QuPWM: Feature Extraction Method for Epileptic Spike Classification

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Abstract—Epilepsy is a neurological disorder ranked as the second most serious neurological disease known to humanity, after stroke. Inter-ictal spiking is an abnormal neuronal discharge after an epileptic seizure. This abnormal activity can originate from one or more cranial lobes, often travels from one lobe to another, and interferes with normal activity from the affected lobe. The common practice for Inter-ictal spike detection of brain signals is via visual scanning of the recordings, which is a subjective and a very time-consuming task. Motivated by that, this paper focuses on using machine learning for epileptic spikes classification in magnetoencephalography (MEG) signals. First, we used the Position Weight Matrix (PWM) method combined with a uniform quantizer to generate useful features from time domain and frequency domain through a Fast Fourier Transform (FFT) of the framed raw MEG signals. Second, the extracted features are fed to standard classifiers for inter-ictal spikes classification. The proposed technique shows great potential in spike classification and reducing the feature vector size. Specifically, the proposed technique achieved average sensitivity up to 87% and specificity up to 97% using 5-folds cross-validation applied to a balanced dataset. These samples are extracted from nine epileptic subjects using a sliding frame of size 95 sample-points with a step-size of 8 sample-points.

Index Terms—magnetoencephalography (MEG), Position Weight Matrix (PWM), Epileptic spike detection, machine learning

I. INTRODUCTION

EPILEPSY is not a singular disease entity but a variety of dysfunctions reflecting brain disorders or abnormal electrical activities that may strike patients of all ages [1]. An epileptic seizure occurs when a burst of electrical impulses in the brain exceeds its normal limits. These pulses spread to neighboring areas in the brain, which may create an uncontrolled storm of electrical activity sent to body organs depending on the size and location of the affected region (see Fig. 1). Epileptic activity may affect brain areas related to motor functions, causing twitches or convulsion. In particular, epileptic patients may stare blankly for a few seconds during

a seizure, while others have uncontrollable jerking movements of the arms and legs. Among the diagnostic tools for epilepsy is the magnetoencephalography (MEG) [2]. The MEG is a recent functional neuro-imaging technology that measures the magnetic activity of the brain. This new technology uses an array of highly sensitive sensors or magnetometers called superconducting quantum interference devices (SQUIDs). However, as the brain magnetic field is very weak compared to surrounding magnetic sources, the MEG measurement needs a shielded room to isolate the patient from the external magnetic fields such as the magnetic field of the earth or the electronic devices. For Epileptic patients, the MEG is used during two main phases of the treatment [3], [4]: first, localizing the region of the brain, which produces the abnormal electrical activities that cause the neurological disorder. If the localized region is not responsible for a vital function in the brain, such as speech, this region is usually extracted surgically if the medications were not effective for the treatment. Second, assessing surgery outcomes.

Fig. 1: Illustration of the brain abnormal activities for different types of epileptic seizures [built based on [5] [6]].

Proper diagnosis and treatment of epilepsy is a major public health goal. An essential routine clinical step inaccurate diagnosis and treatment of epilepsy is the identification and detailed examination of interictal epileptiform discharges (IED) from Electroencephalography (EEG) and, where available, MEG recordings. Currently, the examination of MEG and EEG signals in clinical practice are performed largely manually. Visual identification by expert reviewers is the current gold standard and a widely used procedure for detecting IEDs in both MEG and EEG recordings. This type of manual detection allows much flexibility and adaptability to recordings with largely different and varying baseline levels, artifacts, and IEDs. However, it requires visually analyzing large amounts of data, which is time-consuming, produces fatigue, and is prone

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to errors and inconsistencies. For this reason, automated inter-ictal epileptic spike detection in MEG signals has attracted research interest over the last decade. Four methods, to the best of our knowledge, have been proposed for spike detection of the MEG signals in literature [7], [8]. The first method uses the independent component analysis (ICA). The authors used the ICA decomposition to find statistically independent components in multi-sensor/ multi-channel MEG signals to perform spatial filtering of the MEG data and separate inter-ictal spikes from background activity and then apply clustering technique for the detection [9]. The detection is performed using a thresholding technique. The second method is based on the common spatial patterns (CSP) method and linear discriminant analysis (LDA) (CSP-LDA) [10]. The CSP-LDA performs eigenvalue decomposition of the covariance matrices of the input data to find the most discriminative features. LDA classifier is then employed to perform the spikes detection. The third method is the Amplitude Thresholding and Dynamic Time Warping (AT-DTW) proposed in [11]. This method first uses amplitude thresholding to determine the most likely spiky segments. For the spike detection, the method employs dynamic time warping. The maximum specificity and sensitivity reported in the aforementioned detection methods are 95.8%, and 92.4%, respectively. A more recent detection method has been proposed in [12], where the decomposition of the signal into squared eigenfunctions of the Schrodinger operator was used for detection [13]. This method uses the largest negative eigenfunction in the absolute value of the discrete spectrum of the Schrödinger Operator as a feature with the Random Forest (RF) classifier.

In this work, we propose a novel feature generation method for a multi-channel MEG signal, which improves patient-independent inter-ictal spike detection. This method is based on the combination of the Position Weight Matrix (PWM) method and the uniform quantization scheme. We name this approach QuPWM. This method takes advantage of the efficiency of the PWM method, which is usually used for DNA sequences classification. QuPWM shows great potential in improving the accuracy of the inter-ictal spike detection models.

The paper is organized as follows. Section II includes a description of the MEG dataset and the proposed features extraction process methods based on the PWM method and the used quantization schemes in Section II. Section III presents the obtained results using two MEG experiment: first, healthy versus epileptic patients. Second, using spiky versus non-spiky sample in epileptic patients. Section IV presents a discussion of the findings, where a conducted sensitivity analysis on the proposed feature extraction method is analyzed with respect to the frame length, number of subjects, and using different dataset such as EEG. Finally, Sections V summarizes our concluding remarks.

II. MATERIALS AND METHODS

The proposed methodology consists of three main steps, as shown in Fig. 2. First, the MEG recordings are split into segments using framing technique. For instance, the first

frames of the 24 channels are concatenated to form the first sample, and so on. Then the samples are converted into sequences using a uniform quantization scheme. Second, the quantified samples are mapped to extract two types of PWM-based features. Finally, the classification model SVM is used for spike detection. These three steps are explained in the following sections II-B and II-C.

A. Experimental data acquisition and analysis

MEG data were recorded in a shielded room at National Neural Institute- King Fahad Medical City (NNI-KFMC), Riyadh, Saudi Arabia, with an Elekta Neuromag system. As the MEG signals are much weaker than normal environmental magnetic noise, the shielded room blocks the majority of environmental magnetic fields so that the magnetic fields generated by the brain can be accurately detected. Elekta Neuromag head system (helmet) contains 102 magnetometer and 204 gradiometer sensors. These sensors are further categorized according to the different brain regions. Clinically, the brain is divided into eight regions; left temporal (LT), right temporal (RT), left frontal (LF), right frontal (RF), left parietal (LP), right parietal (RP), left occipital (LO), and right occipital (RO). Each element of the Elekta Neuromag system is comprised of three sensors, one magnetometer, and two gradiometers. Magnetic brain activity was recorded at a sampling frequency of 1 kHz. MEG data was filtered by tSSS (Spatiotemporal signal space separation) method [14]. The data were then off-line band-pass filtered 1-50Hz for visual inspection. A total of 18 MEG data segments, each of 15 minutes duration and 24 channels, were taken from eight epileptic patients and eight healthy patients. These segments are analyzed by specialized neurologists from NNI, KFMC, Riyadh. The neurologists marked the MEG spikes locations, in different brain regions, by visual inspection. The number of sessions, total number of spikes, and the average spike duration in these recordings are described in table I as follows:

TABLE I: Detailed description of the MEG dataset.

Subject ID	#Sessions	#Spikes	Average spikes duration
E001	3	24	53.96 ms
E002	3	17	266.24 ms
E003	2	5	81.60 ms
E004	3	23	89.22 ms
E005	3	11	86.27 ms
E006	3	30	79.83 ms
E007	3	29	90.68 ms
E008	3	16	75.69 ms
E009	3	12	40.83 ms

As mentioned earlier, there are 306 sensors to cover the whole head. These sensors are further marked according to the brain regions. Written informed consent was signed by each participant or responsible adult before they participated

Fig. 2: The experiment 1 framework: MEG records pre-processing, feature generation and classification models.

in the study. The study was conducted in accordance with the approval of the Institutional Review Board at KFMC (IRB log number: 15-086, 2015).

samples suitable for the used feature generation method explained in Sections II-C1 and II-C2.

Fig. 3: Example of healthy and epileptic subject MEG recording. Zoomed plot shows a segment where an epileptic spike event happens in epileptic subject (orange) compared to a healthy subject (black).

B. Multi-channels MEG signal pre-processing

Multi-channels MEG pre-processing aims essentially to prepare classification samples. The pre-processing consists of three steps:

- **signal Framing**: build equitized samples that combine sliding windows or frames from all the 24 MEG channels. These combined frames will represent the raw data samples used as inputs to the classification, which will be quantized in the next step.
- **FFT projection**: with respect to the QuPWM features, the input signals should be preferably aligned in order to get better classification performance. Motivated by that, we consider applying frequency domain projection through a Fast Fourier Transform (FFT) to the framed MEG signals.
- **signal Quantization**: convert the real-values samples to sequences of letters. This step is needed to make the

1) *MEG signal Framing*: The multi-channel MEG signals are segmented into frames using sliding frames using a sliding window of size 100 sample-points with a step of 2 sample-points, as shown in Figures 2 and 3. For instance, the first 100 sample-points of all channels are concatenated together to form the first sample of size 2400 sample-points of the input raw-data. A binary label or class is assigned to each sample as follows:

- **Positive class**: represent samples that have epileptic spike events occurring in MEG records of the epileptic patients.
- **Negative class**: represent samples from uniformly distributed time-locations in MEG records of the healthy patients.

After signal framing, the positive and negative samples will be quantized using a uniform quantizer, as explained in the next section.

2) *FFT projection to frequency domain*: The input framed signal are transformed to the frequency domain using FFT transform of $x(n)$ to frequency domain as $X(k)$ defined as follows:

$$X(k) = \frac{1}{N} \sum_{n=0}^N x(n) e^{\frac{2\pi k n}{N}} \quad (1)$$

where N is the number of sampling-points of the signal $x(n)$.

In the frequency domain version of the signal, each position/sampling-point represents a specific frequency component in all signals forming alignment of the input framed signals. Which allows all input signal to be suitable for position weight matrix method.

3) *MEG signal quantization*: In this work we employed the PWM method for feature extraction as explained in Section II-C1. However, as the PWM method deals only with

sequences, the input MEG samples should be converted into sequences, as shown in Fig. 4. For this reason, we used a uniform quantization scheme. The quantization is utilized to convert the real-valued signal X to a sequence Q of different levels $q_1, q_2, \dots, q_M$ defined as follows [15], [16]:

$$Q(n) = q_i \quad \text{where} \quad i = 1, 2, \dots, M \quad (2)$$

Fig. 4: Example of MEG signal quantization using four levels.

In this classification, the quantization is used to reduce the weight matrices size compared to applying the PWM directly to real-valued signal, because every real value has to be considered as a level in its own. The quantizer will regroup different values of the real-valued input signal into one single level q_i (see Fig. 4). The number of levels M will depend on the probability density of the dataset, as shown in Fig 5. Therefore, two major parameters of the quantization scheme are defined: the desired number of levels M and the resolution r . For an appropriate choice of these parameters, the probability distribution of the signal is analyzed for both classes.

Fig. 5: The quantization of the real-valued sequence with a resolution $r = \sigma$ and $M = 8$. The percentage values reflect the significance of probability of each interval.

Indeed, it is known from probability theory and mathematical statistics that the value of a random variable is considered rare to happen if it lies far from its mean μ by more than 3σ . This observation is called the 3-sigma rule [17] [18]. Therefore, only the most significant variability or randomness characterizing of a Gaussian random variable X is considered, while the other values are neglected. This fact is observed if :

$$|X(n) - \mu| \leq 3\sigma \quad (3)$$

where μ and σ are defined to be the mean and standard deviation of the Gaussian random variable X .

The standard rule is used to define the quantization scheme, as shown in Fig. 5. It is important to note that the probability distribution of X varies from subject to another, which affects the quantization scheme. Therefore and in order to unify the quantization scheme, the mean μ and standard deviation σ are defined as the average mean and standard deviation of all subjects as follows:

$$\mu = \frac{1}{N_s} \sum_{n=1}^{N_s} \mu_n \quad \text{and} \quad \sigma = \frac{1}{N_s} \sum_{n=1}^{N_s} \sigma_n, \quad (4)$$

where N_s is the number of subjects. μ_n and σ_n are the mean and the standard deviation of the data values of the n^{th} subject.

Since the 3-sigma rule indicates that most of the information of a Gaussian random variable is located within $3\sigma + \mu$, the quantization resolution is set to be equal to the standard deviation σ as shown in Fig. 5 and explained in detail in Algorithm 1.

Algorithm 1: Quantization Algorithm

Input : X : Real-valued MEG signal
 M : Number of Quantization levels
 μ : Quantization centroide
 r : Quantization resolution

Output: Q : Output sequence

$N_X \leftarrow$ length of X

for $n \leftarrow 1$ **to** N_X **do**

for $k \leftarrow \frac{2-M}{2}$ **to** $\frac{M}{2}$ **do**

if $X(n) < \mu + \frac{(2-M)r}{2}$ **then**

$Q(n) = q_1;$

else if $\mu + (k-1)r \leq X(n) < \mu + kr$ **then**

$Q(n) = q_{(k+M/2)};$

else

$Q(n) = q_M;$

end

end

C. QuPWM-based features generation

The proposed Quantization-based position weight matrix (QuPWM) feature generation method is based on combining the position weight matrix (PWM) method with Quantization. This method uses two approaches to generate PWM features, as explained in the next section.

1) *Standard PWM-based features* : A position weight matrix (PWM), also known as a position-specific weight matrix (PSWM) or position-specific scoring matrix (PSSM), has been presented for the first time by Gary in [19]. This method is widely used technique for motifs characterization and discovery in biological sequences such as DNA/mRNA [20]–[24]. It showed high potential in sequences characterization and motifs extracting with remarkable binary classification accuracy. For MEG signals, we adapted the PWM-based method to extract relevant features after signal quantization methods. The PWM is based on building two matrices, PWM^+ derived from the positive training set and the second PWM^- represents the negative set. The PWM matrices indicate the significance of each position within input sequences for each class. For binary classification, the two matrices PWM^+ and PWM^- are defined as follows:

$$PWM^+[i, q_j] = \sum_{s=1}^{N_s^+} \xi(Q_s^+(i), q_j) \quad (5)$$

and

$$PWM^-[i, q_j] = \sum_{s=1}^{N_s^-} \xi(Q_s^-(i), q_j) \quad (6)$$

where N_s^+ and N_s^- are the total number of sequences in the positive and negative classes. The $\xi(a, b)$ function is defined as follows:

$$\xi(a, b) = \begin{cases} 1 & \text{if the } a = b \\ 0 & \text{elsewhere} \end{cases} \quad (7)$$

Table II shows an example of a positive matrix PWM^+ . Each column of the matrix represents the frequency of a specific letter q_i in a specific position n among all positive sequences.

TABLE II: Example of a position-wight matrix PWM^+ containing the frequencies of five levels $[q_1, q_2, \dots, q_5]$.

n^{th}	Quantization levels				
position	q_1	q_2	q_3	q_4	q_5
1	1104	257	331	384	372
2	1209	213	271	291	324
3	1217	245	298	336	336
4	987	263	309	409	474
5	941	253	383	442	532
6	1273	243	308	317	367
7	1494	208	243	261	245
8	1301	264	299	364	388
9	61	101	306	829	1331
10	144	88	266	599	1133
..	..	..	..	..	..

Then, these two PWMs are used to generate two scores representing the extracted features. The two scores $Score^+(\mathbf{Q})$

Algorithm 2: k -mers motif extraction

Input $\mathbf{Q}$: the input sequence, k : the order of k -mers to be extracted

Output m_q : the output k -mers motifs of the sequence $\mathbf{Q}$

$i \leftarrow 1$; $N \leftarrow \text{size}(\mathbf{Q})$

$\Omega_k \leftarrow$ all possible combinations composed of k -mers

for each combinations do

$C \leftarrow$ new combination

for $j = 1 : N - k + 1$ **do**

if $Q(j : j + k - 1) = C$ **then**

$k\text{-mers}(i, j) \leftarrow 1$

else

$k\text{-mers}(i, j) \leftarrow 0$

end

$i \leftarrow i + 1$

end

and $Score^-(\mathbf{Q})$ represent the two probabilities of a given sequence to be in the positive or negative class. In other words, for a given sequence Q to be positive, the score induced by PWM^+ should be greater than the score induced by PWM^- . The two scores $Score^+(\mathbf{Q})$ and $Score^-(\mathbf{Q})$ of a sequence Q are defined as as follows:

$$Score^+(\mathbf{Q}) = \frac{\sum_{n=1}^N PWM^+[n, Q(n)]}{\sum_{j=1}^M PWM^+[n, q_j]} \quad (8)$$

and

$$Score^-(\mathbf{Q}) = \frac{\sum_{n=1}^N PWM^-[n, Q(n)]}{\sum_{j=1}^M PWM^-[n, q_j]} \quad (9)$$

where N is the number of sample-points in the data sample/signal Q .

It is very important to mention that the PWMs should be reconstructed only from the training dataset in order not to violate the classification rules.

2) *Motif-based PWM features*: In order to extract more advanced patterns, we adopted a new approach which deals with binary sequences, extracted from the original sequence, that represent the presence of a specific motif of one letter or more in the original sequence, as shown in Fig. 6. We called this approach the motif-based Position Weight Matrix (mPWM). The main idea is to decompose every sequence into binary sequences reflecting a specific pattern of levels in this sequence such as :mono-mers (q_1, q_2, q_3 , etc), di-mers (q_1q_1, q_1q_2, q_1q_3 , etc), tri-mers ($q_1q_1q_1, q_1q_2q_3, q_3q_3q_3$, etc). For instance, a sequence of 3 levels q_1, q_2, q_3 will give: 3 possible mono-mers, $3 \times 3 = 9$ possible di-mers combinations, and $3 \times 3 \times 3 = 27$ possible tri-mers combinations. Fig. 6 shows the different k -mer encodings. For instance, the binary sequence of the mono-mers m_{q_1} is defined as follows:

Input Sequence	$Q(n)$	<table><tr><td>.</td><td>.</td><td>q_1</td><td>q_2</td><td>q_3</td><td>q_2</td><td>q_1</td><td>q_2</td><td>q_3</td><td>q_1</td><td>q_3</td><td>q_1</td><td>q_2</td><td>q_3</td><td>q_2</td><td>q_2</td><td>q_1</td><td>q_2</td><td>q_1</td><td>.</td><td>.</td><td>.</td><td>.</td></tr></table>	.	.	q_1	q_2	q_3	q_2	q_1	q_2	q_3	q_1	q_3	q_1	q_2	q_3	q_2	q_2	q_1	q_2	q_1	.	.	.	.
.	.	q_1	q_2	q_3	q_2	q_1	q_2	q_3	q_1	q_3	q_1	q_2	q_3	q_2	q_2	q_1	q_2	q_1	.	.	.	.			
Mono-nucleotide	$\mathbf{m}_{q_1}(n)$	<table><tr><td>.</td><td>.</td><td>1</td><td>0</td><td>0</td><td>0</td><td>1</td><td>0</td><td>0</td><td>1</td><td>0</td><td>1</td><td>0</td><td>0</td><td>0</td><td>0</td><td>1</td><td>0</td><td>1</td><td>.</td><td>.</td><td>.</td><td>.</td></tr></table>	.	.	1	0	0	0	1	0	0	1	0	1	0	0	0	0	1	0	1	.	.	.	.
.	.	1	0	0	0	1	0	0	1	0	1	0	0	0	0	1	0	1	.	.	.	.			
Di-nucleotide:	$\mathbf{m}_{q_3 q_1}(n)$	<table><tr><td>.</td><td>.</td><td>0</td><td>0</td><td>0</td><td>0</td><td>0</td><td>0</td><td>0</td><td>0</td><td>1</td><td>0</td><td>0</td><td>0</td><td>0</td><td>0</td><td>0</td><td>0</td><td>0</td><td>.</td><td>.</td><td>.</td><td>.</td></tr></table>	.	.	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	.	.	.	.
.	.	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	.	.	.	.			
Tri-nucleotide:	$\mathbf{m}_{q_1 q_2 q_3}(n)$	<table><tr><td>.</td><td>.</td><td>1</td><td>0</td><td>0</td><td>0</td><td>1</td><td>0</td><td>0</td><td>0</td><td>0</td><td>1</td><td>0</td><td>0</td><td>0</td><td>0</td><td>0</td><td>0</td><td>0</td><td>.</td><td>.</td><td>.</td><td>.</td></tr></table>	.	.	1	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	.	.	.	.
.	.	1	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	.	.	.	.			

Fig. 6: Examples of three binary sequences corresponding to mono-mers, di-mers and tri-mers, respectively.

$$m_{q_1}(n) = \begin{cases} 1 & \text{if } Q(n) = q_1 \\ 0 & \text{elsewhere} \end{cases} \quad (10)$$

Similarly, the binary sequence of the di-mers $m_{q_1 q_3}$ is defined as follows:

$$m_{q_1 q_3}(n) = \begin{cases} 1 & \text{if } Q(n) = q_1 \text{ and } Q(n+1) = q_3 \\ 0 & \text{elsewhere} \end{cases} \quad (11)$$

The binary mapping of k -mers motif extraction is summarized in Algorithm 2.

TABLE III: Example of position-wight matrix $PWM_{\mathbf{q}}^+$ containing the frequencies of di-mer motif.

n^{th}	Di-mer motifs (k=2)								
position	$q_1 q_1$	$q_1 q_2$	$q_1 q_3$	$q_1 q_4$	$q_2 q_1$	$q_2 q_2$	$q_2 q_3$	$q_2 q_4$	..
1	15	13	11	14	17	13	11	8	..
2	10	10	12	5	9	11	16	6	..
3	0	0	0	0	0	0	0	0	..
4	0	0	0	0	0	0	0	0	..
5	8	10	8	12	7	14	3	12	..
6	298	290	310	294	303	293	322	299	..
7	93	93	101	112	94	109	89	116	..
8	0	0	0	0	0	0	0	0	..
..	..	..	..	..	..	..	..	..	..

Similarly to the standard PWM, the binary sequences $m_{\mathbf{q}}$, representing the k -mer motifs $\mathbf{q} \in \Omega_k$ and which is defined in Eq. 14, is used to reconstruct multiple pair of PWM matrices $PWM_{\mathbf{q}}^+$ (see Table III) and $PWM_{\mathbf{q}}^-$ defined as follows:

$$PWM_{\mathbf{q}}^+(n) = \sum_{s=1}^{N_s^+} \xi(m_{\mathbf{q},s}^+(n), 1) \quad (12)$$

and

$$PWM_{\mathbf{q}}^-(n) = \sum_{s=1}^{N_s^-} \xi(m_{\mathbf{q},s}^-(n), 0) \quad (13)$$

where $\mathbf{q} \in \Omega$, where $\Omega = \Omega_1 \cup \Omega_2 \cup \dots \cup \Omega_k$ and Ω_k represents the set of the possible k -mers combination defined as:

$$\Omega = \begin{cases} \Omega_1 = q_1, q_2, q_3, \dots & \text{'mono-mers'} \\ \Omega_2 = q_1 q_1, q_1 q_2, q_1 q_3, \dots & \text{'di-mers'} \\ \Omega_3 = q_1 q_1 q_1, q_1 q_2 q_3, q_3 q_3 q_3, \dots & \text{'tri-mers'} \\ \dots & \end{cases} \quad (14)$$

$m_{\mathbf{q},s}$ denotes the motif $m_{\mathbf{q}}$ extracted from the s^{th} sequence Q_s . N_s^+ and N_s^- are the total number of sequences in the positive and negative classes. ξ function is defined in Eq. 7.

Similarly, the two scores $Score^+(m_{\mathbf{q}})$ and $Score^-(m_{\mathbf{q}})$ of a k -mer $m_{\mathbf{q}}$, extracted from a sequence Q , are defined as follows:

$$Score^+(m_{\mathbf{q}}) = \frac{\sum_{n=1}^N m_{\mathbf{q}}(n) PWM_{\mathbf{q}}^+(n)}{\sum_{n=1}^N PWM_{\mathbf{q}}^+(n)} \quad (15)$$

and

$$Score^-(m_{\mathbf{q}}) = \frac{\sum_{n=1}^N (1 - m_{\mathbf{q}}(n)) PWM_{\mathbf{q}}^-(n)}{\sum_{n=1}^N PWM_{\mathbf{q}}^-(n)} \quad (16)$$

where $\mathbf{q} \in \Omega_1 \cup \Omega_2 \cup \dots \cup \Omega_k$ as defined in Eq. 14, where $\mathbf{k}$ is the order of the extracted k -mers in the QuPWM features.

D. Classification models

The input MEG raw data after the pre-processing step has 1734 spiky samples and 1734 healthy samples from different MEG test sessions of eight healthy and eight epileptic patients. The quantified samples are used to generate QuPWM features and then fed to different classification models: K-Nearest Neighbors, Support Vector Machine (SVM), Decision Tree (DT), Random Forest (RF), Multi-layer Perceptron (MLP) and Naive Bayes (NB). The 5-folds cross-validation (CV) process is used, where the data is randomly split into five folds. Each time, four folds are used for training and the remaining fold for testing. The CV performance is measured by average accuracy, sensitivity, and specificity of all five folds. The operation is repeated 10 times in order to study the robustness of the classification model. Finally, the best model which achieves the highest average accuracy is reported.

III. RESULTS

For epileptic patient treatment, the patient needs to take the MEG test to ensure that the abnormal brain activities

Fig. 7: Experiment 2 framework using frequency domain projection.

are absent. Up to now, the visual assessment is the "only" way to assess the MEG signals. Indeed, there is no efficient computer-based aid to analyze MEG signals. Therefore, there is a need for developing machine learning-based algorithms to assist clinicians in quickly and efficiently detecting and predicting abnormalities in MEG signals. In this paper, we will show the utility of the proposed feature generation method for biomedical signal classification. Therefore, the QuPWM features will be used for two different classification experiments. The details of each classification experiments and the obtained results are described in the coming sections III-A and III-B, respectively.

A. Experiments 1 : Spike classification for healthy VS epileptic patients

For this classification, the positive samples are extracted from the spiky region in eight epileptic patients, and the negative samples are from eight healthy patients using MEG signals. This classification investigates the ability of the QuPWM method to learn from normal brain activity in healthy patients to predict inter-ictal spike.

The framework of this experiment is illustrated in Fig. 2. The epileptic spike prediction performance of this classification is shown in Table IV.

TABLE IV: Feature-size reduction comparison of the of proposed PWM features

Method	Parameters	Classifier	Feature size	Accuracy	Sensitivity	Specificity
Raw data	—	—	2400	60.06	78.27	41.84
PWM	M=8, r=0.18	SVM	2	92.10	91.10	93.10
mPWM	M=10, r=0.15 k = 2	SVM	220	98.23	98.07	98.39

B. Experiments 2 : Spike classification for epileptic patients

For this classification, the positive samples are extracted from spiky regions, while the negative samples are from the non-spiky regions of nine different epileptic patients using

MEG signals. This classification is much harder than the previous one, and it challenges the QuPWM ability to distinguish between spiky and non-spiky regions in epileptic patients. The QuPWM feature from the time domain does not achieve good performance because the extracted spiky and non-spiky samples are quite similar in the time domain, as shown in Fig. 8.

Fig. 8: MEG splitting and dataset preparation for the classification experiments 2.

Therefore, the frequency domain is used through a Short-Time Fourier Transform of the MEG signals before applying the QuPWM feature extraction method, as shown in Fig. 7. By doing so, the QuPWM starts extracting frequency-related scores describing the discriminative patterns in the MEG signals spectrum.

C. Subject-independent classification

For epileptic spikes detection, it is important to build subject-independent models that can provide higher specificity

TABLE V: Comparison of the proposed methods with existing methods reported recently in [11]

Method	#Subjects	Feature	Accuracy	Sensitivity	Specificity
ICA [9]	4	Independent Components Analysis	-	86.91	81.19
CSP-LDA [10]	20	Common Spatial Patterns and Linear Discriminant Analysis	-	86.14	90.38
AT-DTW [11]	30	Amplitude Thresholding and Dynamic Time Warping	-	92.45	95.81
QuPWM-SVM	9	di- mers motif-based Position Weight Matrix SVM classifier	92.48	87.20	97.76

and sensitivity for any number of subjects. In order to study the effect of the number of subjects on the detection performance, we studied the combination of randomly combined subjects using an SVM classifier and different frame-lengths $L = \{80, 90, 95, 100, 110\}$. The QuPWM-based features show a constant performance for most of the combinations using the optimal frame-size 95 sample-points, as shown in Table VI. This is because the QuPWM-based features extract the common patterns within the dataset regardless of its size. However, for very big size data, this remark might not hold.

D. Comparison with existing methods

Several detection methods have been proposed for spikes detection using MEG signals. The proposed features generation method is compared to the reported performance of some recent works [11]. Table V shows that the proposed feature generation methodology improves the classification sensitivity and specificity. However, it is worth to be mentioned that the proposed method only works for a balanced dataset due to the limitation of the feature extraction method while the other reported methods were applied to unbalanced datasets.

IV. DISCUSSION

A. Comparison of the PWM-based features

Each of the utilized QuPWM approaches captures a different property of the spikes characteristic. In order to study how these features perform and compare their performances, the different PWM approaches have been tested on the same dataset, using the same classifier, which is the SVM. The obtained results are shown in Tables IV and VII. The results show that the performance of the PWM method can be improved significantly using the mPWM feature. However, the mPWM method needs a larger memory and longer time. This limitation can be addressed using parallelization programming and feature selection to select the most important motif to extract.

B. Choice of the frame length L

As explained in Section II-A, the training and testing data are extracted from the MEG records using a sliding window or frame of size L . The choice of the frame-size is motivated

by the statistical properties of the spikes time-duration for the different eight subjects. Most of the spikes last almost $95ms$, as shown in Fig. 9. Therefore, the frame should be long enough to capture the common characteristics of the different spikes. In order to study how sensitive are the proposed feature generation methods, we performed a sensitivity analysis to study the effect of the frame-length on the classification. The obtained average performance in 5-folds cross-validation using logistic regression classifier with a set of frame-lengths $L = \{80, 90, 95, 100, 110\}$ is presented in Table VII. It shows that a frame-length 95 sample-points= $95ms$ gives better prediction accuracy. Therefore, the optimal frame-length should be around the mean spike duration for all subjects.

Fig. 9: The statistical properties of the epileptic spikes duration for eight epileptic subjects.

C. The effect of classifier type on the performance

In order to study the impact of the classifier on the obtained results, several classifiers were used for spike classification. Specifically, we applied several classifiers: SVM, DT, NB, KNN, and LR. Table VIII shows that the SVM classifier achieves better results using the radial basis function kernel or RBF kernel.

D. Further validation using EEG classification

In order to investigate the usefulness of the proposed method, the QuPMW method is applied to Epileptic Seizure

TABLE VI: . The 5-Folds cross-validation performance for different subjects using LR classifier (mPWM: $M = 6, r = 0.33, k = 1$).

Subject ID	Feature size	Accuracy	Sensitivity	Specificity	Precision	Gmean	F1score	AUC
<i>E001</i>	12	92.18	88.24	96.12	95.79	92.09	91.86	0.96
<i>E002</i>	12	92.10	88.25	95.94	95.60	92.02	91.78	0.96
<i>E003</i>	12	92.10	88.18	96.02	95.68	92.01	91.77	0.96
<i>E004</i>	12	92.08	88.20	95.95	95.61	91.99	91.76	0.96
<i>E005</i>	12	92.10	88.15	96.05	95.72	92.01	91.77	0.96
<i>E006</i>	12	92.04	88.20	95.87	95.52	91.96	91.72	0.96
<i>E007</i>	12	92.15	88.27	96.03	95.70	92.07	91.83	0.96
<i>E008</i>	12	92.11	88.33	95.89	95.55	92.03	91.80	0.96
<i>E009</i>	12	92.22	88.37	96.06	95.73	92.14	91.90	0.96

<i>All subjects</i>	12	92.10	88.40	96.17	95.68	92.09	91.60	0.96
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TABLE VII: The effect of fame length L on 5-Folds cross-validation performance.

#Subjects	Size	L	Step	Method	Parameters	Feature size	Accuracy	Sensitivity	Specificity
9	21800	80	8	PWM	M=5, k=0.25	2	86.39	77.67	95.12
	23142	90					87.53	79.08	95.99
	23754	95					87.49	78.88	96.11
	24270	100					87.19	77.85	96.52
	25122	110					87.07	78.24	95.89
	21800	80	8	mPWM	M=5, r=0.25, k=1	12	90.78	86.29	95.27
	23754	95					92.18	88.24	96.12
	23142	90					91.69	87.82	95.57
	24270	100					91.53	87.36	95.71
	25122	110					91.98	87.95	96.01

prediction using the EEG benchmark Epileptic Seizure Recognition dataset of UCI¹. This dataset contains EEG signals of length 23.6 seconds from 500 different individuals. Then, these EEG signals are framed using sliding windows of length 1 second to reconstruct $23 \times 500 = 11500$ frames of data (row), each frame contains 178 sampling-points for 1 second(column), the last column represents the label $y = \{1, 2, 3, 4, 5\}$ [25].

For epileptic seizure binary classification, Class 0 represent subjects falling in classes 2, 3, 4, and 5. The positive class is represented by all subjects falling in class 1. As the dataset will be unbalanced, we randomly selected a balanced dataset and applied 5-folds cross-validation. The obtained results attain a good prediction of up to 96%. The operation is repeated 10 times in order to study the robustness of the classification model. The average performance of the 10 experiments is

¹url: <https://archive.ics.uci.edu/ml/datasets/Epileptic+Seizure+Recognition>

TABLE VIII: Classification performance using different classifiers [$L = 95$, $step = 8$, $M = 6$, $r = 0.33$].

Classifier	KNN	Linear SVM	RBF SVM	Decision Tree	Random Forest	MLP	NB
Parameters	$K=5$	$kernel="linear"$ $C=0.025$	$kernel="rbf"$ $gamma=2$ $C=1$	$max_depth=5$	$max_depth=5$ $n_estimators=10$ $max_features=1$	$alpha=1$	defaults
Accuracy	92.32	79.10	92.48	85.30	84.03	80.78	69.42
Sensitivity	95.93	91.01	97.76	91.98	91.06	87.14	68.19
Specificity	88.70	67.20	87.20	78.62	77.01	74.42	70.64
Precision	95.62	88.21	97.50	90.75	89.60	85.57	69.07
Recall	88.70	67.20	87.20	78.62	77.01	74.42	70.64
F1-score	92.03	76.27	92.06	84.25	82.81	79.47	69.81
ROC-AUC	0.92	0.79	0.92	0.85	0.84	0.81	0.69

TABLE IX: The 5-Folds cross-validation classification using QuPWM with time and frequency domain for EEG classification from the UCI dataset.

QuPWM	Domain	Parameters	Feature Size	Accuracy	Sensitivity	Specificity
PMW	Time	$M=8, r=1$	2	94.38	92.05	96.72
	Frequency	$M=6, r=0.6$	2	95.71	94.97	96.44
mPWM	Time	$M=10, r=0.6, k=1$	20	94.78	93.58	95.98
	Frequency	$M=6, r=0.6, k=1$	16	96.16	95.55	96.76

reported in table IX.

E. The main limitations of the QuPWM features

The above results show that the proposed QuPWM method is able to extract valuable features and significantly reduce the feature size. However, this method has the following limitations which will be handled in future works:

- QuPWM is more suitable for balanced dataset classification. In the case of highly unbalanced datasets, the samples used to build the PWM matrices should be carefully chosen. For instance, clustering techniques such as k-mean may be used to overcome this challenge.
- In case of a big dataset ($> 10^4$ samples and $> 10^3$ samples-points), the PWM matrices will be bigger and more sparse, which needs more memory and high-speed processors. Therefore, compressing sensing techniques or Principle Component Analysis (PCA) can be used to compress the matrices while keeping similar performance.

V. CONCLUSIONS

We developed a feature extraction method, called QuPWM, for epileptic spikes classification in MEG and EEG signals. This method is based on combining the position weight matrix (PWM) method with digital quantization. The method shows great potential in improving the spike classification accuracy, specifically when using the frequency domain through a Short-Time Fourier Transform of raw input signals. The method is validated using three different classification experiments using MEG and EEG signals. For instance, the QuPWM feature could achieve up to 88% in sensitivity and 97% in specificity for a dataset consisting of nine epileptic patients using the MEG signal. Besides, it achieves up to 95% in sensitivity and 96% in specificity using the EEG dataset. In the future, we are clustering the input sequences to build PWM-specific feature for each cluster of similar subjects, to build a hybrid detection model which might improve the accuracy, especially for outliers samples.

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