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Sleep Apnea Detection Based on Rician Modeling of Feature Variation in Multi-band EEG Signal

Arnab Bhattacharjee, Suvasish Saha, Shaikh Anowarul Fattah*, Wei-Ping Zhu and M. Omair Ahmad, *Fellow, IEEE*

***Abstract*—Sleep apnea, a serious sleep disorder affecting a large population, causes disruptions in breathing during sleep. In this paper, an automatic apnea detection scheme is proposed using single lead electroencephalography (EEG) signal to discriminate apnea patients and healthy subjects as well as to deal with the difficult task of classifying apnea and non-apnea events of an apnea patient. A unique multi-band sub-frame based feature extraction scheme is developed to capture the feature variation pattern within a frame of EEG data, which is shown to exhibit significantly different characteristics in apnea and non-apnea frames. Such within-frame feature variation can be better represented by some statistical measures and characteristic probability density functions. It is found that use of Rician model parameters along with some statistical measures can offer very robust feature qualities in terms of standard performance criteria, such as Bhattacharyya distance and geometric separability index. For the purpose of classification, proposed features are used in K Nearest Neighbor (KNN) classifier. From extensive experimentations and analysis on three different publicly available databases it is found that the proposed method offers superior classification performance in terms of sensitivity, specificity and accuracy.**

***Index Terms*—EEG signals, EEG sub-bands, sleep apnea, entropy, sub-framing, model fitting, Rician model, KNN, goodness of feature, classification.**

I. Introduction

Sleep apnea, a common sleep disorder deteriorating sleep quality of the patients, affects about 5-20% of adult population [1], [2]. According to American Academy of Sleep Medicine (AASM) criteria, apnea is scored where reduction in airflow is $\geq$90% and it stays like so for more than 10 seconds. Hypopnea criterion requires $\geq$30% reduction in airflow for more than 10 seconds in association with either $\geq$3% oxygen desaturation or an arousal [3]. Sleep apnea patients generally experience severe headaches, daytime sleepiness and several cardio-respiratory disorders [4]-[5].

In overnight polysomnography (PSG), the whole night apnea events are manually scored by an expert, which is expensive, tedious, time consuming and prone to human error [6]. As a result, there is a great necessity for an automatic sleep apnea detection algorithm. Different automatic apnea detection schemes using various biomedical signals including EEG are presented in [7]-[13]. For example, in [7], heart rate variability, nasal pressure, EOG, EMG, oronasal temperature, in [8], Oxygen saturation, heart rate variability and the respiratory signals, in [9] EMG signal, in [10] pupil size, in [11] only ECG signal, in [12] oximetric signal, in [13] ECG, EMG, EOG signals are used.

First three authors are with the Department of EEE, BUET, Dhaka, Bangladesh (email: arnabeee10@eee.buet.ac.bd, suvobuet@gmail.com, fattah@eee.buet.ac.bd). Fourth and fifth authors are with the Department of ECE, Concordia University, Quebec, Canada (email: weiping@ece.concordia.ca, omair@ece.concordia.ca)

Instead of utilizing several physiological signals, EEG signal alone is getting special attention by the researches because of its successful application in analyzing sleep related problems [14]-[23]. In [14] non-linear behavior of EEG signal is studied. EEG scaling exponents computed by detrended fluctuation analysis (DFA) are used as features to classify apnea and healthy subjects in [14]. In [15], Hermite decomposition algorithm based on particle swarm optimization is proposed and [16], [17] employ wavelet transform of EEG to identify sleep apnea events. Instead of utilizing the full band EEG signal, an effective way is to divide the EEG signal into well known EEG sub-bands, namely delta, theta, alpha, sigma and beta and analyze the band limited signals. In [18], energy and variance computed from each sub-band are used as features for apnea classification. Bispectral characteristics of EEG signal are studied in [19], where in each sub-band the degree of quadratic phase coupling (QPC) is analyzed. Sleep apnea is detected from the variation of Hilbert spectrum frequency in [20]. Cumulative delta-power ratio of overlapping frames is used for classification in [21] while in [22], multi-band entropy values are used as features to exploit the random characteristics of EEG signal. In [23], statistical features are extracted from the variation of Beta band energy within an EEG frame and used for the purpose of classification.

Most of the reported methods consider classification between apnea and healthy subjects and the difficult task of discriminating apnea and non-apnea events is rarely attempted. In this paper, a sub-frame based model fitting approach is proposed where both these classification scenarios are taken into consideration. First, a multi-band sub-frame based scheme is introduced to extract the feature variation pattern within a frame. Next, the feature variation patterns are processed using statistical analysis and modeled with characteristic probability density function. Resulting model parameters and some statistical measures are used in K nearest neighbor (KNN) classifier to classify apnea and non-apnea frames. Detail experimentations and performance analyses are carried out in three different publicly available databases. The uniqueness of the proposed method lies in modeling the within-frame feature variation pattern and utilizing the fitted model parameters as potential features in the classification scheme, which offers very low feature dimension. Unlike using multiple bio-signals, this paper focuses on automatic detection of sleep apnea using single lead EEG signal which makes the system cost effective and can lead to an auto-diagnostic device favorable for in-home care.

II. Proposed Method

Different major steps involved in the proposed method are illustrated in Fig. 1. A given frame of raw EEG data is first pre-processed, divided into frequency bands, and then proposed sub-frame based feature extraction scheme is employed in each band-limited signal. Finally statistical analysis and modeling are applied to extract the feature vector to be used in the classifier. In what follows, detailed description of each step is presented.

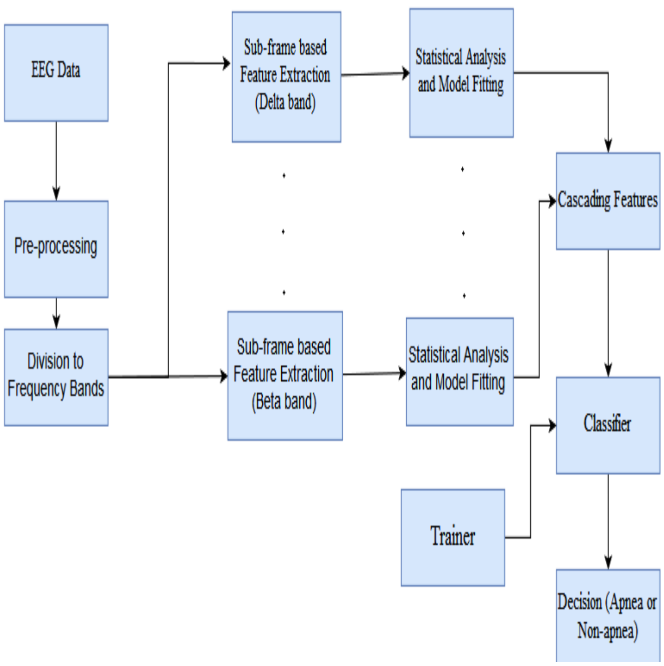

Fig. 1: Block diagram representing the major steps involved in the proposed method

A. Band-limited Signal Extraction

DC offset of a frame of EEG data is removed followed by frame amplitude normalization. During sleep activity level of recorded EEG data changes as the mental state and the sleep stage continuously change with respect to time. As a result, there is a large change in energy content in different EEG frames. Energy normalization is carried out in each frame to counter this phenomena.

EEG signal exhibits significantly different characteristics in different frequency bands. During apnea, carbon dioxide builds up in the bloodstream as breathing is paused, which is identified by the chemoreceptors and brain signals the person sleeping to wake up and breathe in air [24]. Such changes in neural activity level from non-apnea to apnea can cause notable variation in various frequency bands of the EEG data, namely: delta(0.25-4 Hz), theta(4-8 Hz), alpha(8-12 Hz), sigma(12-16 Hz) and beta(16-40 Hz). In the proposed method, five band-pass filters are used to extract the band limited EEG signals which are expected to preserve local information better with respect to full band signal.

B. Multi-band Feature Extraction

For a band limited EEG data, among various statistical features, entropy and log-variance are used in the proposed method. Entropy of a discrete random variable Y with possible values $\{y_0, y_1, y_2, ..., y_M\}$ is defined as

$$H(Y) = E(I(Y)), \tag{1}$$

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

$$I(Y = y_i) = -\log_2(p(y_i)), \tag{2}$$

Using (2), the entropy in (1) can be re-written as

$$H(Y) = -\sum_{i=0}^{M} p(y_i) \times log_2(p(y_i)) \tag{3}$$

where $p(y_i) = n_i/N$, with n_i be the number of occurrence corresponding to y_i value among the N number of values, i.e. $\sum_i n_i = N$. During apnea, normal breathing is hampered and patient may make gasping, grunting or snorting sounds and restless body movements. Since EEG signal contains information regarding different mental and motor-imagery states of the brain, it is expected that for a person at sleep, during apnea events there will be certainly a rapid change in information content in EEG recordings. As entropy is a statistical measure of information content, it is proposed as a potential feature for apnea event detection. For an N length EEG data $s[n]$ with mean value μ, log-variance (LV) is expressed as

$$LV = \log_e\left[\frac{1}{N}\sum_{n=1}^{N}(s[n]-\mu)^2\right]. \tag{4}$$

Similarly, it is expected that variance of EEG signal would be different in both the classes. As variance of EEG is very small, logarithm of variance is used.

C. Temporal Feature Variation Pattern Extraction

In frame by frame analysis, generally the whole duration of a test frame is considered for feature extraction. As an alternate, dividing a frame into overlapping short duration sub-frames offers an advantage of capturing precisely local signal characteristics. In an N length signal with sub-frame length M, shifting by p samples with $p{<<}M{<}N$, there will be a total $\frac{N-M}{p}+1$ number of sub-frames.

If a particular feature is extracted from each sub-frame, a temporal profile of that feature within a frame can be obtained and the properties of that sub-frame based feature sequence can be utilized. A major advantage of using sub-frame based feature extraction is the reduction of the effect of random fluctuation in a given test frame. For example, an

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unexpected value in a test frame can significantly affect the overall feature value. However, in sub-frame based analysis that unexpected value will affect only a mere portion of the total sub-frames. Thus overall analysis carried out using sub-frame based feature values can provide better characteristics of a test frame in comparison to the case where features are calculated using whole test frame. Another key factor is that not the entire N samples of a particular frame correspond to an apneic zone as frame duration is taken higher than the typical apnea duration. Apnea may occur only for a limited period in the whole duration of frame. Sub-framing increases the probability of correctly identifying the particular apneic event since sub-frame based extracted features exhibit sharp changes in its characteristics within an apnea frame, in particular at the transition between apnea and non-apnea events. Considering reasonably large frame size, where apnea duration is less than a frame duration, it is obvious that a transition will exist either from apnea to non-apnea or from non-apnea to apnea or both. Feature extracted from the entire frame at a time, may not be able to characterize such changes.

In order to demonstrate the variation of a feature within a frame in sub-frame based analysis, in Fig. 2, entropy feature patterns extracted from each band limited signal are presented. Here two frames, one apnea and one non-apnea are considered. It is clearly observed from the figure that in different band limited signals, characteristics of the extracted feature patterns differ significantly between apnea to non-apnea cases.

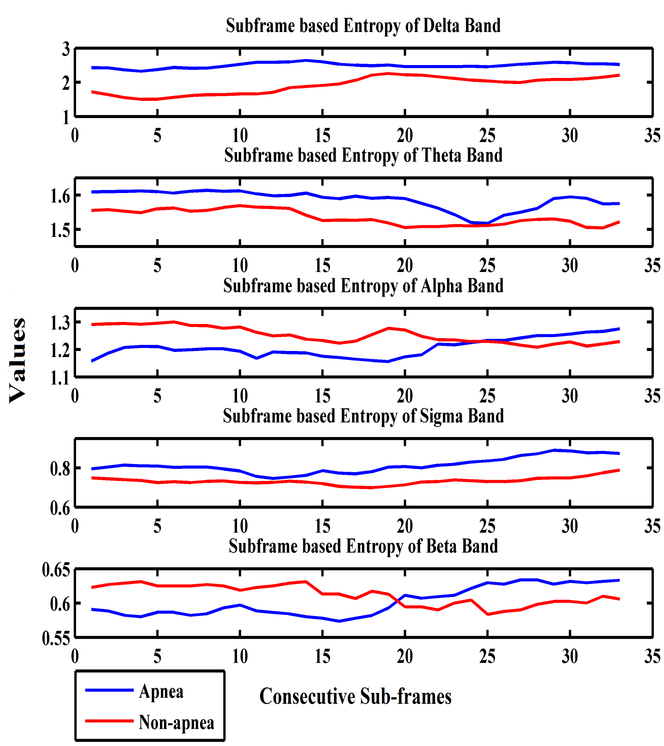

Fig. 2: Variation profile of entropy feature obtained from different band limited EEG signals of test frames (One apnea and one non-apnea frames are considered)

D. Model Fitting of the Extracted Feature Variation Pattern

Characteristic profile of a particular feature obtained from sub-frame based analysis can directly be used as feature for classifying a test frame. However, direct use of the feature sequence involves large feature dimension. As an alternate, efficient processing schemes can be applied on the feature variation pattern to extract distinct information for the purpose of classifying apnea and non-apnea events. One possible way is to extract various statistical features of feature variation pattern. Among different statistical features, mean and variance are considered in the proposed method. In addition to that, with the purpose of quantifying the variation pattern of sub-frame based extracted features, characteristics its amplitude variation can be investigated. In this paper, we propose to fit the sub-frame based extracted feature sequences with characteristic probability density functions (PDFs). The idea is to fit sub-frame based feature variation with a PDF and then use the fitted model parameters as feature. In this case, most of the well known PDFs can be taken into consideration, such as Gaussian, Exponential, Rayleigh... etc. Description of different popular PDFs is given in Table I [25]. This approach will provide an opportunity to capture the variations of statistics of data distributions in apnea and non-apnea. As the number of characteristic parameters is small (most of the cases one or two), feature dimension would be drastically reduced in comparison to using the whole sub-frame based feature sequence. Out of several PDFs, in this paper, we propose to use Rician PDF to fit the feature variation pattern. Detailed analysis using different PDFs is followed in section III. The histograms of feature sequences and corresponding Rician fitting of several apnea and non-apnea frames in different EEG bands are shown in Fig. 3. Here, examples of both entropy and log-variance are presented for all the band limited signals. It is observed from the figure that the histograms of feature variation pattern corresponding to apnea and non-apnea cases differ widely from each other and the fitted Rician PDFs are different and have wide separation. Thus PDF model fitting is expected to offer better feature quality as well as reduced computational burden.

TABLE I: Definition of Characteristic PDFs

Distribution	PDF	Parameters
Normal	$f(x\|\mu,\sigma^2) = \frac{1}{\sigma\sqrt{(2\pi)}} \exp - \frac{-(x-\mu)^2}{2\sigma^2}$	μ, σ
Exponential	$f(x;\lambda) = \begin{cases} \lambda \exp^{-\lambda x}, x \geq 0; \\ 0 \qquad , x < 0 \end{cases}$	λ
Rayleigh	$f(x;\sigma) = \frac{x}{\sigma^2} \exp - \frac{-x^2}{2\sigma^2}, x \geq 0$	σ
Rician	$f(x\|\upsilon,\sigma) = \frac{x}{\sigma^2} e^{-\frac{x^2+\upsilon^2}{2\sigma^2}} I_o(\frac{x\upsilon}{\sigma^2})$	υ, σ
Gamma	$f(x;\alpha,\beta) = \frac{\beta^{\alpha} x^{\alpha-1} \exp^{-\beta x}}{\Gamma(\alpha)};$ $x > 0 \; and \; \alpha > 0 \; \beta > 0$	α, β
Nakagami	$\frac{2m^m}{\Gamma(m)\Omega^m} x^{2m-1} \exp(-\frac{m}{\Omega}x^2),$ $\forall x \geq 0; m \geq 0.5; \Omega > 0$	m, Ω
Weibull	$f(x;\lambda,k) = \begin{cases} \frac{k}{\lambda}(\frac{x}{\lambda})^{k-1} \exp^{(-\frac{x}{\lambda})^k}, x \geq 0; \\ 0 \qquad , x < 0 \end{cases}$	λ, k

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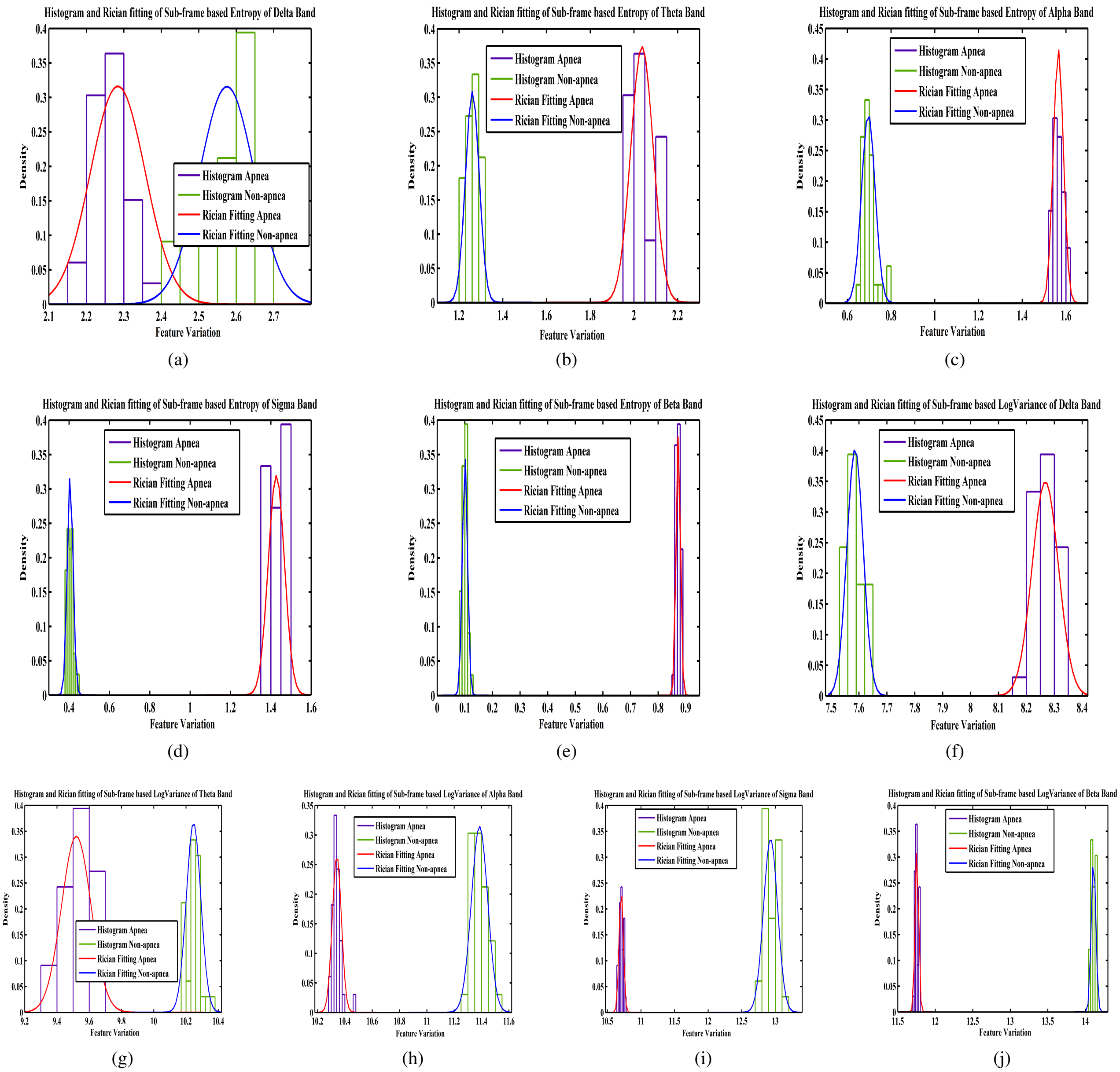

Fig. 3: Histogram of Sub-frame based feature variation patterns of each sub-band and corresponding Rician fitting

The statistical features and the model parameters calculated from each band limited signal of a frame are cascaded as stated in (5),(6) and (7) to form the final feature vector F_{proposed}. Here, $F_{stat,\delta}$ and $F_{mod,\delta}$ are the statistical features and model parameters, respectively extracted from both the sub-frame based entropy and log-variance feature variation patterns in delta band. $F_{\text{statistical}}$ and F_{model} indicate the features obtained from statistical analysis and model fitting, respectively.

$$\mathbf{F}_{statistical} = [\mathbf{F}_{stat,\delta}\ \mathbf{F}_{stat,\theta}\ \mathbf{F}_{stat,\alpha}\ \mathbf{F}_{stat,\sigma}\ \mathbf{F}_{stat,\beta}] \tag{5}$$

$$\mathbf{F}_{model} = [\mathbf{F}_{mod,\delta}\ \mathbf{F}_{mod,\theta}\ \mathbf{F}_{mod,\alpha}\ \mathbf{F}_{mod,\sigma}\ \mathbf{F}_{mod,\beta}] \tag{6}$$

$$\mathbf{F}_{proposed} = [\mathbf{F}_{statistical}\ \mathbf{F}_{model}] \tag{7}$$

E. Classifier

In the proposed method, K-nearest neighborhood (KNN) classifier is used where distance function computed between the features belonging to the EEG pattern in the test set and K neighboring EEG patterns from both apnea and non-apnea group in the training set is considered. The test set EEG pattern is classified based on the K closer class labels of EEG patterns. For the purpose of performance evaluation, M-fold cross validation technique is employed.

III. Result and Discussion

The proposed method involves two stage feature extraction- features mentioned in Section II-B are computed from each sub-frame and the extracted feature variation pattern is used for statistical analysis and model fitting to obtain the final feature

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vector. In view of analyzing the performance of various models, different types of distributions are considered separately in forming the feature vector proposed in (6) and in particular Rician model is used in (7) to form the proposed feature vector. This section presents description of the databases used and the detailed analysis on the choice of proper PDF, quality of the extracted features and classification performance.

A. Database

In order to investigate the proposed method in discriminating apnea patients and healthy subjects as well as apnea and non- apnea frames of an apnea patient, the proposed method is evaluated on three large databases, publicly available in the PhysioNet [26]-[28]. Polysomnograms of healthy subjects are available in [27] while [26] and [28] contain full overnight polysomnograms from subjects with previously diagnosed with sleep apnea. Experienced sleep specialist scored the polysomnograms as apnea or non-apnea which is available as ground truth. Apnea and Hypopnea Index (AHI) defines the severity of apnea and it is measured by the number of occurrence per hour. For the purpose of detailed experimentation, subjects with broad variation in AHI are taken into consideration. In the databases there are different types of apnea and hypopnea, such as obstructive sleep apnea, central sleep apnea, mixed sleep apnea, obstructive sleep hypopnea, central sleep hypoapnea, and mixed sleep hypopnea. The proposed method is targeted to detect apnea frames irrespective of their types. All different categories of apnea and hypopnea events are termed as apnea in this paper. Hence, all types of apnea and hypopnea frames and equivalent number of non-apnea frames for subjects with AHI greater than 5 are selected for experimentation. Depending on the available ground truth, for the databases available in [26] and [28], frame lengths are taken 15s and 30s, respectively. In terms of selecting sub-frame length (M) and corresponding sample shift (p), two factors are to be considered. A small sub-frame length with a moderate sample shift will provide an increased number of feature variation data but it may result into incorrect estimation of the features due to not having enough data. Again, a very small sample shift can be chosen which will provide a large number of feature variation data but it will increase computational complexity. Considering both the issues, in the proposed method, a relatively large sub-frame length of 1280 and 6250 samples are selected for databases- [26] and [28] and 90% overlap between two successive sub-frames are chosen to obtain better estimation of the features as well as considerable amount of data points for model fitting with moderate computational complexity. The information of the subjects used in this study and the number of EEG frames taken are given in Table II.

B. Goodness of Fit

In this sub-section, a comparative analysis on fitting characteristics of different distributions is presented considering conventionally used statistical tools, such as Log Likelihood (LogL), Bayesian Information Criterion (BIC) and Akaike Information Criterion (AIC). The distribution with the largest Log Likelihood value represents statistically the best fit. BIC and AIC are defined as

$$BIC = -2 * ln(likelihood) + [ln(N)](k) \quad (8)$$

$$AIC = -2 * ln(likelihood) + 2(k), \quad (9)$$

where N and k are the number of observations and degree of freedom of model, respectively. The best model in the group compared is the one that minimizes these scores.

In order to demonstrate the comparative fitting performance of various PDFs in multi-band sub-frame based feature variation patterns of each frame, above statistical parameters are calculated. The mean values of these statistical parameters for all the apnea and the non-apnea frames corresponding to a subject are shown in Table III. It is observed from the table the best PDF fitting performance is achieved by the Rician distribution and thus Rician distribution is selected in the proposed method.

TABLE II: Information of the Patients

Database- [26]				Database- [28]			
S/No	Subject ID	AHI	No. of Frames	S/No	Subject ID	AHI	No. of Frames
1	UCDDB003	51	524	1	slp01a	17	74
2	UCDDB005	13	104	2	slp01b	22.3	130
3	UCDDB006	31	148	3	slp02a	34	180
4	UCDDB007	12	142	4	slp02b	22.2	84
5	UCDDB009	12	120	5	slp03	43	382
6	UCDDB010	34	324	6	slp04	59.8	460
7	UCDDB011	8	58	7	slp16	53.1	282
8	UCDDB020	15	132	8	slp32	22.1	100
9	UCDDB021	13	122	9	slp37	100.8	136
10	UCDDB024	24	260	10	slp48	46.8	500
11	UCDDB026	14	160				
	Total Frames		2094		Total Frames		2328

TABLE III: Comparison of fitting of different distributions evaluated in [26]

Distribution	Apnea			Non-apnea		
	LogL	BIC	AIC	LogL	BIC	AIC
Gamma	36.60	-66.21	-69.20	35.56	-64.12	-67.12
Weibull	35.89	-64.78	-67.78	34.51	-62.02	-65.02
Exponential	-60.95	125.39	123.89	-61.33	126.17	124.67
Rayleigh	-38.16	79.81	78.31	-38.54	80.58	79.09
Rician	**36.64**	**-66.29**	**-69.28**	**35.59**	**-64.18**	**-67.18**

C. Goodness of Feature

The quality of the proposed feature is investigated in terms of class separability by the standard goodness of feature measures, namely Bhattacharyya Distance (BD) and Geometrical Separability Index (GSI). For data clusters, BD is computed as [29]

$$BD = \frac{1}{8}(\mu_2 - \mu_1)^T[\frac{1}{2}(\delta)_1 + \delta)_2]^{-1}(\mu_2 - \mu_1) + \frac{1}{2}\ln(\frac{det(\frac{\delta_1+\delta_2}{2})}{\sqrt{det(\delta_1))} * \sqrt{det(\delta_2))}}) \quad (10)$$

Here δ_i and μ_i represent covariance matrix and mean vector of i-th cluster. Bhattacharyya coefficient (BC) is computed as

$$BC = \exp^{-BD} \quad (11)$$

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TABLE IV: Feature Quality in terms of BC evaluated in [26]

S/No.	Gamma	Weibull	Exp.	Ray.	Rician	Proposed
1	0.69	0.53	0.35	0.40	0.08	0.06
2	0.62	0.46	0.22	0.25	0.05	0.02
3	0.78	0.63	0.31	0.42	0.14	0.01
4	0.72	0.52	0.33	0.38	0.09	0.04
5	0.77	0.61	0.53	0.46	0.10	0.03
6	0.42	0.33	0.14	0.13	0.07	0.03
7	0.2	0.13	0.04	0.06	0.01	0.003
8	0.46	0.35	0.19	0.20	0.03	0.01
9	0.49	0.33	0.19	0.19	0.07	0.01
10	0.65	0.46	0.23	0.25	0.07	0.00
11	0.44	0.29	0.16	0.14	0.04	0.01
Mean	0.57	0.42	0.24	0.26	0.07	**0.02**

The GSI provides the measure of the separability of two classes in the nearest neighbor sense and is defined as [30]

$$GSI = \frac{\sum_{i=1}^{N} (f(x_i)) + f(x_i') + 1)\ mod\ 2}{N} \tag{12}$$

where x' is the nearest neighbor of x and N denotes the number of points. Higher value of GSI and lower value of BC represent better the feature quality.

TABLE V: Feature Quality in terms of GSI evaluated in [26]

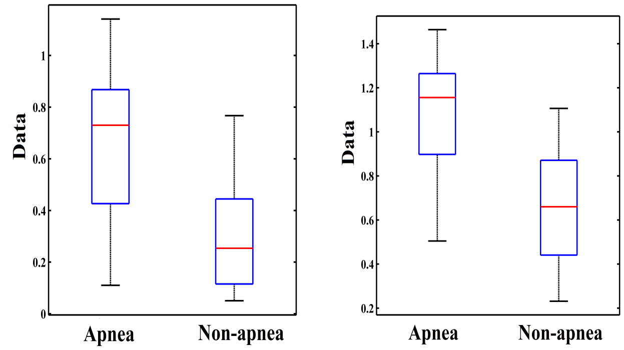
S/No.	Gamma	Weibull	Exp.	Ray.	Rician	Proposed
1	0.53	0.56	0.84	0.84	0.87	0.88
2	0.49	0.56	0.77	0.77	0.79	0.87
3	0.58	0.54	0.70	0.70	0.80	0.86
4	0.50	0.59	0.75	0.75	0.79	0.83
5	0.50	0.47	0.61	0.62	0.81	0.88
6	0.53	0.54	0.90	0.90	0.89	0.92
7	0.52	0.62	0.84	0.84	0.95	0.95
8	0.42	0.61	0.88	0.88	0.91	0.94
9	0.47	0.57	0.73	0.73	0.84	0.89
10	0.62	0.72	0.93	0.92	0.93	0.95
11	0.54	0.69	0.87	0.88	0.96	0.98
Mean	0.52	0.59	0.80	0.80	0.87	**0.90**

In Table IV and II, BC and GSI values are shown, respectively for subjects mentioned in Table II for database [26]. It can be observed from the table that out of several PDFs, the best feature quality, the lowest BC and the highest GSI. is achieved by the Rician distribution and thus Rician distribution is selected to fit the sub-frame based feature sequence in the proposed method. Moreover, it is to be observed that the proposed feature combination of statistical analysis and Rician model parameters, as it is mentioned in (7) offers the best feature quality result.

For the data used in Table II, box plots corresponding to Rician parameters (υ, σ) are shown in Fig. 4 considering entropy variation of Beta band. Here significant separation between the two classes (apnea and non-apnea) are observed.

D. Classification Result

For the purpose of classification, two different cases, (i) classification of apnea and non-apnea frames in the data of apnea patients and (ii) classification of apnea patients and healthy subjects are considered. The KNN classifier is used for classification where cosine distance function and K=9 are chosen. Standard performance measures, namely sensitivity,



(a) Rician Model Parameter υ (b) Rician Model Parameter σ

Fig. 4: Box plot of model parameters

TABLE VI: Definition of Accuracy Measures

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

specificity and accuracy, those are described in (13)-(15), and Table VI, are used.

$$Accuracy(A_{cc}) = \frac{TP + TN}{TP + FP + TN + FN} * 100 \tag{13}$$

$$Sensitivity(S_e) = \frac{TP}{TP + FN} * 100 \tag{14}$$

$$Specificity(S_p) = \frac{TN}{TN + FP} * 100 \tag{15}$$

1) Classification of Apnea and Non-apnea Frames in the data of Apnea Patients: In this case, test and train, both data, are collected from the same subject.

a) Effect of Use of Different PDFs: All three performance criteria obtained for each subject mentioned in Table II by using different PDFs are reported in Tables VII and VIII for two databases using leave-one-out cross validation scheme. In these tables, 'Stat' represents a method that utilizes statistical features ($F_{statistical}$) as described in section II-D. It is found

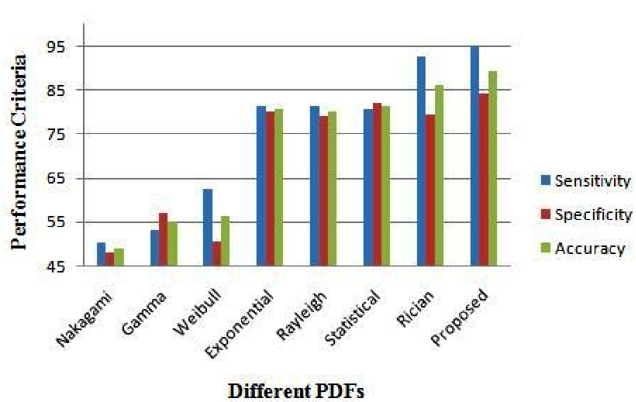


Fig. 5: Performance criteria with different PDFs

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TABLE VII: Classification result of leave-one-out cross validation evaluated in [26]

	Sensitivity(%)					**Specificity**(%)					**Accuracy**(%)				
S/No.	**Exp.**	**Ray.**	**Stat.**	**Rician**	**Proposed**	**Exp.**	**Ray.**	**Stat.**	**Rician**	**Proposed**	**Exp.**	**Ray.**	**Stat.**	**Rician**	**Proposed**
1	82.44	82.44	82.06	90.46	95.80	90.46	90.46	91.22	85.50	87.79	86.45	86.45	86.64	87.98	91.79
2	71.15	71.15	69.23	98.08	100	86.54	86.54	88.46	75	75	78.85	78.85	78.85	86.54	87.5
3	72.97	74.32	72.97	91.78	91.89	75.68	75.68	75.68	67.12	68.92	74.32	75	74.32	79.45	80.41
4	74.65	74.65	71.83	84.51	91.55	73.24	74.65	77.46	73.24	81.69	73.94	74.65	74.65	78.87	86.62
5	68.33	68.33	68.33	86.67	91.67	58.33	58.33	58.33	66.67	75	63.33	63.33	63.33	76.67	83.33
6	96.30	96.91	95.68	96.91	98.15	88.27	87.65	87.65	85.80	89.51	92.28	92.28	91.67	91.36	93.83
7	82.76	82.76	82.76	96.55	100	79.31	79.31	79.31	79.31	89.66	81.03	81.03	81.03	87.93	94.83
8	92.42	92.42	92.42	95.38	95.46	80.30	80.30	80.30	76.92	81.82	86.36	86.36	86.36	86.15	88.64
9	77.05	77.05	77.05	91.80	88.53	91.80	91.80	91.80	85.25	85.25	84.43	84.43	84.43	88.52	86.89
10	91.54	91.54	91.54	93.85	99.23	93.08	93.08	93.08	89.23	91.54	92.31	92.31	92.31	91.54	95.38
11	83.75	83.75	85	93.75	95	92.50	92.50	92.50	91.25	91.25	88.13	88.13	88.75	92.50	93.13
Mean	81.22	81.39	80.81	92.70	**95.21**	82.68	82.75	83.25	79.57	**83.40**	81.95	82.07	82.03	86.14	**89.30**

TABLE VIII: Classification result of leave-one-out cross validation evaluated in [28]

	Sensitivity(%)					**Specificity**(%)					**Accuracy**(%)				
S/No.	**Exp.**	**Ray.**	**Stat.**	**Rician**	**Proposed**	**Exp.**	**Ray.**	**Stat.**	**Rician**	**Proposed**	**Exp.**	**Ray.**	**Stat.**	**Rician**	**Proposed**
1	91.89	91.89	91.89	89.19	94.60	86.49	86.49	86.49	78.38	81.08	89.19	89.19	89.19	83.78	87.84
2	80	80	80	89.23	86.15	83.08	83.08	83.08	73.85	81.54	81.54	81.54	81.54	81.54	83.85
3	77.78	77.78	78.89	86.67	84.44	87.78	87.78	87.78	75.56	85.56	82.78	82.78	83.33	81.11	85
4	73.81	73.81	73.81	78.60	78.57	92.86	92.86	92.86	72	85.71	83.33	83.33	83.33	76.80	82.14
5	68.06	68.06	68.06	92.50	94.24	74.87	74.87	74.87	73.80	75.92	71.47	71.47	71.47	83.15	85.08
6	84.35	84.35	83.48	93.04	96.96	72.61	72.61	72.61	76.97	76.96	78.48	78.48	78.04	85	86.96
7	92.91	92.91	92.91	96.45	95.04	68.09	68.09	68.09	75.18	73.76	80.50	80.50	80.50	85.82	84.40
8	76	76	76	96	94	90	90	90	68	82	83	83	83	82	88
9	100	100	100	100	100	89.71	89.71	89.71	83.82	89.71	94.85	94.85	94.85	92.80	94.12
10	80	80	80	88	92	76	76	76	74	76	78	78	78	81	84
Mean	82.48	82.76	82.78	91.30	**91.60**	82.15	82.83	82.83	75.28	**80.82**	82.31	82.79	82.81	83.56	**86.14**

TABLE IX: Classification result of different cross-validation schemes evaluated in [26]

Cross-validation	Sensitivity (%)					Specificity (%)					Accuracy (%)				
	Exp.	Ray.	Stat.	Rician	Prop.	Exp.	Ray.	Stat.	Rician	Prop.	Exp.	Ray.	Stat.	Rician	Prop.
leave-one-out	81.22	81.39	80.81	92.70	**95.21**	82.68	82.75	83.25	79.57	**83.40**	81.95	82.07	82.03	86.14	**89.30**
10-fold	83.82	85.55	82.85	91.39	**97.10**	79.57	81.79	83.20	76.05	**84.11**	81.80	83.19	83.02	83.00	**90.60**
5-fold	83.19	82.96	83.71	91.66	**95.27**	81.06	82.01	82.63	76.89	**80.93**	82.16	82.08	82.75	83.90	**87.56**
2-fold	82.88	81.97	83.43	90.27	**93.13**	80.55	79.87	79.47	71.12	**78.07**	81.65	80.40	81.21	80.13	**85.37**

that for both datasets, the specificity values obtained by using the proposed feature vector (Rician and statistical parameters) are comparable to those obtained by other methods. However, the sensitivity and accuracy values are found far superior to all other cases, which is the greatest advantage of the proposed scheme. For better understanding, the average of all three performance criteria for various PDFs is shown in Fig. 5. It is clearly observed from the figure that among different PDFs, Rician PDF offers the best sensitivity and accuracy, competitive specificity than that is obtained by other PDFs. At the same time, the proposed method gives the best result in terms of all three performance criteria. For the purpose of evaluating the consistency of the classification due to variation of amount of training data, results obtained by the proposed method by using the leave-one-out, 2-fold, 5-fold and 10-fold cross validation schemes are reported in Table IX. In all cases, similar to previous analyses, the best performance is obtained by the proposed scheme.

b) Comparison of Proposed Method with Other Approaches: One major contribution of the proposed method is the use of two stage feature extraction: sub-frame based feature extraction and fitting the extracted feature variation using Rician PDF to use the model parameters as the feature. The proposed sub-frame based feature variation modeling is compared with the conventional frame based feature extraction method [18], [14], where features are calculated using the entire frame length. In the conventional approach, features mentioned in II-B are extracted from the entire band limited signals and directly used for classification. Instead of modeling the feature variation, another interesting comparison would be to consider the modeling of the data variation of the band limited signals. The proposed method is compared with data modeling where the modeling and statistical analysis are carried out on the pre-processed band limited frame data. The comparison of the proposed method with the conventional approach and data modeling is presented in Table X. It is evident from the table that proposed method offers significant improvement than the other two approaches in each performance criteria. Performance comparison is also carried out in terms of feature quality measure GSI. It is observed from the table that in terms of GSI, the proposed method offers superior feature quality compared to others. This is expected as the proposed sub-frame based feature extraction approach captures local feature information, which offers better local feature variation pattern than the other approaches.

The proposed method is also compared with some existing methods and results are reported in Table XI. In the implementation of the methods, for maintaining a fair comparison, frame length, sub-frame length, frequency limits for sub-bands, band pass filter, classifier parameters are kept same as the proposed method. It is observed from the table that the proposed method outperforms other methods significantly with respect to each performance criterion.

As an alternate, instead of analyzing proposed method individually for each subject, one may consider all frames from 11 subjects in Table II and cross-validation schemes can be applied to evaluate the performance. The result obtained in this case is reported in Table XII. For each of 2-fold, 5-fold and 10-fold cross validation schemes ten independent trials are taken and average result is reported. It is clearly observable from the table that the proposed method offers very high sensitivity, good specificity and high accuracy in this case for all three evaluation schemes.

The proposed method detects all types of apnea and hypopnea as apnea. The sensitivity of the proposed method to different types of apnea and hypopnea are shown in Table XIII. Here, it is evident that proposed method gives very satisfactory classification performances regardless of the type of apnea. The sensitivity of the proposed method is also investigated in terms of the severity of apnea, i.e. the AHI value of the subjects. It is known that AHI below 5 indicates healthy, from 5 to 15 is mild, above 15 to 30 is moderate and higher than 30 is severe [31]. The detailed result is given in Table XIV. It is observed from the table that the method offers very high sensitivity irrespective of the high, low or medium AHI values.

The proposed method is also compared using different classification techniques as shown in Table XV. It is observed from the table that KNN classifier gives the best performance, hence it is selected in the proposed method.

2) Classifying Apnea Patients and Healthy Subjects: Most of the methods available in literature deal with classification of EEG data collected from apnea patients and healthy persons. In this case, for the purpose of testing, EEG signals corresponding to non-apnea events are generally collected from healthy subjects. On the contrary, it is always very challenging when frames of both classes come from a same subject, i.e., the task of discriminating apnea and non-apnea frames of an apnea patient which is already discussed in previous subsection. In this sub-section, results on classifying apnea patients and healthy subjects are reported in Table XVI. Healthy EEG data, used in this simulation are available in [27] and apnea frames of subjects of [26] mentioned in Table II are considered. In Table XVI, leave-one-out, 2-fold, 5-fold, and 10-fold cross-validation results are reported. For each of the 2-fold, 5-fold and 10-fold cross validation schemes ten independent trials are considered and average result is reported. The result shows that the proposed method offers very satisfactory performances

TABLE X: Comparison of the Proposed Method with Other Approaches

Measure	Database- [26]			Database- [28]		
	Data	Conv.	Prop.	Data	Conv.	Prop.
Sensitivity	73.21	81.03	**95.21**	71.06	81.96	**91.60**
Specificity	69.87	81.92	**83.23**	73.04	79.11	**80.82**
Accuracy	71.54	81.48	**89.22**	72.05	80.54	**86.14**
GSI	0.67	0.81	**0.90**	0.66	0.77	**0.87**

TABLE XI: Comparison of the Proposed Method with the Existing Methods

Method	Database- [26]			Database- [28]		
	Se.(%)	Sp.(%)	Acc.(%)	Se.(%)	Sp.(%)	Acc.(%)
[18]	77.69	79.96	78.83	72.143	66.46	69.302
[14]	65.74	59.15	62.45	60.30	56.50	58.40
[22]	81.47	83.28	82.38	80.084	80.647	80.366
[21]	72.40	70.31	71.36	71.62	69.88	70.75
[23]	78.4	76.3	77.35	76.62	74.88	75.75
Proposed	**95.21**	**83.23**	**89.22**	**91.60**	**80.82**	**86.14**

TABLE XII: Classification result with all subjects combined

Cross-Validation	Sensitivity (%)	Specificity (%)	Accuracy (%)
Leave-one-out	98.28	83.76	91.02
10-fold	95.86	82.90	89.37
5-fold	95.80	82.90	89.35
2-fold	94.96	80.70	87.83

TABLE XIII: Sensitivity of the Proposed Method to Different Types of Apnea evaluated in [26]

Types	Total Frames	Detected as Apnea	Sensitivity
Obstructive Apnea	323	321	99.38
Central Apnea	83	83	100
Mixed Apnea	51	51	100
Total Apnea	**457**	**455**	**99.56**
Obstructive Hypopnea	234	228	97.43
Central Hypopnea	277	270	97.47
Mixed Hypopnea	79	76	96.20
Total Hypopnea	**590**	**574**	**97.29**

TABLE XIV: Sensitivity of the Proposed Method to Various AHI

Database- [26]			Database- [28]		
S/No.	AHI	Sensitivity	S/No.	AHI	Sensitivity
1	51	95.80	1	17	94.60
2	13	100	2	22.3	86.15
3	31	91.89	3	34	84.44
4	12	91.55	4	22.2	78.57
5	12	91.67	5	43	94.24
6	34	98.15	6	59.8	96.96
7	8	100	7	53.1	95.04
8	15	95.46	8	22.1	94
9	13	88.53	9	100.8	100
10	24	99.23	10	46.8	92
11	14	95			

TABLE XV: Performance Comparison Using Different Classifiers

Classifier	Sensitivity(%)	Specificity (%)	Accuracy (%)
SVM(Linear)	67	70	68.40
SVM (Polynomial)	87.32	91.28	89.30
SVM(RBF)	63.61	91.79	77.70
ANN	97.90	83.57	90.74
LDA	80.04	100	90.02
KNN	**98.28**	**83.76**	**91.02**

TABLE XVI: Classification result of Apnea and Healthy Data

Cross-Validation	Sensitivity (%)	Specificity (%)	Accuracy (%)
Leave-one-out	98.83	97.21	98.02
10-fold	98.68	96.51	97.61
5-fold	98.64	96.30	97.47
2-fold	98.33	96.24	97.28

with respect to all the standard measures of performance criteria in classifying apnea and healthy EEG data.

IV. Conclusion

In conventional frame-by-frame EEG data analysis only the global characteristics of a frame can be obtained as in that case, features are extracted considering the entire frame at a time. On the contrary, in this paper, two-stage feature extraction method is proposed. First, the feature is computed from small duration overlapping sub-frames within a frame, which can precisely capture sharp changes with respect to time and provide temporal variation of the extracted feature within that frame. Next, statistical analysis and modeling are carried out on the resulting feature variation pattern, which gives an opportunity to utilize both local and global characteristics of a frame. Apart from ensuring such time resolution in feature extraction, use of multi-band signals also ensures frequency resolution. Among various PDF models, it is found that the Rician PDF is offering the best feature quality in terms of Bhattacharyya distance and GSI. Irrespective of the type of apnea, the proposed method can not only classify apnea patient and healthy subject but also classify apnea and non-apnea frames of an apnea patient, which has a great demand in the overnight polysomnography (PSG) to reduce human error, labor and cost. The proposed method is evaluated on three different and large EEG databases and it offers superior classification performance in comparison to some existing methods in terms of sensitivity, specificity and accuracy. It makes the proposed method to be widely applicable in a greater domain of diagnosis.

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Arnab Bhattacharjee received BSc degree from EEE department of Bangladesh University of Engineering and Technology. Currently, he is a masters student of the same department. He is also working as a lecturer in the department. His research interest lies in biomedical signal processing, image processing and machine learning.

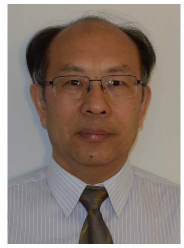
Arnab Bhattacharjee was the Technical Activity Coordinator of IEEE Young Professional Society Bangladesh and currently is the Treasurer of IEEE EMBS Bangladesh Chapter. He is a member of IEEE.

Suvasish Saha received B.Sc. degree in Electrical and Electronic Engineering from Bangladesh University of Engineering and Technology, Dhaka, Bangladesh, in 2016. He is currently pursuing his M.Sc. degree in Electrical and Electronic Engineering at Bangladesh University of Engineering and Technology, Dhaka, Bangladesh. He served as a Lecturer at University of Asia Pacific Bangladesh from August 2016 to July 2017. His research interests include biomedical signal processing, image processing and speech processing.

Shaikh Anowarul Fattah received Ph.D. degree in ECE from Concordia University, Canada. He was a visiting Postdoc and later visiting Research Associate at Princeton University, USA. He received B.Sc. and M.Sc. degrees from BUET, Bangladesh, where he has been serving as a Professor in the Department of EEE. He received several prestigious awards, such as Concordia Universitys Distinguished Doctoral Dissertation Prize in ENS, Dr. Rashid Gold Medal (M.Sc., BUET), NSERC Postdoctoral Fellowship, the URSI Canadian Young Scientist Award 2007, and BAS-TWAS Young Scientists Prize 2014. Dr. Fattah has published more than 170 international journal and conference papers with some best paper awards. His major research interests include biomedical engineering and signal processing. He is regularly delivering Keynote/Invited/Visiting Talks in many countries.

Dr. Fattah is the General Chair of IEEE R10 HTC2017, TPC Chair of IEEE WIECON-ECE 2016, 2017, MediTec 2016, IEEE ICIVPR 20017, an ICAEE 2017. He is the Editor of IEEE PES Enews, Associate Editor of IEEE Access and CSSP (Springer) and was the Editor of Journal of EE, IEB.

Dr. Fattah was 2015-16 Chair of IEEE Bangladesh Section and now Chair (2017) of IEEE EMBS Bangladesh Chapter and founder Chair of IEEE RAS. He is the recipient of 2016 IEEE MGA Achievement Award and 2017 IEEE R10 Humanitarian Technology Activity Outstanding Volunteer Award. He is committee member of IEEE PES (LRPC), IEEE EAB (CEC), IEEE SSSIT (SDHTC), IEEE SIGHT (2016 EAC), 2018 IEEE HAC and R10. He is the Senior Member of IEEE and Fellow of IEB.



Wei-Ping Zhu (SM'97) received the B.E. and M.E. degrees from Nanjing University of Posts and Telecommunications, and the Ph.D. degree from Southeast University, Nanjing, China, in 1982, 1985, and 1991, respectively, all in electrical engineering. He was a Postdoctoral Fellow from 1991 to 1992 and a Research Associate from 1996 to 1998 with the Department of Electrical and Computer Engineering, Concordia University, Montreal, Canada. During 19931996, he was an Associate Professor with the Department of Information Engineering, Nanjing University of Posts and Telecommunications. From 1998 to 2001, he worked with hi-tech companies in Ottawa, Canada, including Nortel Networks and SR Telecom Inc. Since July 2001, he has been with Concordias Electrical and Computer Engineering Department as a full-time faculty member, where he is presently a Full Professor. His research interests include digital signal processing fundamentals, speech and statistical signal processing, and signal processing for wireless communication with a particular focus on MIMO systems and cooperative communication.

Dr. Zhu served as an Associate Editor for the IEEE Transactions on Circuits and Systems Part I: Fundamental Theory and Applications during 2001-2003, an Associate Editor for Circuits, Systems and Signal Processing during 2006-2009, and an Associate Editor for the IEEE Transactions on Circuits and Systems Part II: Transactions Briefs during 2011-2015. He was also a Guest Editor for the IEEE Journal on Selected Areas in Communications for the special issues of: Broadband Wireless Communications for High Speed Vehicles, and Virtual MIMO during 2011-2013. Currently, he is an Associate Editor of Journal of The Franklin Institute. Dr. Zhu was the Chair-Elect of Digital Signal Processing Technical Committee (DSPTC) of the IEEE Circuits and System Society during June 2012-May 2014, and the Chair of the DSPTC during June 2014-May 2016.

M. Omair Ahmad (S'69-M'78-SM'83-F'01) received the B.Eng. degree from Sir George Williams University, Montreal, QC, Canada, and the Ph.D. degree from Concordia University, Montreal, QC, Canada, both in electrical engineering. From 1978 to 1979, he was a Faculty Member with the New York University College, Buffalo, NY, USA. In September 1979, he joined the Faculty of Concordia University as an Assistant Professor of computer science. He joined the Department of Electrical and Computer Engineering, Concordia University, where he was the Chair with the department from June 2002 to May 2005 and is currently a Professor. He holds the Concordia University Research Chair (Tier I) in Multimedia Signal Processing. He has published extensively in the area of signal processing and holds four patents. His current research interests include the areas of multidimensional filter design, speech, image and video processing, nonlinear signal processing, communication DSP, artificial neural networks, and VLSI circuits for signal processing. He was a Founding Researcher at Micronet from its inception in 1990 as a Canadian Network of Centers of Excellence until its expiration in 2004. Previously, he was an Examiner of the Order of Engineers of Quebec. Dr. Ahmad was an Associate Editor of the IEEE TRANSACTIONS ON CIRCUITS AND SYSTEMS PART I: FUNDAMENTAL THEORY AND APPLICATIONS from June 1999 to December 2001. He was the Local Arrangements Chairman of the 1984 IEEE International Symposium on Circuits and Systems. In 1988, he was a member of the Admission and Advancement Committee of the IEEE. He has served as the Program Co-Chair for the 1995 IEEE International Conference on Neural Networks and Signal Processing, the 2003 IEEE International Conference on Neural Networks and Signal Processing, and the 2004 IEEE International Midwest Symposium on Circuits and Systems. He was a General Co-Chair for the 2008 IEEE International Conference on Neural Networks and Signal Processing. He is the Chair of the Montreal Chapter IEEE Circuits and Systems Society. He is a recipient of numerous honors and awards, including the Wighton Fellowship from the Sandford Fleming Foundation, an induction to Provosts Circle of Distinction for Career Achievements, and the Award of Excellence in Doctoral Supervision from the Faculty of Engineering and Computer Science of Concordia University.