IEEE Access
Multidisciplinary | Rapid Review | Open Access Journal

Received September 23, 2018, accepted October 31, 2018, date of publication December 10, 2018,
date of current version December 31, 2018.

Digital Object Identifier 10.1109/ACCESS.2018.2883062

VMD-RiM: Rician Modeling of Temporal Feature Variation Extracted From Variational Mode Decomposed EEG Signal for Automatic Sleep Apnea Detection

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ABSTRACT Electroencephalogram (EEG) is getting special attention of late in the detection of sleep apnea as it is directly related to the neural activity. But apnea detection through visual monitoring of EEG signal by an expert is expensive, difficult, and susceptible to human error. To counter this problem, an automatic apnea detection scheme is proposed in this paper using a single lead EEG signal, which can differentiate apnea patients and healthy subjects and also classify apnea and non-apnea frames in the data of an apnea patient. Each sub-frame of a given frame of EEG data is first decomposed into band-limited intrinsic mode functions (BLIMFs) by using the variational mode decomposition (VMD). The advantage of using VMD is to obtain compact BLIMFs with adaptive center frequencies, which give an opportunity to capture the local information corresponding to varying neural activity. Furthermore, by extracting features from each BLIMF, a temporal within-frame feature variation pattern is obtained for each mode. We propose to fit the resulting pattern with the Rician model (RiM) and utilize the fitted model parameters as features. The use of such VMD-RiM features not only offers better feature quality but also ensures very low feature dimension. In order to evaluate the performance of the proposed method, K nearest neighbor classifier is used and various cross-validation schemes are carried out. Detailed experimentation is carried out on several apnea and healthy subjects of various apnea-hypopnea indices from three publicly available datasets and it is found that the proposed method achieves superior classification performances in comparison to those obtained by the existing methods, in terms of sensitivity, specificity, and accuracy.

INDEX TERMS EEG signal, entropy, goodness of feature, KNN classifier, model fitting, Rician model, sleep apnea, sub-framing, variational mode decomposition.

I. INTRODUCTION

Sleep apnea, a prevalent sleep disorder disrupting sleep quality of the patients, affects about 6-17% of the general population where among the elderly, this may be as high as 49% [1], [2]. Apnea is defined as complete closure of airflow where repetitive cessation of breathing during sleep occur lasting for few seconds to minutes. Patients usually suffer from daytime sleepiness, headaches, and various cardio-respiratory disorders [3], [4].

The study of overnight polysomnography (PSG) is a standard method for sleep apnea diagnosis where, in a sleep lab, the patient spends the whole night and several accessible bio-signals are collected and with the help of these signals, expert scores the apnea events manually. Visual identification of sleep apnea events with the help of a sleep expert is costly, time consuming and erroneous. Hence, it is of great necessity to develop an algorithm for automatic apnea detection. There are many automatic detection methods available in the

literature, however, most of them utilize multiple biomedical signals including EEG. For example, in [5], oxygen saturation, heart rate variability and the respiratory signals, in [6], EOG, EMG, heart rate variability, oronasal temperature, nasal pressure, in [7] oximetric signal, in [8] pupil size, in [9] EMG signal, in [10] EOG, EMG, ECG signals are utilized. However, use of multiple (or multi-channel) bio-signals has several disadvantages, such as the cost of additional sensors, discomfort for the patient, excessive data acquisition and processing requirement and computational expense in terms of time and implementation. Hence apnea detection with a single channel bio-signal is of great necessity. The advancement in wearable EEG data acquisition system has opened up a new direction for various EEG based disease analysis and thus apnea detection from EEG signal is now getting special attention by the researchers [11]–[22].

In [11], detrended fluctuation analysis (DFA) is used to compute EEG scaling exponents which are utilized as features for classifying apnea and healthy subjects. Here, the result is reported for six apnea and six healthy subjects where 360 epochs for both the cases are considered only. In [12], [13], wavelet transform of EEG is employed to identify sleep apnea events and in [14], particle swarm optimization based hermite decomposition algorithm is proposed. Instead of using the full band EEG signal, an effective way is to divide the EEG signal into well-known EEG sub-bands and analyze the band-limited signals. But for band-limited signal extraction bandpass filters with fixed bandwidth are used whereas neural activity varies from time to time, person to person. Hence, the possible benefits in analysis with the use of adaptive bandwidth based decomposition for band limited signal extraction is yet to be explored. Recently in [15], sub-frame based features are modeled for band-limited signals, where the signals are obtained by simple bandpass filtering. However, in the method, the effect of including higher frequency bands (>40Hz) in apnea detection is not considered. In [16], for apnea classification, energy and variance are computed from each sub-band. In [17], random characteristics of EEG signal is exploited by multi-band entropy values to use as features while in [18], the cumulative delta-power ratio of overlapping frames is used. Variation of within frame EEG beta band energy is studied and various statistical features are extracted in [19]. In [20], intrinsic mode functions (IMF) of empirical mode decomposed EEG signal are separated into amplitude modulated (AM) and frequency modulated (FM) components using Teager energy operator which are used for feature extraction. The extracted features from separated components are given as input to support vector machine. Bispectral characteristics of EEG signal are investigated in [21], where the degree of quadratic phase coupling (QPC) is analyzed for each sub-band. In [22], variation of Hilbert spectrum frequency is studied. However, most of the reported methods, classify between apnea and healthy subjects and the challenging task of differentiating apnea and non-apnea frames of an apnea patient is not much investigated.

Instead of using multiple bio-signals, this paper focuses on automatic sleep apnea detection using a single lead EEG signal. In this paper, both classification scenarios- classifying apnea and non-apnea frames in the data of an apnea patient and classification of apnea and healthy subjects, are taken into consideration. The given raw EEG frame is pre-processed and divided into overlapping sub-frames. Variational mode decomposition (VMD) analysis is introduced in each sub-frame and features are extracted from each mode. VMD gives an opportunity to obtain compact BLIMFs with adaptive center frequencies in direct relevance to the varying neural activity of the brain. Instead of directly using the extracted feature vector, within frame feature value variation pattern is modeled with a suitable characteristic probability distribution function (PDF) and the fitted model parameters are then used in K nearest neighbor (KNN) classifier to classify apnea and non-apnea frames. Publicly available three large databases are used for detailed experimentations and performance analyses.

II. PROPOSED METHOD

Features are extracted from the mode functions obtained from each sub-frame by applying VMD and finally, temporal variation of each feature is modeled with a suitable PDF. Different major steps involved in the proposed method is presented in Fig. 1. A detailed description of the steps is presented in this section.

A. ANALYSIS WITH SUB-FRAMING

DC offset removal and frame amplitude normalization are performed in each frame for pre-processing. The neural activity level of the recorded EEG signal changes with respect to time during sleep. Hence, in different EEG frames, there exists a large variation in energy content. To counter this phenomenon, in each frame, energy normalization is also applied. Usually, in the frame by frame analysis, the analysis of a test frame is carried on the full duration. In this paper, as an alternate, the sub-frame based analysis is proposed where the test frame is divided into a shorter frame duration (to be called sub-frame) and a reasonable amount of time overlap is kept between successive sub-frames to obtain several sub-frames.

For example, from the frame of N length, with sub-frame duration of M samples and shifting it by p samples, the second sub-frame can be found from $(p+1)th$ sample to $(p+M)th$ sample. This procedure can be continued until reaching the end of the frame. Considering $p << M < N$, total $\frac{N-M}{p}+1$ sub-frames can be obtained. Figure 2 shows the procedure of sub-frame operation.

Sub-frame based analysis can minimize the effect of random fluctuations in the test frame. For example, an unexpected value in the original data can significantly hamper the overall analysis carried out on the entire frame. On the contrary, in the sub-frame based analysis, only a few sub-frames will be affected by that unexpected value. Thus analysis using sub-frames is expected to obtain better characteristics

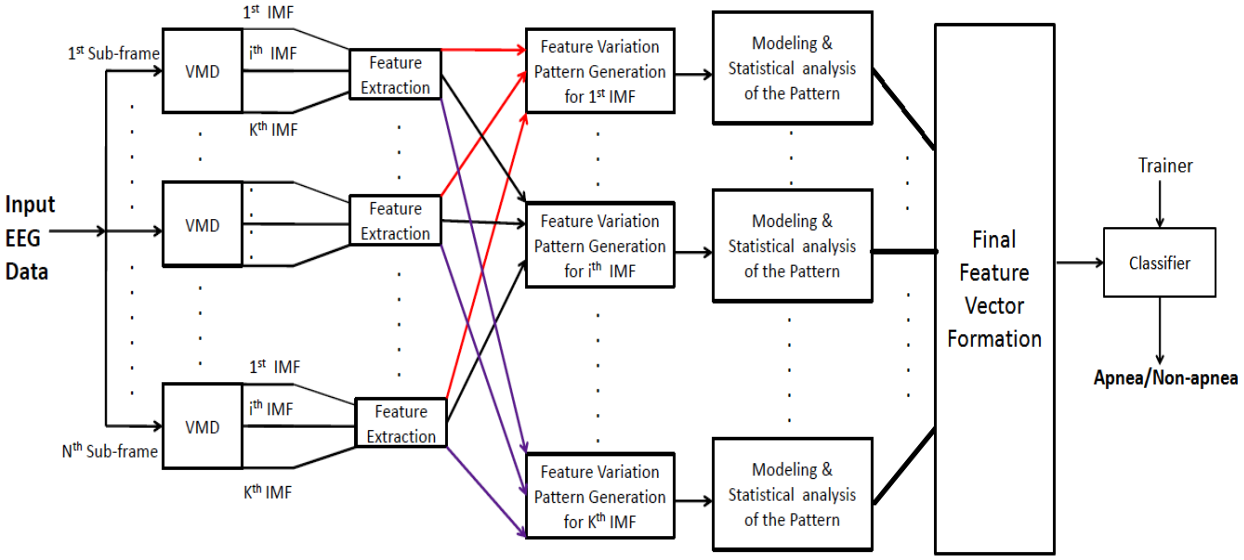

FIGURE 1. Flow chart of the proposed method.

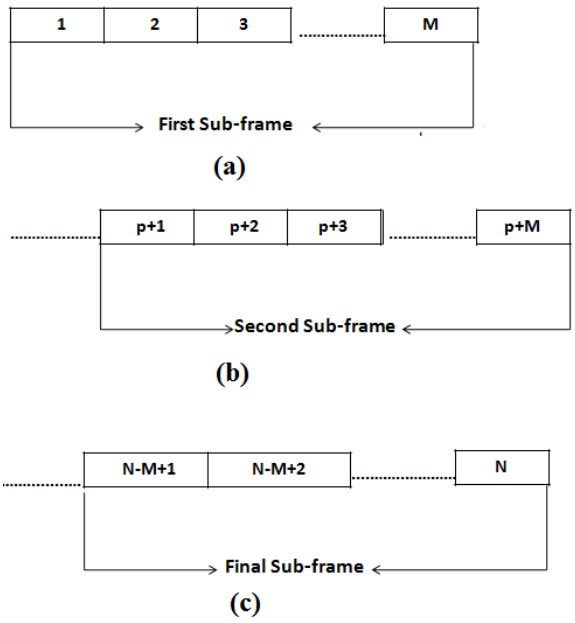

FIGURE 2. a) First Sub-frame b) Second Sub-frame c) Last Sub-frame.

in comparison to working with the entire test frame at a time. Such use of sub-frame based analysis ensures extraction of local information better within a frame.

Another key point is that not only a portion of the frame correspond to apnea as generally apnea duration is lesser than the frame duration taken. A limited period of the entire duration of the frame may be the occurrence of apnea. As sub-framing provides an opportunity for analysis with high temporal resolution, it allows to capture changes in characteristics within an apnea frame, especially at the transition between apnea and non-apnea events. Analyzing the entire frame one at a time is unlikely to represent such changes. Hence, in the proposed scheme, the sub-frame based analysis is being adapted.

B. SHORT DESCRIPTION OF VARIATIONAL MODE DECOMPOSITION (VMD)

The VMD algorithm decomposes any input signal adaptively into k discrete number of band-limited intrinsic mode functions (u_k). Here each mode is mostly compact around the respective center frequency ω_k. The algorithm searches for a given number of u_k and the corresponding center frequencies ω_k utilizing alternate direction method of multipliers (ADMM). The input signal can be reproduced either exactly or in the least square sense by using these modes. A detailed description of the VMD algorithm can be found in [23]. The major steps involved in the VMD algorithm can be briefly summarized as-

i) for each mode u_k, the associated analytic signal is computed using Hilbert transform in order to obtain a unilateral frequency spectrum

ii) Mode's frequency spectrum is shifted by mixing with an exponential tuned to the respective calculated center frequency

iii) Bandwidth is estimated through Gaussian smoothness of the demodulated signal

To search for u_k and ω_k, it is required to solve a constrained variational problem, which is described by the following equation:

$$\begin{pmatrix} min \\ u_k,\, \omega_k \end{pmatrix} = \left\{ \sum_k \left\| \partial_t \left[(\delta(t) + \frac{j}{\pi t}) * u_k(t) \right] e^{-j\omega_k t} \right\|_2 \right\}, \tag{1}$$

$$\sum_k u_k = f \tag{2}$$

where t is the time script, $\delta(\cdot)$ is the Dirac distribution and * denotes convolution operator, f is the signal to be decomposed and k is the number of modes.

The number of modes has to be predefined in the application of VMD and its value (underbinning or overbinning) has a considerable impact on the quality of decomposed signals. In different applications, EEG signal is divided into five frequency band-limited signals, namely- delta (0.25-4 Hz), theta (4-8 Hz), alpha (8-12 Hz), sigma (12-16 Hz) and beta (16-40 Hz), where the frequency bands are well established in literature and exhibit differences in frequency (Hz), amplitude and activity level. Delta, theta and alpha bands correspond to deep sleep, mild sleep and relax state, respectively while sigma and beta bands refer to alert states [24], [25]. During apnea, as the breathing is paused, the level of carbon dioxide rises in the bloodstream. Increased carbon dioxide level in the bloodstream is recognized by the chemoreceptors. As a result, person sleeping is signaled by the brain to breathe in air and wake up [26]. Hence, there can be significant variation in different EEG frequency bands due to the above-mentioned changes in neural activity from non-apnea to apnea. However, in a particular band, it is expected that the dominant frequencies caused by neural activity shift slightly from time to time and person to person.

Hence, simple bandpass filtering of EEG data with fixed center frequency will not be able to capture the shifts. VMD analysis results in band-limited IMFs where the center frequencies are dynamically calculated. This allows the center frequency to shift and accurately represent the neural activity. Moreover, in order to correspond with the variation of neural activity in different frequency bands, the number of VMD modes should be chosen in such a way that both lower and higher frequency bands are covered. In order to present variation in spectral representation for a various number of modes, in Fig. 4, a frame of EEG data is considered and the corresponding power spectral densities are plotted. It is clearly observed that $K = 3$ and 4 do not have modes covering frequency above 30 Hz. Moreover, $K = 4$ has a mode at around 10 Hz, representing the original alpha state, which is missing for $K = 3$. For $K = 5$ the earlier four modes stay on their positions and an extra mode appears covering higher frequency band (>40 Hz). The higher frequency band is further divided into an increased number of modes as the value of K is taken greater than five. As EEG data mostly have significant information lying in lower bands (frequency<40 Hz), it is redundant to have too many modes in higher frequency. Division of higher frequency band into more bands corresponding to new modes does not provide necessary information for apnea detection. Moreover, the increase in a number of modes increases computational complexity. Hence, in this paper $k = 5$ is proposed to utilize the entire frequency band and to have modes representing conventional EEG Sub-bands. Moreover, it also ensures not having redundant modes increasing the computational complexity. Detailed performance comparison with a various number of modes is given in section III.

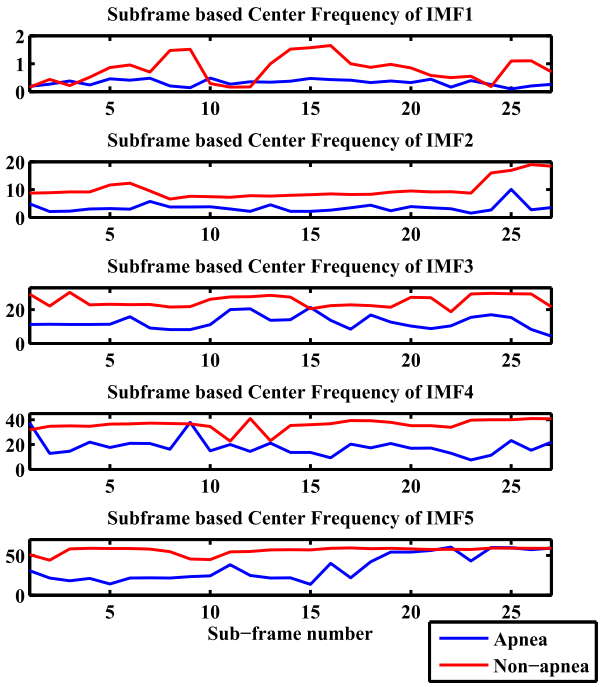

FIGURE 3. Frequency signature of the proposed method.

The frequency characteristics can be further presented by demonstrating the variation of center frequencies of each IMF of the sub-frames within a frame for both apnea and non-apnea. The frequency signature is presented in Fig. 3. Here for each sub-frame center frequencies are calculated and plotted for each IMF. As it is mentioned above that different VMD IMFs represent different frequency bands, which is clearly visible from the figure.

C. PROPOSED FEATURES FOR EACH MODE

During apnea, patients experience a disturbance in normal breathing and this can lead to grunting, gasping, body movements. Hence, it is expected that there will be changes in information content in the EEG signal during apnea events as EEG corresponds directly with various neural activity level. Moreover, variation in EEG data increases during apnea than non-apnea instances. Such changes in information content and the data variation are expected to be better reflected in different VMD modes of sub-frame EEG data than the whole duration frame. In order to capture the changes, in the proposed method, entropy and log-variance are chosen as features to be extracted from each VMD mode of sub-frame EEG data.

Entropy of a discrete random variable Y with $(M + 1)$ number of possible values $\{y_0, y_1, y_2, \ldots, y_M\}$ is defined as

$$H(Y) = E(I(Y)), \tag{3}$$

where $E(\cdot)$ denotes the expectation operator and $I(Y)$ represents the information content. For a particular value y_i of Y, the information content can be expressed as

$$I(Y = y_i) = -\log_2(p(y_i)), \tag{4}$$

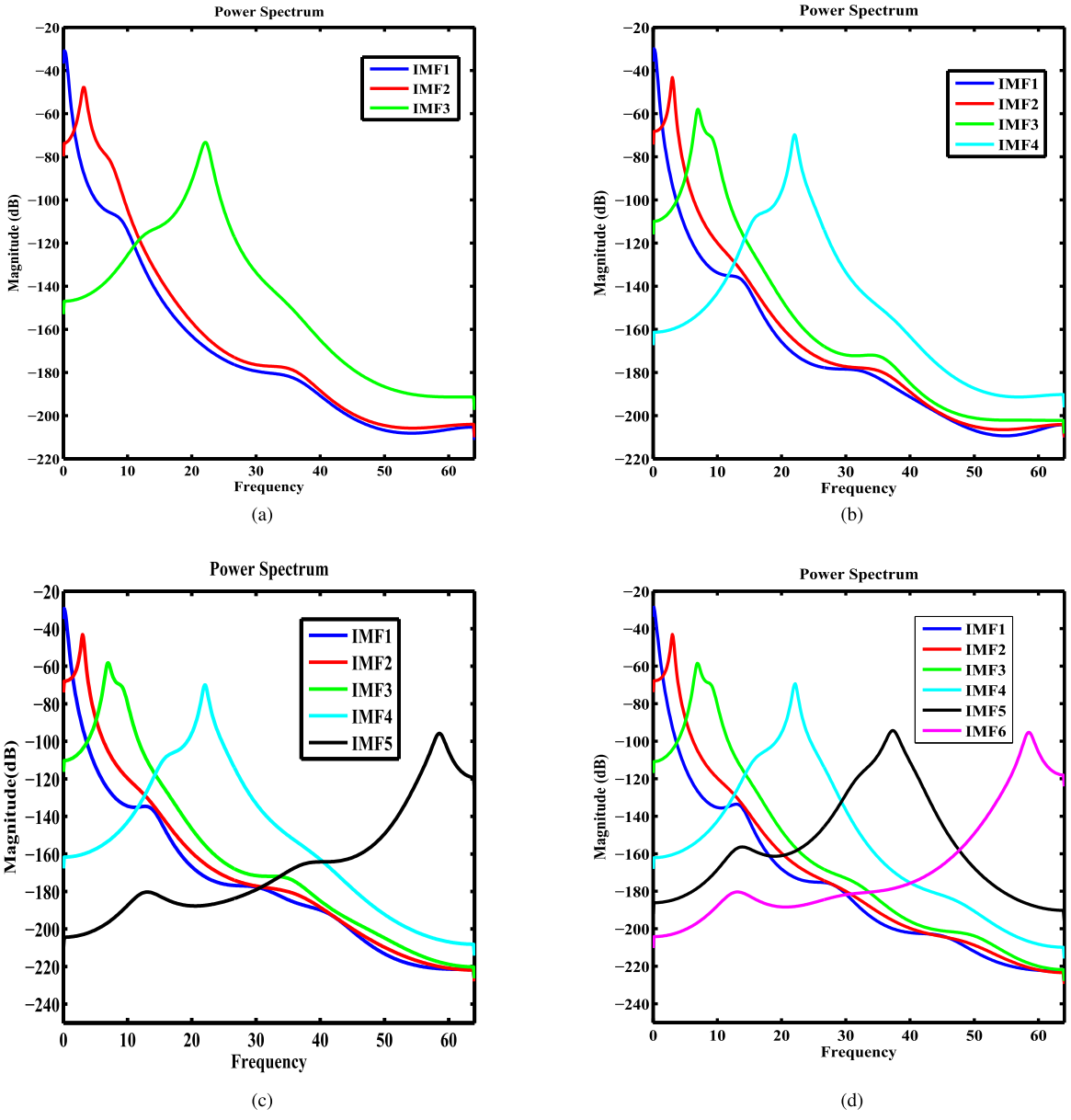

FIGURE 4. Power spectrum densities of K number of VMD modes of an EEG frame (a)K=3 (b)K=4 (c)K=5 (d)K=6.

where $p(y_i) = n_i/N$, denotes the probability of occurrence of y_i, with n_i be the number of occurrence of coefficients in a bin in proximity of y_i value among the N number of values, i.e. $\sum_i n_i = N$. Using (4), the entropy in (3) can be re-written as

$$H(Y) = -\sum_{i=0}^{M} p(y_i) \times log_2(p(y_i)), \tag{5}$$

here $p(y_i) = n_i/N$, with n_i be the number of occurrence of coefficients in a bin in proximity of y_i value among the N number of values, i.e. $\sum_i n_i = N$.

For data $x[n]$ with length N and mean μ, Log-variance (LV) is calculated as

$$LV = \log_e[\frac{1}{N}\sum_{n=1}^{N}(x[n] - \mu)^2]. \tag{6}$$

D. FEATURE VARIATION PATTERN GENERATION

In the proposed sub-frame based VMD analysis scheme, features are extracted from each mode of overlapping sub-frames. If the amount of frame shifting (p) in sub-framing is kept small, features extracted for each mode in sub-frame based VMD analysis can provide a precise variation profile of that feature characteristic. Such use of sub-frame and VMD provides an opportunity to obtain a temporal variation profile of a particular feature for a specific mode within a frame. If there are W number of sub-frames, the within frame feature variation pattern for kth mode can be generated as

$$Variation\ Pattern = [F_{1k}, F_{2k}, F_{3k}, \ldots\ldots\ldots F_{Wk}], \tag{7}$$

where F_{Wk} denotes the feature calculated from the kth mode of the Wth sub-frame.

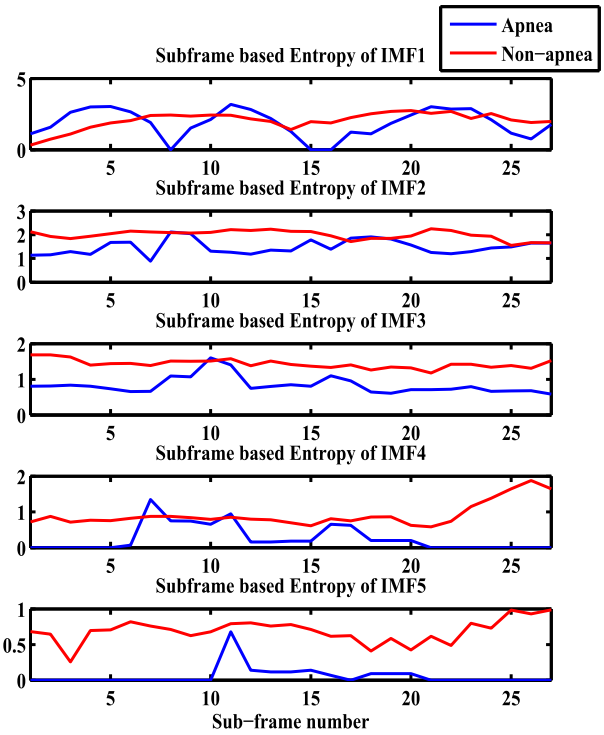

FIGURE 5. Entropy feature variation profile obtained from different IMFs of VMD of both apnea and non-apnea. Here, the test frame is divided into multiple sub-frames and each sub-frame is variational mode decomposed. Entropy is calculated from each resulting IMF and the variation profile of with-in frame entropy feature is plotted.

In order to represent the within frame feature variation in different VMD modes, in Fig. 5, entropy values calculated from different modes are presented for both apnea and non-apnea. Entropy values are calculated in proposed sub-frame based VMD analysis from each mode and the variation patterns of entropy values are shown. It is evident from the figure that in different modes, characteristics of feature variation is different from apnea to non-apnea.

E. PROCESSING OF THE EXTRACTED FEATURE SEQUENCE

Within frame feature variation pattern can be directly given as input to the classifier. But sub-framing calculates more features for a single frame than compared to conventional feature extraction method. Hence, if sub-frame based extracted features are directly utilized for classification, it will increase the feature dimension considerably, which will in a way affect the computational time and cost. As an alternate, characteristics of feature variation profile can be investigated for classifying apnea and non-apnea frames. One idea can be to carry out statistical analysis on feature variation pattern. Among various statistical features, in the proposed method, mean and variance are used.

Furthermore, the amplitude variation of the feature variation pattern of each VMD mode can be investigated. In this paper, we propose to fit the sub-frame based feature variation pattern with probability density function (PDF). The motivation is to use the parameters of the fitted PDF as features. In the choice of different PDFs, well-known PDFs can be considered. Such an approach can investigate the data distributions of feature variation profile. As model parameters are mostly one or two, the problem regarding large feature dimension is eliminated and the computational burden is reduced. Among different PDFs, in this paper, we propose to fit the feature variation pattern with Rician PDF.

Detailed analyses with different PDFs are covered in section III. Histograms of feature variation patterns and the corresponding Rician fittings of various apnea and non-apnea frames for different VMD modes are presented in Fig. 6. It is evident from the figure that the fitted Rician PDFs for apnea and non-apnea frames differ widely and there is minimum overlap between the two. Hence the fitted parameters are expected to quantify the variation pattern better and to have better feature quality.

The statistical features ($F_{\text{statistical}}$) and the model parameters (F_{model}) calculated from each mode of overlapping sub-frames of a frame are cascaded as equation (8),(9) and (10) to obtain the final feature vector (F). Here, $F_{\text{mod},1}$ and $F_{\text{stat},1}$ are the model parameters and statistical features, respectively, calculated from the feature variation patterns of mode 1.

$$F_{statistical} = [F_{stat,1}\ F_{stat,2}\ \ldots..F_{stat,n}] \quad (8)$$

$$F_{model} = [F_{mod,1}\ F_{mod,2}\ \ldots\ldots\ldots\ldots.F_{mod,n}] \quad (9)$$

$$F = [F_{statistical}\ F_{model}] \quad (10)$$

F. KNN CLASSIFIER

K-nearest neighborhood (KNN) classifier is utilized in the proposed method where distance function is computed between the features belonging to the EEG pattern in the test set and the K neighboring EEG patterns in the training set. Based on the K closest class labels, the test set is classified. M-fold cross-validation is followed for performance evaluation. M-fold means, the dataset is partitioned into M portions. Each portion is tested while remaining (M-1) portions are used as trainers. The classification is done at least M times to report the result.

III. RESULT AND DISCUSSION

In the proposed method, a frame of EEG data is preprocessed and divided into overlapping sub-frames. VMD analysis is performed on each sub-frame signal. Features mentioned in section IIC, are calculated for each mode. The feature variation patterns obtained for each mode are subjected to model fitting and statistical analysis and the final feature vector is formed according to (8),(9) and (10). In the following sections, the database description, feature quality analysis and the classification results of sleep apnea detection are presented.

A. DATABASE

For the purpose of experimentation, publicly available three large databases are used [27], [28] and [29], where [29]

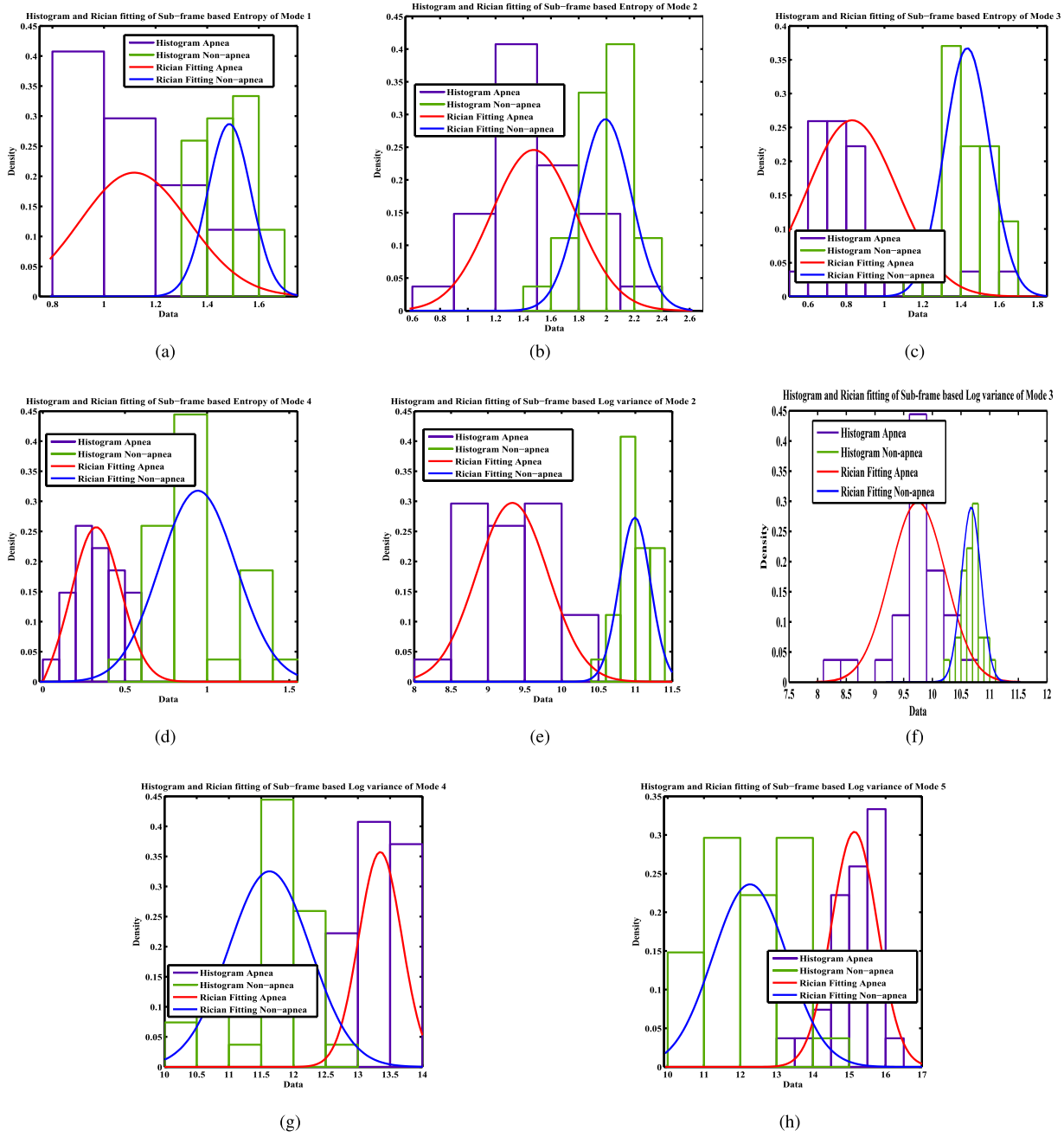

FIGURE 6. Test frame is divided into multiple sub-frames and each sub-frame is variational mode decomposed. Entropy and log-variance are calculated from each resulting IMF. Histograms of the calculated feature variation patterns and the corresponding Rician fittings of various VMD modes are shown for both apnea and non-apnea frames.

contain the data of healthy subjects and the data of apnea subjects are available in [27] and [28]. Polysomnograms scored as apnea or non-apnea by the experts are available as ground truth in the databases. Apnea and Hypopnea Index (AHI) defines the severity of apnea and it is measured by the number of occurrence per hour. It is known that AHI below 5 is healthy, 5 to 15 indicates mild, the range of 15 to 30 is moderate and greater than 30 is severe [30]. For [27] and [28], frame durations taken are 15s and 30s, respectively, depending on the respective ground truths. There are two considerations to make in the selection of sub-frame duration and the size of overlap. A big sub-frame length with large overlap will not provide enough data for feature variation pattern and thus the corresponding model fitting will be biased. On the other hand, a very small sub-frame length with large overlap is an option but very short sub-frame length might provide an incorrect estimate of features, such as entropy and log-variance. Moreover, a large overlap between consecutive sub-frames

TABLE 1. Subjects used for the evaluation of the proposed method.

Data for Apnea patients												Data for Healthy Subjects				
Database- [27]						Database- [28]						Database- [29]				
S/No	Study No.	AHI	Elecrode	Frame No.	Frame Length	S/No	Study No.	AHI	Elecrode	Frame No.	Frame Length	S/No	Study No.	Electrode	Frame No.	Frame Length
1	UCDDB002	23	C3-A2	100		1	slp01a	17	C4-A1	70		1	SC4002E0	Fpz-Cz	300	
2	UCDDB003	51	C3-A2	488		2	slp01b	22.3	C4-A1	130		2	SC4032E0	Fpz-Cz	300	
3	UCDDB005	13	C3-A2	100		3	slp02a	34	O2-A1	180		3	SC4042E0	Fpz-Cz	300	
4	UCDDB006	31	C3-A2	148		4	slp02b	22.2	O2-A1	84		4	SC4072E0	Fpz-Cz	300	
5	UCDDB007	12	C3-A2	142		5	slp03	43	C3-O1	382		5	SC4082E0	Fpz-Cz	300	
6	UCDDB009	12	C3-A2	94		6	slp04	59.8	C3-O1	460		6	SC4102E0	Fpz-Cz	300	
7	UCDDB010	34	C3-A2	254		7	slp14	30.7	C3-O1	366		7	SC4001E0	Fpz-Cz	300	
8	UCDDB011	8	C3-A2	58		8	slp16	53.1	C3-O1	262		8	SC4031E0	Fpz-Cz	300	
9	UCDDB012	25	C3-A2	376		9	slp32	22.1	C4-A1	100		9	SC4011E0	Fpz-Cz	300	
10	UCDDB013	16	C3-A2	110	15s	10	slp37	100.8	C4-A1	128	30s	10	SC4021E0	Fpz-Cz	300	15s
11	UCDDB014	36	C3-A2	416		11	slp48	46.8	C3-O1	546		11	SC4022E0	Fpz-Cz	300	
12	UCDDB017	12	C3-A2	102		12	slp59	55.3	C3-O1	140		12	SC4041E0	Fpz-Cz	300	
13	UCDDB018	2	C3-A2	18		13	slp60	59.2	C3-O1	200		13	SC4051E0	Fpz-Cz	300	
14	UCDDB019	16	C3-A2	156		14	slp61	41.2	C3-O1	100		14	SC4052E0	Fpz-Cz	300	
15	UCDDB020	15	C3-A2	122		15	slp66	65.5	C3-O1	98		15	SC4061E0	Fpz-Cz	300	
16	UCDDB021	13	C3-A2	114												
17	UCDDB022	7	C3-A2	38												
18	UCDDB023	39	C3-A2	280												
19	UCDDB024	24	C3-A2	224												
20	UCDDB025	91	C3-A2	80												
21	UCDDB026	14	C3-A2	130												
22	UCDDB027	55	C3-A2	424												
23	UCDDB028	46	C3-A2	312												
	Total Frames			**4286**			**Total Frames**			**3246**			**Total Frames**		**4500**	

will result in a large number of feature variation data that will increase the computational complexity. Hence, keeping both the issues in consideration, in this paper a moderate sub-frame length of 2s and 4s are used for databases- [27] and [28], respectively and 80% overlap between two successive sub-frames are maintained to ensure enough data points for model fitting with moderate computational complexity. Detailed information of the subjects used in this paper is presented in Table 1.

B. GOODNESS OF FEATURE

Quality of the proposed feature vector is analyzed by the goodness of feature measures, such as Geometrical Separability Index (GSI). GSI, called Thornton's separability index as well, gives the measure of the separability in the nearest neighbor sense of two classes. It is defined as the fraction of a set of data points whose labels for classification are similar to those of their nearest neighbors. It is defined as [31]

$$s = \frac{\sum_{i=1}^{N}(f(x_i)) + f(x_i') + 1) \; mod \; 2}{N}, \tag{11}$$

where N is the number of data points and x' is the nearest neighbor of x.

From (11) it is understandable that separability index, s approximates to one when two classes are separable and zero for inseparable classes, hence higher the GSI value, better the feature quality. In Table 2, GSI values are given for the purpose of comparison among method of different distribution fitting to multi-band feature variation pattern and the proposed method. From Table 2 it is evident that out of different PDFs, Rician PDF fitting gives better performance, while the proposed method of combining Rician PDF parameter and statistical features, offers the best GSI index.

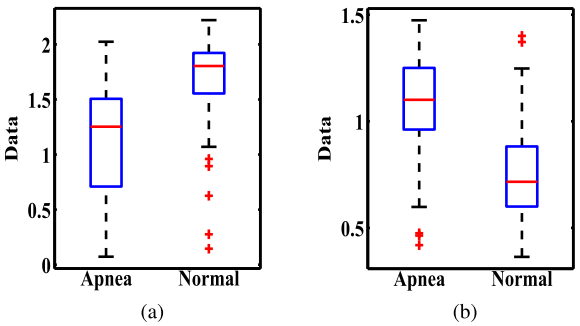

FIGURE 7. Distribution of model parameters. (a) Rician Model Parameter (υ). (b) Rician Model Parameter (σ).

TABLE 3. Definition of accuracy measures.

	Apnea	**Non-Apnea**
Apnea	True Positive (TP)	False Negative (FN)
Non-apnea	False Positive (FP)	True Negative (TN)

The distribution of Rician parameters (υ, σ) is presented in Fig. 7 via boxplot using the data of Table 1. Here entropy feature variation in mode 5 is considered. It is obvious from the figure that there is are a significant separation in the distribution of the parameters between apnea and non-apnea.

C. CLASSIFICATION RESULT

For classification purpose, two distinct cases are considered, (i) apnea and non-apnea classification in the data of apnea patients and (ii) apnea patients and healthy subjects classification. In KNN classifier, cosine distance function and K equal to 9 are chosen. Standard performance measures described in (12)-(14) are used to evaluate the performance

TABLE 2. Feature quality by GSI.

Database- [27]							Database- [28]						
S/No.	**Gamma**	**Rayleigh**	**Exp**	**Stat**	**Rician**	**Proposed**	**S/No.**	**Gamma**	**Rayleigh**	**Exp**	**Stat**	**Rician**	**Proposed**
1	0.71	0.84	0.84	0.84	0.81	0.92	1	0.69	0.93	0.91	0.91	0.86	0.94
2	0.73	0.93	0.92	0.96	0.84	0.99	2	0.72	0.81	0.82	0.82	0.83	0.92
3	0.63	0.76	0.75	0.79	0.66	0.85	3	0.71	0.84	0.84	0.84	0.77	0.91
4	0.49	0.64	0.65	0.64	0.58	0.75	4	0.63	0.73	0.74	0.73	0.73	0.87
5	0.73	0.72	0.70	0.70	0.75	0.75	5	0.52	0.65	0.66	0.69	0.73	0.89
6	0.63	0.86	0.83	0.79	0.69	0.87	6	0.71	0.85	0.85	0.84	0.83	0.95
7	0.78	0.80	0.80	0.92	0.93	0.94	7	0.55	0.74	0.73	0.85	0.80	0.95
8	0.84	0.78	0.76	0.88	0.86	0.95	8	0.63	0.78	0.79	0.78	0.82	0.89
9	0.79	0.87	0.86	0.89	0.84	0.95	9	0.56	0.73	0.72	0.79	0.69	0.88
10	0.66	0.76	0.73	0.69	0.72	0.83	10	0.77	0.95	0.95	0.94	0.95	0.94
11	0.80	0.91	0.89	0.92	0.84	0.93	11	0.47	0.60	0.59	0.65	0.63	0.86
12	0.78	0.94	0.94	0.97	0.94	0.99	12	0.64	0.77	0.78	0.84	0.78	0.96
13	0.76	0.83	0.83	0.89	0.72	0.94	13	0.79	0.96	0.96	0.94	0.94	0.97
14	0.82	0.95	0.93	0.93	0.95	0.97	14	0.68	0.86	0.86	0.91	0.85	0.89
15	0.64	0.85	0.84	0.84	0.86	0.92	15	0.61	0.77	0.78	0.72	0.77	0.78
16	0.66	0.84	0.81	0.90	0.77	0.95							
17	0.77	0.84	0.82	0.84	0.87	0.92							
18	0.63	0.68	0.69	0.67	0.74	0.88							
19	0.72	0.83	0.82	0.89	0.89	0.95							
20	0.76	0.93	0.93	0.90	0.86	0.91							
21	0.72	0.83	0.81	0.92	0.85	0.98							
22	0.67	0.71	0.68	0.73	0.87	0.89							
23	0.69	0.78	0.76	0.81	0.81	0.92							
Mean	0.71	0.82	0.81	0.84	0.81	**0.91**	**Mean**	0.65	0.80	0.80	0.82	0.80	**0.91**

TABLE 4. Performance analysis of the proposed method for various PDf fitting using leave-one-out cross validation (database- [27]).

	Sensitivity(%)					**Specificity**(%)					**Accuracy**(%)				
S/No.	**Exp.**	**Ray.**	**Stat.**	**Rician**	**Prop.**	**Exp.**	**Ray.**	**Stat.**	**Rician**	**Prop.**	**Exp.**	**Ray.**	**Stat.**	**Rician**	**Prop.**
1	86	86	88	98	92	92	90	86	82	90	89	88	87	90	91
2	92.62	94.67	94.67	97.13	98.36	93.44	96.72	96.72	80.33	96.72	93.03	95.70	95.70	88.73	97.54
3	82	82	88	74	90	80	80	88	68	86	81	81	88	71	88
4	62.16	58.11	58.11	58.11	77.03	78.38	75.68	81.08	71.62	71.62	70.27	66.89	69.59	64.86	74.32
5	71.83	73.24	76.06	77.46	83.10	80.28	80.28	77.46	76.06	81.69	76.06	76.76	76.76	76.76	82.39
6	76.60	78.72	72.34	95.74	100	82.98	82.98	78.72	65.96	87.23	79.79	80.85	75.53	80.85	93.62
7	70.08	69.29	85.83	98.43	96.06	93.70	96.06	92.13	89.76	91.34	81.89	82.68	88.98	94.09	93.70
8	75.86	68.97	68.97	93.10	82.76	79.31	86.21	86.21	82.76	86.21	77.59	77.59	77.59	87.93	84.48
9	92.55	92.02	90.96	92.55	98.40	84.04	86.17	86.70	80.85	88.30	88.30	89.10	88.83	86.70	93.35
10	76.36	76.36	81.82	87.27	90.91	83.64	83.64	74.55	61.82	85.45	80	80	78.18	74.55	88.18
11	87.98	89.90	87.50	97.12	98.56	87.98	87.98	89.42	79.81	87.02	87.98	88.94	88.46	88.46	92.79
12	94.12	94.12	94.12	94.12	96.08	100	100	100	100	100	97.06	97.06	97.06	97.06	98.04
13	88.89	88.89	88.89	88.89	88.89	100	100	88.89	100	100	94.44	94.44	88.89	94.44	94.44
14	97.44	97.44	91.03	100	94.87	93.59	94.87	97.44	92.31	97.44	95.51	96.15	94.23	96.15	96.15
15	91.80	93.44	91.80	96.72	98.36	81.97	78.69	83.61	77.05	73.77	86.89	86.07	87.70	86.89	86.07
16	84.21	87.72	92.98	92.98	98.25	94.74	94.74	89.47	78.95	89.47	89.47	91.23	91.23	85.96	93.86
17	94.74	89.47	89.47	100	100	73.68	73.68	68.42	73.68	73.68	84.21	81.58	78.95	86.84	86.84
18	75.71	75	74.29	93.57	97.14	67.14	68.57	71.43	65	72.14	71.43	71.79	72.86	79.29	84.64
19	93.75	92.86	91.07	94.64	96.43	86.61	86.61	88.39	92.86	92.86	90.18	89.73	89.73	93.75	94.64
20	95	97.5	95	95	97.50	85	85	87.50	82.50	80	90	91.25	91.25	88.75	88.75
21	80	75.38	89.23	98.46	92.31	92.31	95.38	93.85	84.62	96.92	86.15	85.38	91.54	91.54	94.62
22	80.19	81.13	81.60	94.81	97.64	66.51	66.51	72.17	80.66	81.60	73.35	73.82	76.89	87.74	89.62
23	81.41	83.33	84.62	89.74	97.44	82.69	83.33	85.90	74.36	89.74	82.05	83.33	85.26	82.05	93.59
Mean	83.97	83.72	85.06	91.65	**94**	85.22	85.79	85.39	80.04	**86.92**	84.59	84.75	85.23	85.84	**90.46**

of the proposed method. These were computed using TP, FP, FN, and TN values [32] as shown in Table 3.

$$Accuracy(A_{cc}) = \frac{TP + TN}{TP + FP + TN + FN} * 100 \quad (12)$$

$$Sensitivity(S_e) = \frac{TP}{TP + FN} * 100 \quad (13)$$

$$Specificity(S_p) = \frac{TN}{TN + FP} * 100 \quad (14)$$

1) CLASSIFICATION OF APNEA AND NON-APNEA FRAMES IN THE DATA OF APNEA PATIENTS

Here, only apnea patients are considered, where test and train data are from the same patient.

a: PERFORMANCE ANALYSIS OF DIFFERENT PDFs

For every subject mentioned in Table 1 the proposed method is evaluated for different PDFs. Performance analyses using

TABLE 5. Performance analysis of the proposed method for various PDF fitting using leave-one-out cross validation (database- [28]).

S/No.	Sensitivity(%)					Specificity(%)					Accuracy(%)				
	Exp.	Ray.	Stat.	Rician	Prop.	Exp.	Ray.	Stat.	Rician	Prop.	Exp.	Ray.	Stat.	Rician	Prop.
1	85.71	82.86	91.43	88.57	94.29	88.57	88.57	97.14	94.29	94.29	87.14	85.71	94.29	91.43	94.29
2	81.54	83.08	84.62	90.77	95.38	86.15	87.69	83.08	69.23	83.08	83.85	85.38	83.85	80	89.23
3	76.67	77.78	82.22	83.33	90.00	88.89	88.89	88.89	73.33	83.33	82.78	83.33	85.56	78.33	86.67
4	80.95	80.95	69.05	78.57	78.57	83.33	85.71	90.48	69.05	76.19	82.14	83.33	79.76	73.81	77.38
5	75.39	74.87	70.16	81.68	97.38	73.82	74.35	78.53	73.30	76.96	74.61	74.61	74.35	77.49	87.17
6	95.65	95.65	93.04	78.26	100	73.48	74.78	77.39	66.52	85.22	84.57	85.22	85.22	72.39	92.61
7	78.69	75.41	86.34	87.43	96.72	77.05	81.97	85.25	74.86	90.16	77.87	78.69	85.79	81.15	93.44
8	83.21	82.44	80.15	89.31	96.18	78.63	80.15	68.70	71.76	76.34	80.92	81.30	74.43	80.53	86.26
9	88	88	82	94	92.00	72	72	76	58	76.00	80	80	79	76	84.00
10	100	100	100	100	100.00	89.06	89.06	89.06	89.06	89.06	94.53	94.53	94.53	94.53	94.53
11	75.82	72.53	79.49	81.32	97.80	55.31	53.11	56.41	59.71	72.89	65.57	62.82	67.95	70.51	85.35
12	92.86	91.43	95.71	75.71	100.00	64.29	70	77.14	75.71	92.86	78.57	80.71	86.43	75.71	96.43
13	100	100	100	98	100.00	90	90	91	85	92.00	95	95	95.50	91.50	96.00
14	90	90	82	86	96.00	90	88	86	80	86.00	90	89	84	83	91.00
15	83.67	81.63	87.76	85.71	95.92	73.47	71.43	67.35	71.43	63.27	78.57	76.53	77.55	78.57	79.59
Mean	85.88	85.11	85.60	86.58	**95.43**	78.94	79.71	80.83	74.08	**81.56**	82.41	82.41	83.21	80.33	**88.49**

leave-one-out cross validation technique for each PDF are reported in Tables 4 and 5 for databases [27] and [28], respectively.

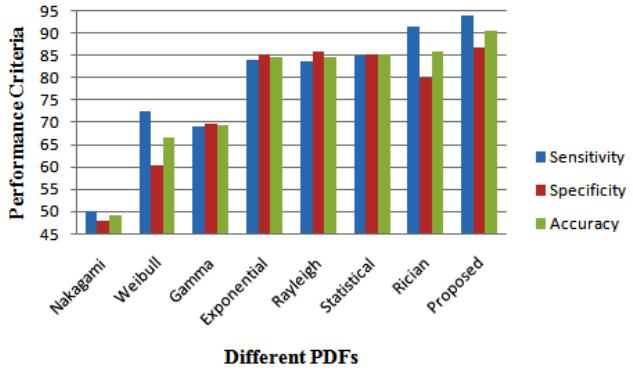

FIGURE 8. Variation profile of with-in frame feature is modeled with different PDFs and model parameters are used as input to classifiers. Mean of all the performance criteria are plotted for various PDFs.

In the tables, 'Stat' represents the method utilizing statistical features ($F_{statistical}$) as mentioned in (8). From the results reported in Tables 4 and 5, it is found that for both the datasets, specificity values acquired by the proposed feature set (Rician parameters and statistical analyses) are similar to those achieved by other PDFs. But, the sensitivity and the accuracy values are found to be far better compared to all other cases. Greater sensitivity means high apnea detection performance, hence it serves as a big advantage of the proposed method. The mean of the performance criteria for different PDFs is presented in Fig. 8. As found earlier, among different PDFs, Rician PDF offers the best sensitivity and accuracy and competitive specificity whereas, the proposed method achieves the best performance in each criterion.

b: COMPARISON OF PROPOSED METHOD WITH OTHER APPROACHES

Comparison of the proposed sub-frame based analysis is carried out with the conventional feature extraction method.

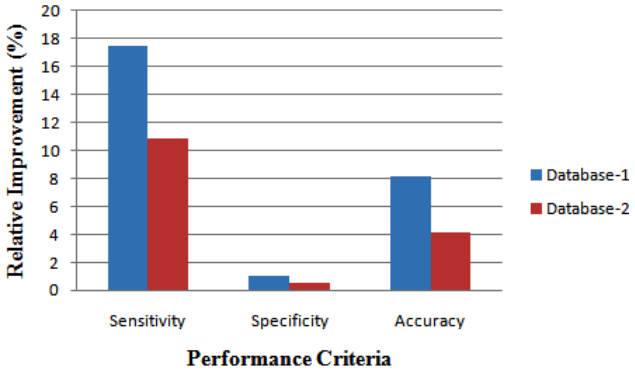

FIGURE 9. Relative Improvement with the proposed method comparing to the conventional approach. In the conventional approach,unlike sub-frame based analysis, entire frame is used for feature extraction and those are given as inputs directly to the classifier.

In the conventional approach, instead of using sun-framing, the features are computed using the entire frame duration and directly used as input to the classifier. The relative improvement achieved for both the datasets by the proposed approach with respect to the conventional approach is reported in Fig. 9. It is readily observable from the figure that there is relatively a large improvement in sensitivity and accuracy for both the databases.

Instead of modeling the within frame feature variation pattern, another alternative could be to model the data variation of the given frame. Pre-processed frame data are being subjected to the modeling and statistical analysis and the performance comparison of is made with the proposed method. The results are shown in Fig. 10. It is clearly shown from the figure that the proposed method offers significant improvement than modeling the original pre-processed data.

It is generally regarded that most information in scalp EEG lies in low frequencies (<40Hz). However, a recent study shows that neural activity extends far beyond the conventional frequency ranges. At high frequencies of EEG signal, rhythmic band activities are identified and it is shown that their

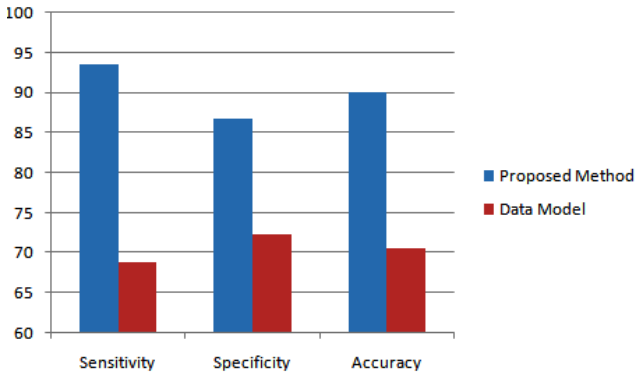

FIGURE 10. Comparison of Proposed Method with Data Modeling. In data modeling, unlike using the feature variation profile, modeling is applied on the pre-processed EEG data.

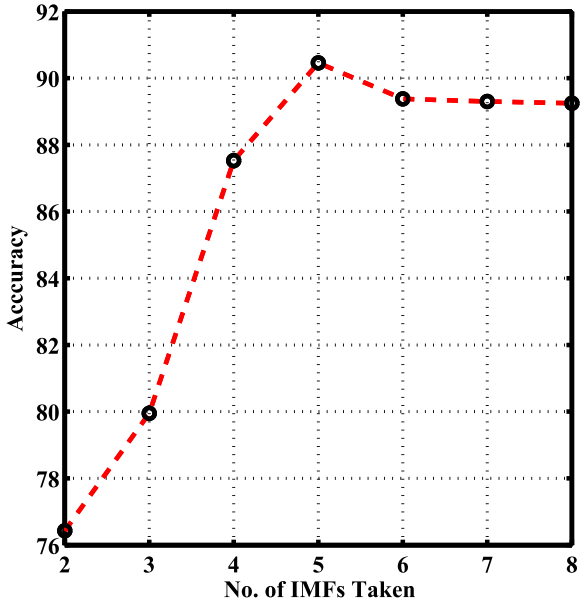

FIGURE 11. Classification Accuracy with different number of VMD modes taken.

properties depend on the state of vigilance [33]. In this paper, the analysis is carried on with various numbers of IMFs. Figure 11 shows the accuracy of the proposed method using a various number of modes. It is shown that the utilization of higher frequency IMFs improves the overall result significantly. The analyses with a number of modes above five have higher accuracies compared to the analyses with a number of modes below five. It is also seen that analysis with five modes provides the best accuracy, which is recommended in this paper. As is discussed in section IIB, number of modes below five provides low accuracy as they fail to encapsulate the higher frequency band and for the number of modes above five the accuracies are similar indicating redundant high-frequency modes.

To show the effect of modeling, the proposed method is compared with the use of the extracted feature variation pattern as a direct input to the classifier. It is revealed from Table 6 that the proposed method offers significantly better

TABLE 6. Effect of model fitting on classification performance (results with and without using the proposed model fitting).

Method	Se.(%)	Sp.(%)	Acc.(%)	GSI
without modeling	65.33	65.02	65.17	0.69
Proposed Method	94	86.92	90.46	0.91

classification performance and GSI value. It shows the effectiveness of modeling and statistical analysis in quantifying the feature variation pattern and providing a discriminative set of features.

TABLE 7. Performance comparison with the methods available in literature.

	Database- [27]			Database- [28]		
Method	Se.(%)	Sp.(%)	Acc.(%)	Se.(%)	Sp.(%)	Acc.(%)
[11]	65.74	59.15	62.45	60.30	56.50	58.40
[16]	77.69	79.96	78.83	72.143	66.46	69.302
[17]	81.47	83.28	82.38	80.084	80.647	80.366
[18]	72.40	70.31	71.36	71.62	69.88	70.75
[19]	78.4	76.3	77.35	76.62	74.88	75.75
[15]	93.7	83.61	88.65	94.2	80.41	87.31
Proposed	**94**	**86.92**	**90.46**	**95.43**	**81.56**	**88.49**

Comparison of the proposed method is made with the existing methods for the subjects mentioned in Table 1 and the result is reported in Table 7. From the Table, it is evident that the proposed method provides a better result compared to the existing methods. It can be seen that the performance of [15] is close to the proposed method. However, in [15] EEG signal is divided into sub-bands using fixed bandwidth bandpass which may fail to capture the variation in dominant frequencies from person to person, time to time due to changes neural activity which is discussed in section IIB. Moreover, unlike the proposed method, high frequency (>40Hz) EEG data are not taken for analysis.

In order to evaluate the performance of the proposed method, instead of subject-specific analysis, one idea could be to apply cross-validation schemes on all frames from all subjects mentioned in Table 1 for [27] together. The result achieved for this approach is shown in Table 8. It is evident from the Table that the proposed method shows very satisfactory performance in classifying apnea and non-apnea frames.

TABLE 8. Classification performance with all subjects combined.

Cross-Validation	Sensitivity (%)	Specificity (%)	Accuracy (%)
leave-one-out	96.90	87.93	92.42
10-fold	97.18	87.72	92.36
5-fold	96.22	87.08	91.59
2-fold	96.39	85.95	91.17

EEG signals reflect the underlying cortical activation, and therefore different electrodes exhibit distinct functional roles during sleep. According to the recommendations of Rechtschaffen and Kales [34], it requires one EEG lead with electrodes placed either at C4-A1 or C3-A2 according to the 10-20 system of electroencephalography electrodes placement on the skull. In agreement with this view,

the 2007 AASM Manual [35] recommended the use of three standard EEG electrodes for the scoring of sleep; including central, frontal and occipital electrodes. However, [36] showed that no differences are observed in arousal scoring statistics when the only central electrode is used compared to using three electrodes (frontal, central, and occipital). In the proposed method, the databases used for apnea patients utilized different electrodes for data acquisition. The performance of apnea detection of the proposed method with respect to electrode position is presented in Table 9. It is interesting to note that the result very well supports the recommendation of Rechtschaffen and Kales. Here the electrodes with a central position (C3-A2, C4-A1) have significantly better apnea detection performance compared to other positions.

TABLE 9. Effect of position of electrode in apnea detection.

Electrode Position	No. of Subjects	Sensitivity (%)	Specificity (%)	Accuracy (%)
C4-A1	4	95.42	85.61	90.51
C3-A2	23	94	86.92	90.46
O2-A1	2	84.29	79.76	82.02
C3-O1	9	97.78	81.74	89.76

TABLE 10. Performance of different classifiers.

Classifier	Sensitivity	Specificity	Accuracy
SVM (linear)	68.3	75.2	71.75
SVM (Polynomial)	71.04	83.3	77.17
SVM (RBF)	70.86	94.13	82.50
LDA	77.27	78.87	78.07
KNN	**96.90**	**87.93**	**92.42**

TABLE 11. Performance of different distance function in KNN classifier.

Distance Function	Sensitivity	Specificity	Accuracy
Euclidean	95.84	87.69	91.76
Cityblock	94.77	87.30	91.04
Correlation	96.16	86.15	91.16
Cosine	**96.90**	**87.93**	**92.42**

The proposed method is tested with various classifiers. The performance of different classifiers is presented in Table 10. It is to be found that out of several classifiers KNN provides the best result, hence it is selected in the proposed method. Moreover, in KNN, different distance functions can be used for classification. In this paper, the performance of KNN with different distance functions is investigated and it is reported in Table 11. From the table it is evident that all the functions have quite similar performances, however, out of these functions, cosine distance function gives the best performance. Hence, cosine distance function has been adopted in this paper. Alongside the distance function, the classification performance of KNN also depends upon the value of K used. Figure 12 presents the detailed performance analysis of the classifier with various values of K. It is observed from the figure that the performances are quite similar for K upto 12. However, the specificity declines onwards, hence the overall accuracy also falls. In order to have a consistent performance, in this paper K = 9 is selected.

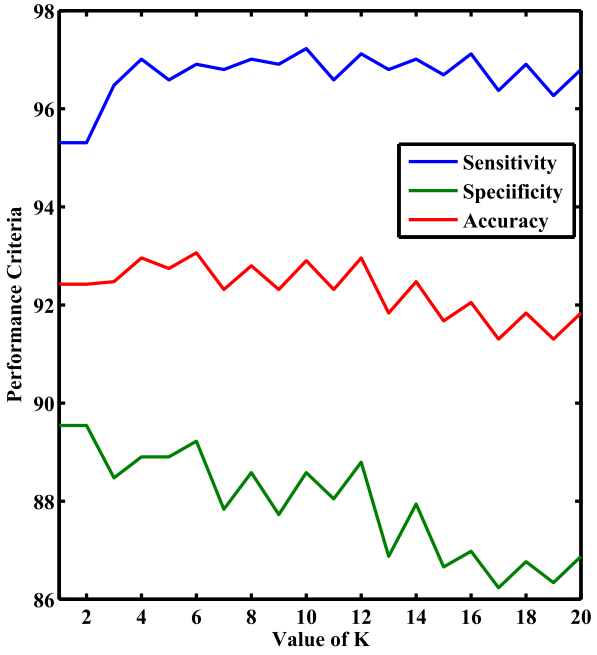

FIGURE 12. Performance of KNN classifier in the proposed method with different values of K.

TABLE 12. Performance of the proposed method in classifying apnea and healthy subjects.

Cross-Validation	Sensitivity (%)	Specificity (%)	Accuracy (%)
leave-one-out	98.83	97.55	98.19
10-fold	98.80	98.15	98.45
5-fold	98.82	97.73	98.27
2-fold	98.55	97.52	98.03

2) CLASSIFYING APNEA PATIENTS AND HEALTHY SUBJECTS

Here, non-apnea frames are taken from healthy subjects and the task of classifying apnea and healthy subjects is considered. Different cross-validation schemes are applied for performance evaluation and the details of the result are reported in Table 12. For each cross-validation scheme, the average result of ten independent trials is reported. From the Table, it is evident that the proposed method achieves superior performances in classifying apnea and healthy subjects in terms of all performance criteria.

IV. CONCLUSION

In this paper, instead of considering the entire frame of given EEG data at a time, a unique sub-frame based VMD analysis is followed. VMD divides a signal into K band-limited intrinsic mode functions (BLIMFs) which are compact around a center frequency calculated solving a constrained variational problem. Such BLIMFs with adaptive center frequency can represent neural activity better compared to band limited EEG signal collected by bandpass filtering with definite center frequency and bandwidth. Moreover, it is shown that for EEG data, the number of VMD modes can be taken as five ensuring better result and limited computational complexity. Features expected to be discriminative for apnea detection are computed from each BLIMF of small duration sub-frame EEG data and temporal variation of features are generated for each mode. Unlike analysis over the entire frame, such

small duration sub-frame based analysis and feature extraction can preserve local characteristics better. It is shown that if the extracted temporal feature variations are directly used for classification, it yields a poor result. Hence, modeling and statistical analysis are carried out on the extracted feature variation pattern, which provides an opportunity to characterize the amplitude variation of it. Among different PDF models, it is discovered that in terms of GSI Rician PDF offers the best feature quality. Unlike the established methods, the proposed is employed to classify apnea and non-apnea frames of apnea patients as well as discriminate apnea and healthy subjects, which has a great demand in the field of diagnosis. The proposed method is evaluated on three different and large public databases of apnea patients with wide variation in AHI and healthy subjects and three different criteria of classification have been adopted to measure the effectiveness of the proposed method. In each of the cases, the proposed method offers significantly better classification performance in comparison to some existing methods in terms of sensitivity, specificity, and accuracy. As a result, the proposed scheme can be employed in clinical applications to reduce the burden of the clinicians in apnea detection.

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