 0.8285, 0.4904, and 0.5. The best hyperparameter for the learning rate and momentum are 0.001 and 0.2, respectively. The details about hyperparameter tuning for network weight initializer can be seen. The accuracy and standard deviation achieved for normal, he_normal, uniform, lecun_uniform, normal, zero, glorot_normal, glorot_uniform, and network weight initializer are (0.7161 and 0.0306), (1,0), (0.5000 and 0.0116), (0.8380 and 0.2289), (0.8380 and 0.2289), (0.4904 and 0.0067), (0.6619 and 0.2391), and (0.5000 and 0.0116). The best network initializer in this hyperparameter tuning is he_uniform according to the highest accuracy achieved.

The accuracy and standard deviation achieved for activation functions such as softmax, softplus, softsign, relu, tanh, sigmoid, hard_sigmoid, and linear activation functions are (0.6419 and 0.0205), (0.6329 and 0.0085), (0.7213 and 0.0289), (0.7381 and 0.0230), (0.7096 and 0.0120), (0.6549 and 0.0157), (0.6601 and 0.0095), and (0.7135 and 0.0147), respectively. The best optimizer for the activation function according to the highest accuracy achieved is the

ReLu optimizer. The accuracy is the best when the dropout rate is zero with some weight constraint. The accuracy and standard deviation achieved for the dropout rate and weight constraint (0 and 0.3), (0 and 1), (0.1 and 2), and (0.5 and 4) are (0.7135 and 0.2352), (0.8380 and 0.2289), (0.7285 and 0.2063) and (0.8380 and 0.2289), respectively. The accuracy and standard deviation achieved for the number of neurons 20, 40, 60, and 100 are (0.7174 and 0.0112), (0.7112 and 0.1241), (0.8132 and 0.8913), and (0.8913 and 0.0151). The best optimizer for the number of neurons in the hidden layer is 100 according to the highest accuracy achieved.

4. Performance Evaluation

The performance evaluation section includes the evaluation metrics which explains the accuracy, sensitivity, specificity, precision, and recall based on the true positive, true negative, false positive, false negative result, and classification result of the ZleepNet CNN.

4.1. Evaluation Metrics. The metrics used for performance evaluation of the sleep apnea detection includes accuracy (AC), sensitivity (SE), and specificity (SP), which are calculated from true positive (TP), true negative (TN), false positive (FP), and false negative (FN) in this study. We also calculated precision (PR), recall (RE), and *F1* score (*F1*). It can be seen that three empirical studies are made using the accuracy metrics of the proposed deep convolutional neural network model using fifty patients, and each empirical study includes 3700 to 4000 sample data of ten patients. Each empirical study illustrates two figures in which one is for accuracy and the other is for loss. It becomes more stable after 20 iterations. The stable condition for training prediction loss ranged from 20 to 100 iterations.

4.2. Classification Result. The clinical studies express association in terms of sensitivity and specificity [41]. According to Table 3, the SpO₂ signals are used for the comparison between the proposed model and other classifiers. The proposed model outperformed the other models with the accuracy of 91.3085% and the split rate of 0.2% in which the training data are 20% (794 samples) and testing data are 80% (3178 data samples).

TABLE 2: Hyperparameter tuning for epoch size.

Mean/accuracy	Std dev	First attribute	Second attribute	
0.6080	0.0331	Batch size =>	80	Epoch 50
0.8380	0.2289	Batch size =>	100	Epoch 100
0.6467	0.1873	Batch size =>	60	Epoch 100
0.2289	0.2289	Optimizer =>	SGD	
0.5000	0.0116	Optimizer =>	RMSprop	—
0.5095	0.0067	Optimizer =>	Adagrad	—
0.3285	0.0116	Optimizer =>	Adadelata	—
0.8380	0.2289	Optimizer =>	Adam	—
0.5190	0.0178	Optimizer =>	AdamMax	—
0.4904	0.0067	Optimizer =>	Nadam	—
0.8285	0.2424	Learning rate =>	0.001	Momentum => 0.2
0.4904	0.0067	Learning rate =>	0.01	Momentum => 0.2
0.5000	0.0116	Learning rate =>	0.2	Momentum => 0.4
0.7161	0.0306	Network weight initializer =>	Normal	—
1.0000	0	Network weight initializer =>	he_normal	—
0.5000	0.0116	Network weight initializer =>	Uniform	—
0.8380	0.2289	Network weight initializer =>	lecun_uniform	—
0.8380	0.2289	Network weight initializer =>	Normal	—
0.4904	0.0067	Network weight initializer =>	Zero	—
0.6619	0.2391	Network weight initializer =>	glorot_normal	—
0.5000	0.0116	Network weight initializer =>	glorot_uniform	—
1.0000	0	Network weight initializer =>	he_uniform	—
0.6419	0.0205	Activation function =>	Softmax	—
0.6329	0.0085	Activation function =>	Softplus	—
0.7213	0.0289	Activation function =>	Softsign	—
0.7381	0.0230	Activation function =>	Relu	—
0.7096	0.0120	Activation function =>	Tanh	—
0.6549	0.0157	Activation function =>	Sigmoid	—
0.6601	0.0095	Activation function =>	hard_sigmoid	—
0.7135	0.0147	Activation function =>	Linear	—
0.7135	0.2352	Dropout rate=>	0.0	Weight constraint => 3.0
0.8380	0.2289	Dropout rate=>	0.0	Weight constraint => 1
0.7285	0.2063	Dropout rate=>	0.1	Weight constraint => 2.0
0.8380	0.2289	Dropout rate=>	0.5	Weight constraint => 4.0
0.7174	0.0112	Number of neurons in the hidden layer =>	20	—
0.7112	0.1241	Number of neurons in the hidden layer =>	40	—
0.8132	0.2424	Number of neurons in the hidden layer =>	60	—
0.8913	0.0151	Number of neurons in the hidden layer =>	100	—

TABLE 3: The performance of ZleepNet convolutional neural network on the three datasets.

	Dataset 1	Dataset 2	Dataset 3
Accuracy	90.3	91.3	89.7
Sensitivity	0.9183	91.31	96.49
Specificity	0.9000	94.33	86.79
Precision	90.41	87.23	88.70
Recall	0.9125	91.07	96.49
F1	0.9142	89.10	92.43

5. Limitations and Future Work

There are some challenges in using the deep convolutional neural network for type 4 studies. The nature of the SpO₂ signal is stored in one-dimensional many row and one-column format. Then, segmentation of the signal can lead to missing important information for detection. The features are made up of 16 Hz in a 30 second format. There will be 484 values of the SpO₂ signal in 30 seconds. Assuming that the sleep apnea event happens between first

and second consecutive features, this kind of sleep event will not be detected.

However, the threshold for the detection of sleep apnea events is the cessation of airflow for at least 10 seconds. The use of 484 for a 30 second feature format will reduce such kinds of missing detection to a certain degree. However, missing data due to the segmentation will not be eliminated with 484 feature format within 30 seconds, and it can be reduced to certain acceptable degrees in a 30 second segment. The other challenge is that the data-driven method

TABLE 4: Comparison between different types of classifier for sleep apnea detection.

Ref	Types of classifier	Split rate	Training data (%)	Testing data (%)	Accuracy
[26]	LDA	0.5	50	50	86.5
Proposed model	CNN	0.5	50	50	90.33
[33]	SVM	0.3	70	30	90
Proposed model	CNN	0.3	70	30	91.56
[34]	Bagging rep tree	0.1	90	10	84.80
Proposed model	CNN	0.1	90	10	90.89
[50]	Artificial neural network	0.17	83	17	90.30
Proposed model	CNN	0.17	83	17	91.30

always depends on the training data. When the ground truth of the real data is corrupted, it will not produce the accurate result, so the alternative to this method is the use of unsupervised and reinforcement learning as the future direction. The other factor that should be considered is the privacy of the patients when collecting information for sleep monitoring. Attaching microphones or many sensors and recording video make the patient feel very uncomfortable and difficult to fall asleep for sleep recording [21].

6. Conclusion

Table 4 illustrates the comparison between different types of classifiers, such as LDA, SVM, bagging representation tree, and artificial neural network for sleep apnea detection by giving the same parameter setting in the split rate; the percentage of training data; and testing data. In fact, we run the model with the use of the best hyperparameter achieved from the previous table in the hyperparameter tuning section. Compared to linear discriminant analysis (LDA), the split rate is 0.5 with 50% of training data and 50% of testing data.

According to Table 4, the accuracy of the proposed CNN is 90.33% when the LDA achieved 86.5% accuracy with the use of 50% for training data and 50% for testing data with the split rate of 0.5. The accuracy of the SVM is 90% when the split rate is 0.3% with the use of 70% for training data and 30% for testing data. On the other hand, the accuracy of the proposed CNN is 91.56%. When comparing with bagging representation tree, the accuracy of proposed CNN is 90.89%, using the split rate 0.1% with 90% of data will be training and the other 10% will be testing. When the proposed model achieved 91.30% accuracy when comparing with the artificial neural network (90.30% accuracy) using the split rate 0.17% in which 83% is used for training data and the other 17% is used for testing data. In conclusion, the proposed model outperformed LDA, SVM, bagging representation tree, and artificial neural network when comparing their accuracy by doing the same parameter setting for the split rate and the percentage of training and testing data.

Data Availability

The nature of the data is one-dimensional time series data which is separated into 30-second segment. These data labels for each segment are apnea or not apnea which is identified

by the doctor. The data used to support the findings of this study are available on request to the ethical committee of the Songklanagarind Hospital.

Ethical Approval

The Songklagarind Hospital prioritize patient privacy.

Conflicts of Interest

The authors declare that they have no conflicts of interest.

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