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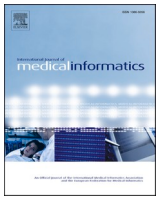

An intelligent model involving multi-channels spectrum patterns based features for automatic sleep stage classification

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ABSTRACT

Effective sleep monitoring from electroencephalogram (EEG) signals is meaningful for the diagnosis of sleep disorders, such as sleep Apnea, Insomnia, Snoring, Sleep Hypoventilation, and restless legs syndrome. Hence, developing an automatic sleep stage scoring method based on EEGs has attracted extensive research attention in recent years. The existing methods of sleep stage classification are insufficient to investigate waveform patterns, texture patterns, and temporal transformation of EEG signals, which are most associated with sleep stages scoring. To address these issues, we proposed an intelligence model based on multi-channels texture colour analysis to automatically classify sleep staging. In the proposed model, a short-time Fourier transform is applied to each EEG 30 s segment to convert it into an image form. Then the resulted spectrum image is analysed using Multiple channels Information Local Binary Pattern (MILBP). The extracted information using MILBP is then deployed to differentiate EEG sleep stages. The extracted features are tested, and the most effective ones are used to the represented EEG sleep stages. The selected characteristics are fed to an ensemble classifier integrated with a genetic algorithm which is used to select the optimal weight for each classifier, to classify EEG signal into designated sleep stages. The experimental results on two benchmark sleep datasets showed that the proposed model obtained the best performance compared with several baseline methods, including accuracy of 0.96 and 0.95, and F1-score of 0.94 and 0.93, thus demonstrating the effectiveness of our proposed model.

1. Introduction

Sleep is an essential physiological phenomenon to maintain healthy life [1]. Lack of adequate sleep, due to daily life and environmental factors, has a profound impact on learning capacity, brain functions, and concentration, which can contribute further to sleep issues such as apnea and insomnia [2,3]. A normal healthy sleep is clinically defined as a good quality, sufficient duration with an appropriate timing, and the absence of sleep disturbances [4]. Medical reports have demonstrated that up to 70 million people in the US endure chronic sleep disorders [5,6] which could impact their daily life and health. Another report released by World sleep day origination[1] showed that every year around 71,000 people suffer serious injuries from car accidents due to sleep-problems.

Polysomnogram (PSG) is used as a standard tool for monitoring sleep stages. It consists of a bunch of biomedical signals including Electro-encephalogram (EEG), Electromyogram (EMG), Electrooculogram (EOG), ElectrocardiogTram (ECG), and other kinds of bio-signals. Sleep staging based on biomedical signals is a fundamental task to understand sleep regularity and disorders. According to the American Academy of Sleep Medicine (AASM), EEG signals are classified into 30-s intervals, and each segment is visually categorised by a sleep expert into one of five sleep stages, including Wake (W), non-Rapid Eye Movement (NREM) and Rapid Eye Movement (REM) (R) where the NREM is further classified into (S1, S2, S3).

Visual inspection is the standard way of sleep monitoring which is used to characterise EEG recordings based on patterns and waveforms associated with each sleep stage, such as alpha rhythms in stage W, and

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K-complexes or sleep spindles in stage S2. However, the use of manual inspection to analyse a whole-night sleep is time-consuming and laborious. Therefore, extracting representative features from EEG to classify sleep stage automatically has attracted significant research interest in recent years.

Traditional EEG sleep classification methods usually extract representative features from EEG signals using transformation models such as Fourier Transform (FT) and Wavelet Transform (WT), then those features are fed into the Support Vector Machine (SVM) or Hidden Markov k-means for sleep staging. For example, Dhok et al., [8] extracted rényi entropy and Wigner–Ville distribution to analyse EEG signals. The extracted features were used as inputs for a gaussian kernel-based support vector machine. Taran et al, [12] applied an optimize flexible analytic wavelet transform to classify a single channel EEG signal. Each EEG epoch was passed through optimize flexible analytic wavelet transform (OFAWT) to extract the desired features for EEG sleep stages. Then several classifiers including a decision tree, discriminant analysis, ensemble, and k-nearest neighbour classifiers were employed to classify EEG features into five sleep stages. Huang et al., [13] combined joint quaternion valued singular spectrum with ensemble empirical mode decomposition to identify sleep stages. A fast Fourier transform was used in that study to decompose EEG signals. A bootstrap aggregating classification-based model was designed for classifying the extracted features. da Silveira et al.,[14] applied a discrete wavelet transform to analyse sleep EEG characteristics. Two statistical features, kurtosis, skewness, and variance were extracted from wavelet coefficients, then were sent to a random forest classifier. Prerau et al., [15] proposed a multitaper spectral analysis approach to analyse EEG sleep stages and compared their results with traditional spectral estimation techniques.

Although feature extraction based on transformation techniques could improve the efficiency, some shortcomings are still evident. For example, some features may be suitable for a specific dataset, but could receive worse performance on other datasets, and using the same features set to classify all sleep stages could not be adequate. To obtain a higher accuracy of sleep stage classification, a superior method needs better generalization and efficiency.

With the development of deep learning, many researchers focus on applying deep neural networks for feature extraction of EEG signals. These methods could improve the generalization and accuracy by their capacity of learning complicated nonlinear features. Chambon et al. [16] used CNN to obtain intra-local feature of each segment, and directly sending a feature sequence to the classifier for sleep staging. Supratak et al. [17] and Seo et al. [18] suggested intra-local feature vectors produced by CNN, and then the extracted features were fed into LSTM. Xiang et al. [19] introduced a semantic learning based on CNN-LSTM structure. Jia et al. [20] designed a graph convolutional network model to extract spatial temporal features from EEG signals. Huang et al. [21] tested different kernel sizes in CNN to extract multi-scale intra-local features. Dong et al. [22] extracted hand-crafted features of spectrum from EEG signals and feed them into LSTM for sleep staging. The proposed model was trained with an adversarial concept for sleep staging. Ghasemzadeh et al., [7] classified EEG sleep stages based on logistic smooth transition autoregressive (LSTAR). A double-density dual-tree discrete wavelet transform was applied to decompose EEG segment into time–frequency sub-bands. Then, LSTAR was employed to extract a features vector from sub-bands. The final set of features was sent into a classifier to classify EEG segments into sleep stages. Jadhav et al., [9] utilised a convolution neural network model with time frequency image to classify EEG sleep stages. Each EEG segment is passed through a continuous wavelet transform to obtain a time frequency image and then it was used as an input to the convolution neural network model. Sundar et al., [10] proposed a deep learning model based on a Bidirectional Recurrent Neural to classify EEG sleep stages. EEG signals were pr-processed and then each 30 s segment was fed to the proposed model. Tang set al., [11] designed an end-to-end deep adaptation model for sleep stages classification. ECG signals were used in that study as inputs to the proposed model.

Although the above-mentioned approaches based on deep learning approaches achieved an acceptable performance, investigating the waveform characters and texture patterns of sleep stages should be further investigated and considered. Those methods could not fully consider these patterns, which means it needs a model to extract this information and fit the actual sleep staging process, improving the accuracy of classification. Understanding the patterns associated with EEG sleep stages could help design a suitable model for sleep stage classification.

To overcome the above shortcomings and incorporate the patterns of EEG, we propose a novel sleep stages classification model combining multiple channels information local binary pattern technique and ensemble classifier based on genetic algorithm. The objective of the proposed model is to capture and investigate the most representative texture features including structural patterns, and multi-channel information. Firstly, EEG signals are segmented into 30 s interval, then each EEG segment is passed through a short-time Fourier transform. As a result, each 30 s segment is converted into an image form. The MILPB is applied to extract the desired texture features to differentiate sleep stages. The extracted features are sent to an ensemble classifier to categorise them into five sleep stages.

2. Proposed methodology

In this study, an intelligence model is proposed to classify EEG sleep stages. To transfer EEG signal into an image form, A short-time Fourier transform is applied to each EEG 30 s segment. The extracted spectrogram image is analysed using multiple channels information local binary pattern (MILBP) approach. Texture features are pulled out from each spectrogram image to represent EEG sleep stages. The extracted texture features are investigated to select the most significant ones. The selected EEG features are sent into the proposed ensemble classifier based on genetic algorithm. The genetic algorithm is utilised to select the optimal weights for each classifier to improve the classification accuracy. This model is implemented in a desktop computer system with the following specifications: Windows 10 Pro operating system, 8 GB RAM, and Intel core i7 @ 3.3 GHz. MATLAB Software, image processing toolbox, EEG signal processing software are used in the design of the proposed model. Fig. 1 shows the schematic diagram of the proposed model for sleep stages classification.

2.1. Transferring EEG signals to logarithmic spectrogram image form

As EEG signals are high dimensional and non-stationary time series, time–frequency domain techniques are considered an efficient tool to reveal the important characteristics by representing EEG data in both the frequency and time domains [23–25]. In this paper, we adopted the logarithmic spectrogram image to analyse EEG sleep stages as it is considered one of the efficient techniques time–frequency domain techniques [25].

According to previous studies, this technique can expose the hidden characteristics of signals. It has been employed in many applications to identify the abnormal events in brain signals. In this design, we applied a short-time Fourier transform (STFT) to each 30 s EEG sleep segment to logarithmic spectrogram images using the following formula:

$$X[f] = \sum_{k=0}^{K-1} x[k]zx[k]e^{\frac{-2\pi k}{K}}, f = 0, 1, \cdots.., K-1 \quad (1)$$

Where, k refers to the discrete time index, f defines as a discrete frequency index, z refers to the Hamming window, while ($z_f = \frac{2f\pi_.}{K}$) denotes to the frequency in radians. In this study, we adopted a window size of 256 datapoints with an overlap of 50 % to transfer EEG epochs to spectrogram images from using the following formulae:

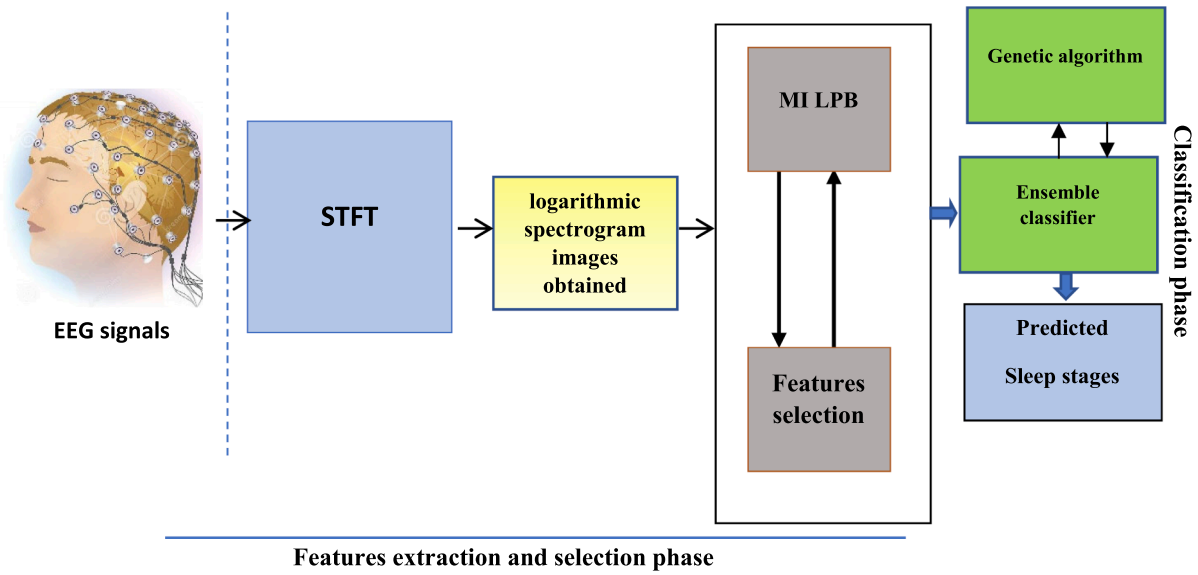

Fig. 1. The proposed model for EEG sleep stages classification.

$$S(f,j) = |X(f)| \tag{2}$$

$$IS(f,j) = \log(S(f,j)) \tag{3}$$

Where $IS(f,j)$ denotes to the obtained spectrogram image. It is represented by a two-dimension matrix. While f refers to the frequency bin falls between 1 and 129, and j refers to the number of time frames. Each 30 s EEG sleep segment is converted into an image of 2049x43. Then, the dimensionality of the obtained image is resized to a 50x50 matrix. This reduction is adopted to minimise the execution time of the proposed model. Fig. 2 illustrates an example of 30 s sleep stages segment is being converted into a spectrogram image form. The axis of image represents the frequency and time. The colours scales refer to the amplitude of the frequency of produced spectrogram image. In this example, five sleep stages are converted into images using STFT. Based on our simulation, it is noticed that sleep stages produced different values of the magnitude and frequency that could be used to differentiate sleep stages.

2.2. Multiple channels information local binary pattern (MCILBP)

To improve the discriminant ability of classic LBP in the sleep stages classification, a multiple channels information local binary pattern (MILBP) is proposed to analyse EEG signals [26–28]. The proposed MILBP method uses the characteristics in a single colour channel and integrates it with the correlation information among multiple colour channels to extract the most discrimination information from images produced from EEG signals. As a colour image consists of three channels R, G, B, the proposed model extracts, and investigates the information of each channel and the cross-channel feature information.

The results showed that the cross-channel local information among image's channels provides high discriminative information. As a result, LBP is employed to extract EEG sleep stages features from three different combinations of channels R-G-B, G-B-R, and B-R-G, respectively. In this paper, we adopted the LBP histogram features from each colour channel sequence. In addition, the extracted information from each channel is investigated individually. Then, the nine histograms of LBP are combined in one set to form the final features vector that represents a colour texture of spectrogram image. The main steps of the proposed model are described as follow:

1. When sampling radius R = 3, 18 neighbourhood points are considered in each local cub of 3x3x3. The cube is divided into three different channels. The centre point of G channel is used as a threshold value. Then, the three orthogonal planes of cube are binarized using the threshold. We named the orthogonal planes as plane z, plane ×, plane y. From each plane, LBP code is obtained. Then, three LBP codes are gained to form MILBP descriptor using Eq. (5). The LBP three codes are

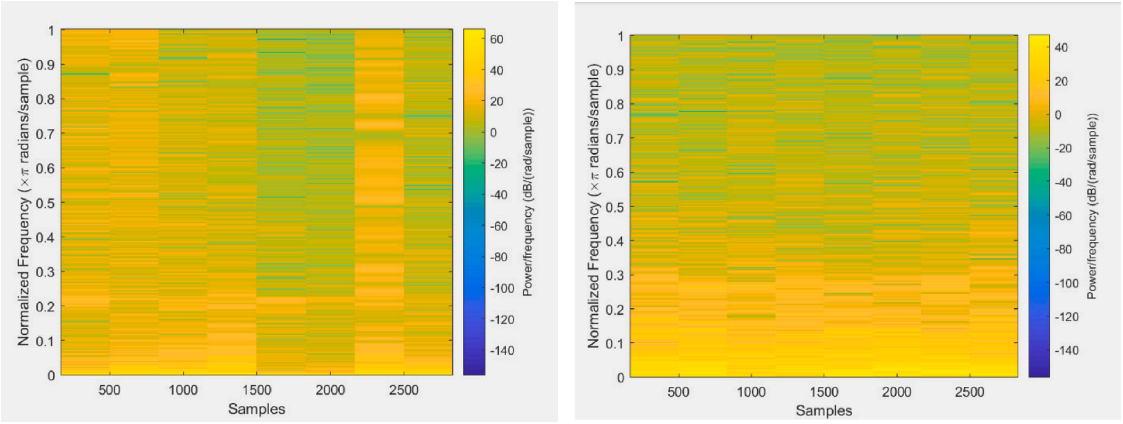

Fig. 2. An example of 30 s sleep stages is converted into an image.

described as: the LBP of y plane denotes to the local texture feature, while the LBP of z, and × represent the multi-channel features Fig. 3(d).

$$MCILBP_{I,R,N}(i,j) = \sum_{m=1}^{N} \delta_I(r_n - r_c)^{2^{m-1}} \tag{4}$$

$$\delta_I(u) = \begin{cases} 1, u \geq 1 \\ 0, u < 0 \end{cases}$$

Where $I = 1,2,3$, is the index of three channels ×, y, z. For instance, the binary number of X is 100001, the equivalent value of LBP is 33 and the LBP^{u2} value is 2.

3 Then, the MCI_LBP histograms for a spectrogram image of are calculated as follows

$$hist_{MCILBP_I}(k) = \sum_{i=1}^{m} \sum_{j=1}^{n} h\left(MCILBP_{I,R,N}(i,j), k\right) \tag{5}$$

where $MCILBP_1, MCILBP_2, MCILBP_3$ are the histograms of plane ×, y, and z respectively. $MCILBP_2$ denotes the LBP feature describing the texture colour in a single channel, while $MCILBP_3$, and $MCILBP_1$ represent features cross channels. In this paper, we integrated the features of three histograms in one set to create one set represented by $MCILBP^{R,G,B}{}_{I,R,N}$ for each spectrogram image where

$$MCILBP^{R,G,B}{}_{I,R,N} = [MCILBP_1, MCILBP_2, MCILBP_3] \tag{5}$$

3. The correlation and dependencies between channels sequences are considered in this paper. The three colour channels of RGB space are shifted to GBR and BRG. As a result, we obtained a new set representation called *MCILB* and$hist_{MCILBP} = \left[MCILBP^{R,\ G,\ B}{}_{I,R,N},\ MCILBP^{G,\ B,R}{}_{I,R,N},\ MCILBP^{B,\ R,\ G}{}_{I,R,N}\right]$.. The obtained three united set of different sequences are normalised to [1, 0]. Then they are integrated as $hist_{MCILBP}$ to represent each colour image.

$$hist_{MCILBP} = \left[MCILBP^{R,\ G,\ B}{}_{I,R,N},\ MCILBP^{G,\ B,R}{}_{I,R,N},\ MCILBP^{B,\ R,\ G}{}_{I,R,N}\right] \tag{6}$$

2.2.1. MCILBP magnitude

The colour differences magnitudes of the generated images are also investigated and used to extend MCI_LBP to MCI_LBPM to enhance its discriminative ability. Previous studies showed that magnitude information of an image provides a high discriminative information regarding cross channel features. The MCI_LBP contains attributes extracted from three planes y, z, and ×, for example, nine colour values on plane × is considered and the centre is marked as a reference point. Based on Eq. (9), the local absolute differences $R_n^{'}(n = 1,2,3,\cdots r = 8)$ is obtained by subtracting the reference point from the neighbourhood points. For a colour image of M × N dimension, (M−2L) × (N-2L) references can be obtained. As a result, we obtained (M−2L) × (N-2L) × 8 local absolute references. The average value *Av* for all the $R_n^{'}$ in the entire image is calculated.

$$Av = \frac{1}{(M-2L)x(N-2L)xr} \sum_{i=r+1}^{M-R} \sum_{j=r+1}^{N-r} \sum_{k=1}^{P} R_n^{'} \tag{7}$$

Then $MCILBPM_{I,r,P}$ is defined as

$$MCILBPM_{I,r,P}(i,j) = \sum_{n=1}^{P} \delta_I\left(R_n^{'} - Av\right)2^{n-1} \tag{8}$$

The extended histograms $hist_{MCILBPM}$ is obtained by combining $hist_{MCILBPM}$ and $hist_{MCILBP}$ as

$$hist_{MCILBPM} = [hist_{MCILBPM}, hist_{MCILBP}] \tag{9}$$

The R, and P parameters produced a total of P (P − 1) + 2 uniform codes. However, the other nonuniform codes are considered as one code. The LBP^{u2} is represented as P(P − 1) + 3. In this paper, we chosen the sampling range as 8, 12, 16 and 24, and the R is set to 1, 2, and 3, respectively. As a result, the feature dimension is 59, 135, 243 and 555. Then, we cascaded all the features as one descriptor.

As colour images comprise of three colour channels, the radius of Z-axis can be 1, when the *R* >1. In our simulation, we set the value of *P* as p = 8, p = 12, and p = 16 for planes Z, and X. In addition, the R set to R = 1, R = 2, and R = 3, respectively. With the plane Y, *P* value is set as 8, 16, and 24, and the R is set as 1, 2, and 3, respectively. The dimensions of MCI_LBP are 531(=59 × 3 × 3), 1539(= (243 + 135 × 2) × 3) and 3123 (= (555 + 243 × 2) × 3).

2.3. The proposed ensemble model

Ensemble algorithms are machine learning models that are built using a set of classifiers [29–31]. They assign labels to new cases according to the voting decision that is form from their predictions. One of the solutions used to make the decision is to perform a voting process based on the outputs of different classifiers [32]. In this paper, we suggested a design based on threshold algorithms. The new ensemble model integrated with the genetic model to identify the best weight value for classifiers that made up the ensemble. Fig. 3 shows the proposed classification model. The proposed model consists of three phases.

- Training phase: In the first phase, the original dataset is partitioned into three sets. The first set is used to train the classifiers. The second set is utilised for the training the genetic algorithm to obtain the weights, while the third set is employed for the validation of the proposed model. The training set is employed to train *M* models that are used to form the ensemble based on a matrix cost *N*. After training *M* classifiers, two matrices named Set_{opt}, Set_{val} are obtained with number of rows corresponding to the optimisation and validation sets, and columns number equal to the number of classifiers.
- Optimisation phase: In this phase, an optimisation method based on D_{opt} is used to determine the weights for each classifier to deliver the

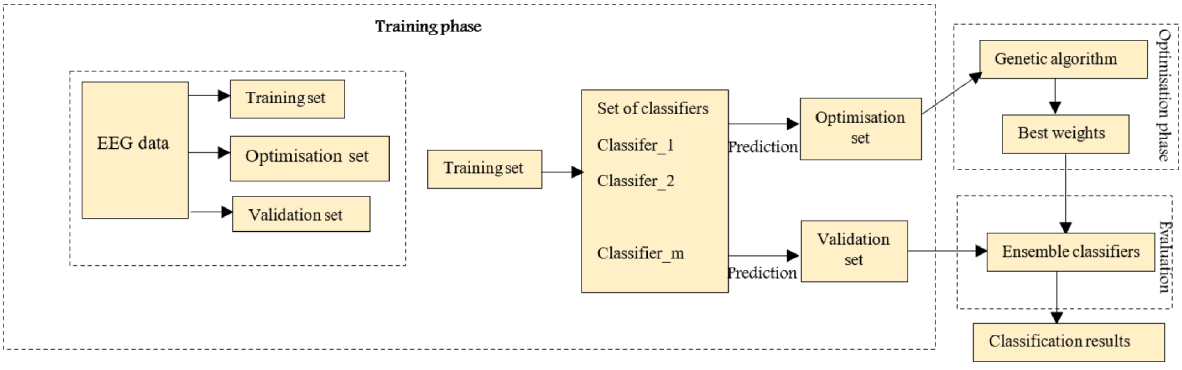

Fig. 3. The proposed ensemble classifier.

best solution. The optimisation phase searches for the optimal weights that is carried out using genetic algorithms.
- Evaluation phase: In this phase, the predictions achieved in the first stage are examined using the validation set Set_{val}.

We detailed each step. First, we explained the predication matrices that are employed as inputs to the genetic algorithm. Then, the classifiers and their parameters are explained. Secondly, optimisation process is explained in detail. Finally, we explained the metrics used to evaluate the proposed model.

2.3.1. Training phase

The data of the genetic algorithm are generated. we used a set of classifiers to design the ensemble model. A cost-sensitive function was employed using a cost matrix M to produce a model with a low cost. The cost matrix moves the classified samples from one class to another. Let $Ts = \{(f_1, l_1), (f_2, l_2), \cdots\cdots, (f_n, l_n)\}$ is an input dataset, where f_i is feature values, and l_i is a label. The cost matrix is described as a matrix of N elements. The elements of cost matrix $N(i,j)$ represent the predicted label j and the real i.

The dataset is divided into three sets named Set_{train}, Set_{tval}, and Set_{opt}. Cost matrix N and Set_{train} are employed to train the ensemble model. As a result, two prediction matrixes are achieved D_{opt}, D_{val} as shown in Fig. 3.

2.3.2. Optimisation phase

The purpose of designing an ensemble classifier is to improve the results of sleep classification produced by individual classifiers. Different strategies are used to merge the output of classifiers to form the ensemble. Most of ensemble techniques used a weighting vote approach by which assigns a specific weight to each classifier. The main issue with this approach is how to assign the best weight to each model used to from the ensemble. In this paper, the genetic algorithm is used to assign the optimal wight to each of the classifiers. The genetic algorithm is employed to find the wights for each classifier of the ensemble to classy new instances. Five main steps are repeated until the desired criteria is reached.

- **Initialisation**: In this step, the weight assigned to each classifier is represented by chromosome. Positional encoding is used to represent genes. Each gene i_{th} represents the weight of i_{th} classifier. Chromosome *Chro* is defined as

$$Chro = (ch_1, ch_2, \cdots, ch_k) \tag{10}$$

Where k refers to the number of classifiers used to form the ensemble, each member in the genetic algorithm is contained n Chromosomes.

- **Evaluation:** The phase is performed using an error function f. The error function is calculated according to the cost of the label predicted for each entity in the dataset. We considered the vote carried out with weight associated with each classifier. It is the total sum of all costs of each entity in the dataset. The cost matrix N is employed to calculate the costs. The following steps are considered to calculate the error function. Each classifier's weight is calculated using chromosome *ch*, prediction matrix *pre*, and instance e for the possible label in the dataset.

$$w(ch, pre, e_i, l) = \sum_{j=1}^{M} w_j [pre_{i,j} == l] = \begin{cases} 1, if pre_{i,j} = l \\ 0, otherwise \end{cases}$$

The successful label L_i is calculated for each instance e_i as follow.

$L_i = armaxw(ch, pre, e_i, l)$. Then, the error function is calculated as a sum of costs as follow:

$$f(ch, pre, datset) = \sum_{i=1}^{M} N(l_i L_i) \tag{11}$$

Where l_i is the actual label for the instance i_{th}.

- **Selection**: Deterministic approach is used to make a selection by which several tournaments are run among few chromosomes that are chosen arbitrarily from the population. The number of selected chromosomes is called selection pressure and denoted by $pres_{selected}$. The selection pressure determined the probability of worse individuals that were involved in the competition. In each competition, it is selected the winning chromosome which obtains the smallest error value.
- **Crossover and Reproduction**: In this paper, uniform crossover is used in this research as it is a powerful method used to find all possibilities when parents are re-joined. Each gene has the same probability that belong to one or other parent. We refer n_{th} to the total number of children produced by two fathers.
- **Mutation**: Uniform mutation is utilised in this research. Mutation operator mu_{press} is employed in this paper. A gene mutation mu_{press} probability is assigned to each member in the new population.

2.3.3. Evaluation procedure

Once the optimal weights are collected from the optimisation phase. Those obtained weights are passed to the predication matrix to obtain predications. This predication is then employed to compute validation measures named MZ, and ME. Where MZ is the mean of the total differences between the actual set and the predication set, while ME is the rate of error of each classifier.

$$MZ = \frac{1}{n}\sum_{k=1}^{k=n} |y_k - \overline{y_k}| \tag{12}$$

$$ME = \frac{1}{n}\sum_{k=1}^{k=n} |y_k - \overline{y}_k| = 1 - Acc \tag{13}$$

3. Experimental results

In this section, the performance of the proposed model was evaluated on two sleep datasets, and it was compared with several state-of-the art EEG sleep stages classification models. The proposed model was implemented with MATLAB 2021b using Machine learning toolbox, Image processing toolbox. We adopted 10-fold cross validation to obtain the average results ensuring the effectiveness of experiments. The ratio of training, and test sets was set in accordance with the number of subjects. The Hamming window with 1-s window size and 50 % overlap was chosen as the STFT function.

3.1. Experimental EEG dataset

Two open access EEG sleep datasets were used in this paper to evaluate the proposed model. The datasets were collected from Physionet Sleep-EDF, and UCD.

3.1.1 Dataset-1 (Physionet Sleep-EDF): This dataset contains 197 whole-night PSG recordings [33]. Each PSG recording contains EEG (from Pz-Oz and Fpz-Cz channels), submental chin EMG, EOG and event marker. The EEG and EOG signals were sampled at 100 Hz. Dataset also contains hypnogram files that have sleep patterns corresponding to the PSGs. Each 30 s PSG segment was manually scored by an expert according to the Rechtschaffen and Kales (R&K) rules [34]. In addition, this dataset has two different data subsets, one was recorded from healthy people, the other was collected from the people with mild difficulty falling asleep. Due to some PSGs have many unknown annotations, only 180 whole-night PSGs with three channels (2 EEG and 1 EOG) were selected, where 143 PSGs from healthy dataset and 37 PSGs from unhealthy dataset.

3.1.2 Dataset-2 (UCD): This dataset was collected by St. Vincent's University Hospital Sleep Disorders Clinic, which contains 25 full overnight PSG recordings [35]. The dataset is free publicly available at https://archive.physionet.org/physiobank/database/ucddb/. All PSG recordings were collected from adult subjects with suspected sleep disordered breathing. Each PSG recording consists of 14 channels,

mainly including EEG and ECG at 128 Hz, EMG and EOG at 64 Hz. Each 30-s segment was scored by a sleep expert sleep based on R&K rules. Six channels (2 EEG, 2 EOG, 1 EMG and 1 ECG) of all PSGs were selected in this study. To balance the amount of each sleep stage, stage N3 and N4 were combined into stage N3 according to the AASM standard. The final task of classification includes five stages (W, N1, N2, N3, R). the amount of EEG segments on two datasets is shown in Fig. 4.

3.2. Ensemble algorithm settings

In this experiment, the base classifiers that were used to form the ensemble classifiers, were chosen carefully. The parameters for the genetic algorithm were selected to obtain the best classification results. We used Weka software to implement the proposed ensemble classifiers. Table lists the classifiers model used to construct the ensemble model. As mentioned before the genetic algorithm was adopted used to choose the optimal weights to improve the weighting vote phase. In this paper, five basic steps in genetic algorithms were implemented as mentioned in section 2.3.2. All parameters were selected carefully based on the obtained results. As a result, the population size was set 200 to initialise the population. In the evaluation phase, the basis of error function was employed for each class of the dataset. The voting process was carried out based on the weights associated with each individual classifier. In the selection phase, the deterministic tournament technique was selected in this research. In the final phase, the Uniform crossover was applied in the reproduction and crossover. The total number of children produced from two parents is two, as shown in Fig. 5.

3.3. Results

3.3.1. The performance of the proposed model in different colour spaces

The effects of the use of different combination of sequences of channels with different number of radiuses on sleep stages classification were investigated. In this experiment, the three channels of the RGB space were arranged in different sequences, namely, G-B-R, R-G-B, and B-R-G, respectively. Table 1 reports the average of classification accuracy in different channel sequences with different scales. The results showed that the proposed model MCILBP improved significantly when all planes were considerd and R = 3. As a results, the textures features extracted from all the planes of all the channel-sequences were adopted in our paper to classify EEG sleep stages.

3.3.2. The effects of combine magnitude information with MCILBP

To verify the effects of combined magnitude information with the textures features MILBP on EEG sleep stages classification, a new experiment was conducted in which the effectiveness of magnitude information on classification accuracy was investigated. In this experiment, the MILBP features with and without, and magnitude information were extracted from each EEG segment, and then sent into the proposed ensemble classifier. It can be noticed that the accuracy of sleep stages classification was significantly improved when the textures features were combined with the magnitude information. In addition, we noticed that the best results were obtained in the case of R = 3. However, when the cascaded descriptor was adopted the classification performance was improved by 3 %. Table 2 reports the classification results based on different combination of features.

The reason was that both stage N2 and stage N3 produced similar texture features corresponding to sleep spindles, which made them had similar features. This was happened more clearly in UCD dataset, which means sleep apnea could make EEG characteristics of stage N2 appears in stage N3. It also noticed that the classification of stage N1 was degraded in Dataset-1 because some samples were misclassified into stage W and N2.

Based on previous studies stage N1 was usually considered as a transitional stage between stage W and N2 [5,26], [50]. It produces similar alpha rhythm and low amplitude compared with stage W and N2 which made the classification of stage N1 more complicated [22]. In addition, the number of N1 segments in Dataset-1 (12.1 %) is less than UCD dataset (16.4 %), resulting in the weak performance in the latter dataset.

3.3.3. Comparisons with classic machine learning models

To obtain an accurate detection of sleep disorders, and to understand the relationship among sleep stages, we need to classify different categories of sleep-stages. The differentiation between REM and NREM is necessary for sleep experts to identify several sleep disorders such as catalepsy. In addition, the evaluation of sleep quality is essential to identify any abnormality in AW and sleep-stages. In this paper, we formed several combinations sleep stages categories as presented in Table 3. This type of experiment delivers a fair performance comparison among the suggested model and the state-of-the-art methods designed for sleep stages classification.

The classification performance of the proposed ensemble model was

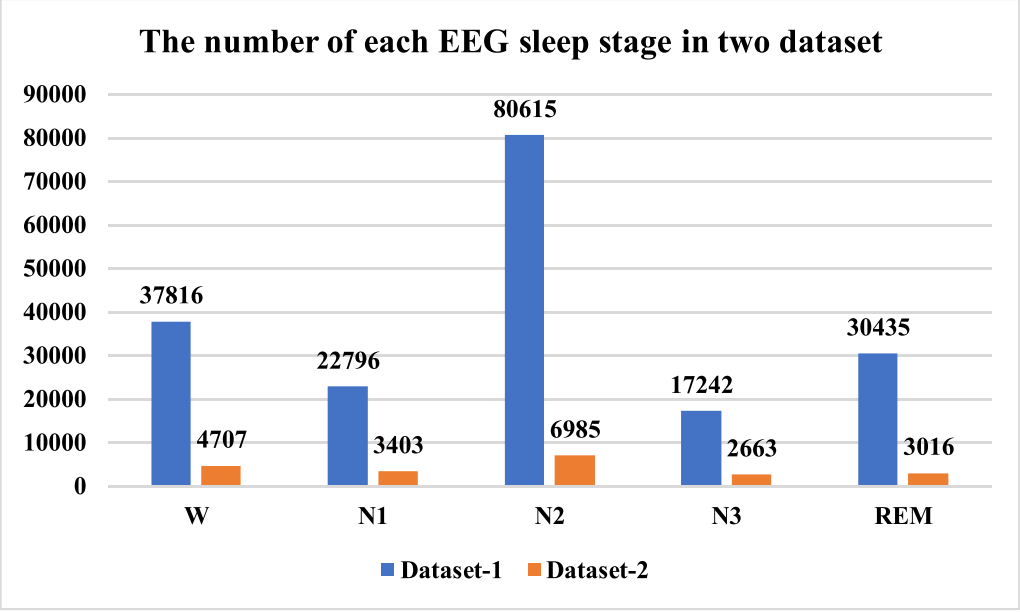

Fig. 4. The proposed ensemble classifier.

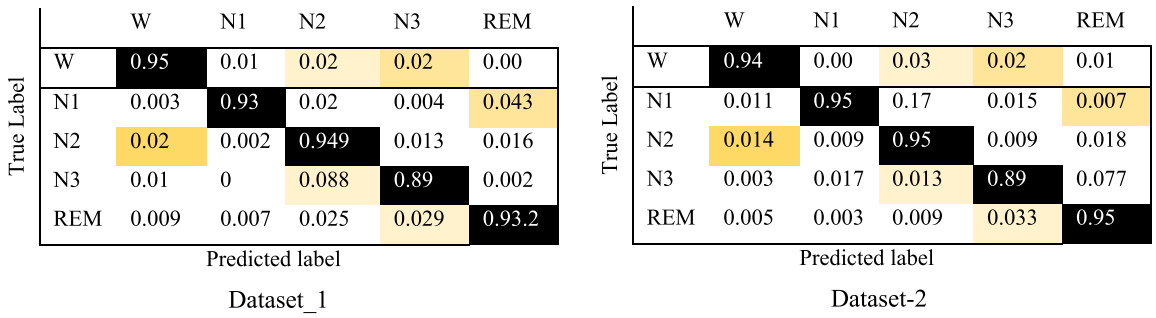

Fig. 5. Confusion matrix of the proposed model.

Table 1
The average of classification accuracy of the proposed model with different planes and colour channels sequences.

Plane Y			
Sequences	R = 1	R = 2	R = 3
R-G-B	67.10 %	69.45 %	72.22 %
G-B-R	61.12 %	70.51 %	71.51 %
B-R-G	82.2 %	83.7 %	86.19 %
Sequences Cascaded	84.48 %	85.14 %	86.11 %
Plane X and Z			
R-G-B	80.12 %	82.67 %	83.21 %
G-B-R	78 %65	80.37 %	82.72 %
B-R-G	84.69 %	86.58 %	87.13 %
Sequences Cascaded	89.32 %	87.27 %	90.15 %
All planes (Y, Z,X)			
R-G-B	92.12 %	90.59 %	92.82 %
G-B-R	90.18 %	91.36 %	91.95 %
B-R-G	93.43 %	93.66 %	94.24 %
Sequences Cascaded	**93.75 %**	**93.98 %**	**94.01 %**

Table 2
Classification accuracy of the proposed model with and without magnitude information.

Features	Radius	Accuracy	Sensitivity
Textures features	1	87.13 %	86.16 %
	2	88.11 %	87.80 %
	3	88.27 %	87.99 %
	Cascaded	89.24 %	88.87 %
Textures features with magnitude information	1	89.87 %	88.76 %
	2	90.12 %	89.90 %
	3	91.65 %	91.98 %
	Cascaded	**94.32 %**	**94.12 %**

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Table 3
Different categories of sleep stages.

Classification class	Sleep stages
Six sleep stages	AW, N1, N2, N3, N4 and REM
Five sleep stages	AW, N1, N2, SWS (N3, N4) and REM
Four sleep stages	AW, SHS (N1, N2), SWS, and REM
Three sleep stages	AW, NREM, and REM
Two sleep stages	AW, and sleep (N1-N4, REM)

evaluated with several machine learning techniques named SVM, ensemble algorithms, and KNN. Each algorithm performance was assessed using the 10-folds cross-validation metric. In this experiment, the EEG data were randomly separated into 10 groups. At each experiment, one set was involved in the testing and remaining sets were used in the training, the process was repeated ten times, and all results were recorded. Tables 4–8 report the comparisons of all classification results of models.

In the comparisons, the average of classification accuracy, specificity and sensitivity were adopted as performance comparison parameters for the classifiers. The comparison results showed that the proposed ensemble model based on genetic algorithm provided better results as than other classification models. It obtained the highest classification rates with all five-sleep stages categories. The highest accuracy of 99.98 % was gained with 2 sleep stages category. The second highest accuracy across the sleep stages categories was recorded by the ensemble boosted classifier. However, the KNN and SVM recorded the lowest accuracy rates. Based on the results, the proposed model based on genetic algorithm scored a high classification rate for all sleep stages compared with the classic ensemble classifier. The results demonstrated that the use of genetic algorithm to calculate the weights for the classifiers improved the performance of the ensemble.

4. Discussion

In the current study, we found that a combination of textures features, and magnitude information improve EEG sleep stages classification by 4 %. In this section, the main findings are summarised as follow:

1. The performance of the proposed model was evaluated based on two EEG channels Pz-Oz, and Fpz-Cz. Table 9 present the classification results in terms of accuracy, sensitivity, specificity, and kappa coefficients. The textures features and magnitude features were extracted from both channels and then they sent to several classifies. It was noticed that the proposed model achieved a high performance on two EEG channels. The Kappa values of Pz-Oz, and Fpz-Cz were 0.93, and 0.95 respectively. The obtained results indicated that the agreement between manual scoring and the proposed model was excellent.
2. The performance of the proposed model was evaluated in term of leave-one-subject-out (LOSO) cross-validation strategy. In this experiment, one subject was utilised for the testing phase, while the remaining subjects was employed for the training purposes. Table 10 reports the classification accuracy based on LOSO metric for two datasets. The highest values were highlighted in bold. The proposed model obtained an accuracy of 0.93.1 % with Dataset-1 (Physionet Sleep-EDF), and 0.93.2 with Dataset-2 (UCD) respectively.To assess the effectiveness of the proposed model for EEG sleep stages classification, comparisons were made with other existing sleep classification methods. The results of comparisons were presented in Table 11. The comparisons were made based on the most common performance metrics for sleep stages classification ACC and kappa that were used by previous methods. In addition, five and six sleep stages classification classes were reported in this table. We can notice that the classification accuracy of previous methods for six and five sleep stages dropped in the ranges of 61–96 and 71–94 %. The results of comparisons indicate that the proposed model can add a meaningful impact in the field of EEG sleep stages analysis. It can be implemented in hardware systems to be used in health care units for identifying of sleep-related disorders.

Table 4
Six sleep stages identification results of the proposed model compared with several machine learning models.

Classifier	R = 1			R = 2			R = 3		
	Acc.	Sen.	Spec.	Acc.	Sen.	Spec.	Acc.	Sen.	Spec.
KNN	67.11 %	66.45 %	66.56 %	69.76 %	69.12 %	68.87 %	60.12 %	60.43 %	69.98 %
SVM	73.3 %	72.12 %	72.02 %	74.87 %	74.31 %	73.89 %	76.32 %	76.23 %	75.92 %
Ensemble Bagged	78.31 %	78.20 %	78.01 %	80.38 %	79.87 %	79.69 %	82.22 %	81.98 %	82.01 %
Ensemble Boosted	80.54 %	80.21 %	80.31 %	83.20 %	82.98 %	82.84 %	84.55 %	84.12 %	84.38 %
The proposed model	**93.75 %**	93.26 %	92.79 %	93.98 %	93.22 %	93.10 %	94.01	94.00 %	93.99 %

Table 5
Five sleep stages identification results of the proposed model compared with several machine learning models.

Classifier	R = 1			R = 2			R = 3		
	Acc.	Sen.	Spec.	Acc.	Sen.	Spec.	Acc.	Sen.	Spec.
KNN	68.54 %	68.07 %	68.24 %	69.99 %	69.84 %	69.45 %	70.26 %	70.19 %	70.31 %
SVM	76.54 %	76.13 %	76.11 %	77.32 %	78.78 %	77.10 %	79.42 %	79.01 %	78.99 %
Ensemble Bagged	80.74 %	80.35 %	80.11 %	81.99 %	81.21 %	81.01 %	83.73 %	83.12 %	82.51 %
Ensemble Boosted	84.99 %	84.11 %	84.20 %	85.02 %	84.79 %	84.82 %	85.90 %	85.14 %	85.30 %
The proposed model	94.12 %	93.97 %	93.90 %	94.87 %	94.01 %	94.24 %	95.32 %	95.15 %	94.96 %

Table 6
Three sleep stages identification results of the proposed model compared with several machine learning models.

Classifier	R = 1			R = 2			R = 3		
	Acc.	Sen.	Spec.	Acc.	Sen.	Spec.	Acc.	Sen.	Spec.
KNN	83.94 %	83.67 %	83.74 %	83.89 %	83.74 %	83.65 %	84.86 %	84.79 %	84.35 %
SVM	86.04 %	85.93 %	86.90 %	87.82 %	87.28 %	87.14 %	88.41 %	87.71 %	88.59 %
Ensemble Bagged	88.14 %	88.04 %	88.00 %	89.00 %	88.91 %	88.83 %	90.83 %	90.10 %	90.01 %
Ensemble Boosted	92.39 %	92.31 %	92.21 %	93.42 %	93.09 %	93.02 %	94.60 %	94.34 %	94.41 %
The proposed model	96.9 %	96.27 %	96.10 %	97.27 %	97.51 %	97.14 %	98.32 %	98.11 %	98.16 %

Table 7
Four sleep stages identification results of the proposed model compared with several machine learning models.

Classifier	R = 1			R = 2			R = 3		
	Acc.	Sen.	Spec.	Acc.	Sen.	Spec.	Acc.	Sen.	Spec.
KNN	71.24 %	71.00 %	71.04 %	72.19 %	72.30 %	72.10 %	73.93 %	73.59 %	73.50 %
SVM	79.34 %	78.87 %	78.61 %	80.22 %	80.18 %	80.29 %	82.52 %	82.47 %	82.54 %
Ensemble Bagged	83.24 %	83.00 %	82.98 %	84.40 %	84.01 %	84.32 %	85.08 %	84.99 %	85.00 %
Ensemble Boosted	86.10 %	85.41 %	55.83 %	87.43 %	87.00 %	87.12 %	88.30 %	88.10 %	88.00 %
The proposed model	96.72 %	96.31 %	96.75 %	97.27 %	97.14 %	97.01 %	98.12 %	97.97 %	97.99 %

Table 8
Two sleep stages identification results of the proposed model compared with several machine learning models.

Classifier	R = 1			R = 2			R = 3		
	Acc.	Sen.	Spec.	Acc.	Sen.	Spec.	Acc.	Sen.	Spec.
KNN	90.17 %	90.01 %	90.14 %	91.12 %	9103 %	90.95 %	92.36 %	92.24 %	92.17 %
SVM	93.24 %	93.10 %	93.30 %	93.99 %	93.68 %	93.60 %	94.72 %	93.81 %	93.39 %
Ensemble Bagged	94.79 %	94.15 %	94.21 %	96.89 %	96.93 %	96.51 %	96.12 %	95.89 %	96.00 %
Ensemble Boosted	97.19 %	97.21 %	97.25 %	97.99 %	97.12 %	97.00 %	97.91 %	97.94 %	75.70 %
The proposed model	98.92 %	98.97 %	98.30 %	98.17 %	98.21 %	98.04 %	99.92 %	99.85 %	99.96 %

Table 9
Six sleep stages identification results accuracy based on different EEG signals.

Classifier	Pz-Oz				Fpz_Cz			
	Acc.	Sen.	Spec.	kappa	Acc.	Sen.	Spec.	kappa
KNN	67.11 %	66.45 %	66.56 %	0.65	65.17 %	63.91 %	63.02 %	0.62
SVM	73.30 %	72.12 %	72.02 %	0.70	72.22 %	72.43 %	72.32 %	0.71
Ensemble Bagged	78.31 %	78.20 %	78.01 %	0.77	77.32 %	77.71 %	77.61 %	0.77
Ensemble Boosted	80.54 %	80.21 %	80.31 %	0.79	79.21 %	78.00 %	79.14 %	0.78
The proposed model	93.75 %	93.26 %	92.79 %	0.93	92.41 %	91.19 %	92.01 %	0.92

Table 10
Six sleep stages classification accuracy based on LOSO.

Classifier	Dataset-1		Dataset-2	
	Acc.	*F_score*	*Acc.*	*F_score*
KNN	66.99 %	0.65	65.86	0.65
SVM	73.10 %	0.72	73.12	0.73
Ensemble Boosted	77.45 %	0.76	76.98 %	0.75
Ensemble Bagged	81.01 %	0.80	80.95 %	0.80
The proposed model	**93.21 %**	**0.92**	**92.93 %**	**0.93 %**

Table 11
Comparisons among the proposed model with previous methods.

Authors	Approach	Channels	Classification rates R&K	AASM
Doroshenkov et al., [36]	Amplitude features based HMM classifier	Fpz-Cz, Pz-OZ	ACC: 61.08 %	–
Ebrahimi et al., [37]	Wavelet transform coupled with ANN	Fpz-Cz, Pz-OZ	–	7 ACC: 1.93 %
Hassan et al., [38]	TQWT with random forest	Pz-Oz	ACC: 93.38 %	ACC: 95.42 %
Hassan et al., [39]	TQWT based on Bagging	Pz-Oz	ACC: 92.43 %	ACC: 93.69 %
Hsu et al., [40]	Energy features-based approach coupled with ERNN	Fpz-Cz, Pz-OZ	–	ACC: 83.60 % Kapp:0.7452 %
Liang et al., [41]	AR model with LDA	Fpz-Cz	ACC:76.70 %	
Zhu et al., [42]	Visibility graph based SVM	Fpz-Cz	ACC:87.50 % Kappa:0.81 %	
Berthomier et al., [43]	Fuzzy logic based iterative method with fuzzy classifier	Fpz-Cz	–	ACC:71.2 %
Ronzhina et al., [44]	Power spectral density with LDA	Pz-OZ	ACC:76.70 %	
Abdulla et al., [45]	Correlation graph-based ensemble classifier	Pz-OZ	ACC:93 %	
Diykh et al., [46]	Weighted undirected graph-based LS-SVM	Pz-OZ, C3-A2	ACC:95.5	
Diykh et al., [46]	Structural graph-based k-means	Pz-OZ	ACC:92.1	
The proposed model	STFT based MILPB with ensemble classifier	Pz-OZ	ACC:94 % Kappa:94 %	ACC:93 % Kappa:93 %

5. Conclusions

In order to improve the EEG sleep classification accuracy, the MLBP model coupled with an ensemble classifier was suggested to classify EEG sleep stages. Two EEG channels named Pz-Oz, and Fpz-Cz were used to test the effectiveness of the proposed model. Our findings demonstrated that the accuracy of sleep stages classification was significantly improved when the textures features was combined with the magnitude information. The GA algorithm was adopted to select the optimal weight for each classifier. The results showed that the genetic algorithm improved the classification performance of the ensemble classifier when it was used in the weighting calculation. The proposed method shows competitive results for two, three, four, five and six sleep class classification. Therefore, the proposed method. The proposed automatic sleep stages classification model can be implemented in a portable hardware model to perform real-time sleep stages classification.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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