Analysis of Multi Codebook GLVQ versus Standard GLVQ in Discriminating Sleep Stages

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***Abstract*—Sleep is an essential phase in human circadian rhythm with importance in restoring human vigour and vitality. Conventional sleep examination is done using Polysomnography with many sensors connected to various parts of human body. Recently, research in sleep is geared toward alternative feasibility of using only ECG signal. In this research, sleep stages classification using only features derived from single-lead ECG is conducted. The capability of Generalized Learning Vector Quantization (GLVQ) in discriminating sleep stages is tested. We showed that GLVQ which is configured with multi codebooks shows promising result in discriminating complex sleep stages data.**

I. Introduction

Sleep is an important phase in human daily life where human body gets restoration and renewal, both physically and mentally. The people who deprived of sleep often associated with a number of both physical and emotional disturbances. Sleep deprivation may become hazardous as it is the cause of accidents in transportation and factory plant [1]. One of the way to measure the human sleep quality is through sleep stages analysis. American Academy of Sleep Medicine (AASM) had published the manual for diagnosing sleep stages and their significance in sleep quality [2]. According to this standard, there are five classes of sleep stages consisting of Wake, NREM 1, NREM 2, NREM 3, and REM. Main differences with the previously defined standard after Rechtschaffen and Kales in 1968 are the inclusion of body movement in either wake or sleep stages plus categorizing stage 3 and 4 in R&K as NREM 3 or slow wave stage [3].

The common method to examine sleep stages is through Polysomnography (PSG) device. PSG is multi-parameter test designed to monitor multiple signals that are related to human body such as heart, brain, and muscle. There are Electrocardiography (ECG) which measures human electric activity, Electroencephalography (EEG) which measures brain activity, Electromyography (EMG) which measures muscles movement, and Electrooculography (EOG) which measures eye movement [3].

The measurement with PSG must be done on sleep laboratory with dedicated personnel to attend the patient via overnight observation. The cost for examination is also rather high. This difficult and costly procedure, combined with the scarcity of the facility, lead the many scientists to investigate an alternative way to evaluate the sleep stages and various sleeps disorders [4], [5], [6], [7], [8], [9].

Heart rate variability for the past decades has been extensively researched for measuring sleep stages to certain extent. Chazal et al. has managed to distinguish normal patient and apnea patient remarkably well with 100% accuracy using extracted Heart Rate Variability (HRV) features [4]. Penzel et al. used Detrended Fluctuation Analysis and Spectral Analysis for analysing sleep and sleep apnea [10]. Shinar et al. studied LF/HF ratio of HRV to discriminate Slow-Wave-Sleep with the rest of sleep stages [5]. Yilmaz et al. used SVM with HRV features and achieved 76.9% accuracy [6]. Another experiment using SVM in measuring multi class sleep stages is done by Bsoul et al. [7]. Another research which looking for additional features other than HRV is also performed by Adnane et al who proposed windowed detrended fluctuation analysis (WDFA) [8].

ECG signals from which HRV are calculated need to be annotated by specialist or it need to be applied with accurate QRS detector before the features can be derived. Noviyanto et al. proposed the usage of raw ECG features which is not dependent on QRS annotator to estimate sleep stages [9]. The usage of respiratory features are also actively investigated. Redmond et al. used Ribcage Respiratory Effort features from EEG channel C4-A1 aside from HRV features to boost sleep stages detection accuracy [11]. Karlen et al. also used direct respiratory signals to classify wake versus sleep [12]. Indirect respiratory effort features such as ECG Derived Respiratory (EDR) was also computed to boost the detection accuracy [4], [7], [8], [11]. Looking at the result, the usage of alternate method to gauge sleep shows promising result for sleep disorder detection [4], [10]. However, ECG based features are only partially successful in distinguishing certain class subsets of sleep stages like in two classes mode [7], [5], [8] or three classes mode [11].

Learning vector quantization (LVQ) as introduced by Kohonen has simple learning mechanism [13], yet robust to be applied in various areas [14], [15]. Generalized learning vector quantization (GLVQ) is an improvement over original LVQ which handles the problem of the sensitivity of original weight initialization [16]. Its several variants are also successfully tested against different kind of data [17], [18]. Setiawan et al. introduced fuzzy-neuro generalized learning vector quantization (FNGLVQ) as one of the latest GLVQ variants [19]. It has been applied to classify different types of arrhythmia heart beat with good performance. FNGLVQ was designed with single prototype in mind. In highly complex data the performance may degrade.

In this paper, we analyse the performance of GLVQ with single codebook for each class and GLVQ with multiple codebooks which we dubbed as Many Prototype GLVQ (MPGLVQ) by applying them to sleep data. The high degree of data inseparability forced single codebook GLVQ to reach low performance. In contrary, GLVQ with many codebooks increase the accuracy value. The result of the experiment will be used to extend FNGLVQ with many prototypes.

The organization for the rest of this paper is described as follows. Section II explains the dataset and features used in this experiment. The classifier is briefly explained in section III. In section IV, the experiment and its results are presented. Lastly, section V discusses the conclusion of this paper.

II. Dataset and Feature Extraction

MIT-BIH Polysomnographic Database (slpdb) is freely available on Physionet site [20]. This dataset consists of 18 sleep records which come from 16 male subjects, aged 32 to 56 (mean age 43), with weights ranging from 89 to 152 kg (mean weight 119 kg) for total recording of 85 hours. Each record contains 4 different channels including ECG, EEG, blood pressure, and respiratory data. The record may be divided into three category as normal sleepers, mixed normal and insomniac sleepers, and heavy insomniac [8]. Furthermore, each record may have duration as short as 1:17 hours and maximum 6 hours with variance of 3:06 hours.

It is also important to see how well the classifier performed against healthy patients. Past researches had attempted in manually collecting sleep stages recording from various patient with different kind of sleep disorder condition as done by Chazal et al. [4], Yilmaz et al. [6], and Redmond et al. [11]. However, not once the records comes from healthy patient. This encourages us to collaborate with Mitra Kemayoran Hospital, Jakarta to collect sleep records of 10 subjects consist of 7 male, aged from 23 - 40. Each of them was recorded for 9 hours of sleep duration, and in total 21 physiologic channel is monitored including ECG, EEG, and EMG. Sleep stages is annotated per 30 seconds (one epoch) following AASM recommendation [2]. These two datasets are used in our experiment.

There are three different features set for sleep stages. The first feature set is based from Heart Rate Variability (HRV) calculated from RR interval, the second is variability of ECG Derived Respiratory (EDR) features, and the third is features that are calculated directly from raw ECG signal. Before HRV is computed, we need to calculate the length of every adjacent R peaks. In order to do that, we need to know the position of R peak in the ECG signal. MIT-BIH data had already annotation for R peak done by doctors, whereas for MITRA data we need to run ecgpuwave of WFDB tools to annotate the R peak automatically [20]. This program is based from improved version of Pan and Tompkins algorithm with wave form limiting factor [21], [22]. From 10 records of Mitra database, three records are excluded because QRS detector is considered as failed in detecting the correct QRS annotation. The other two records, while recorded from healthy patient, had the ECG signal recording that hardly resemble healthy heart waves. Hence, only five records were used for the experiment.

From the list of RR interval of one epoch of 30 seconds, we can calculate the Heart Rate Variability (HRV) features. The HRV features can be differentiated as time domain features and frequency features. The time domain features are,

- NN/RR, the ratio between numbers of normal RR interval (NN) with the actual number of RR interval.
- AVNN, the average of all NN interval within one epoch.
- SDNN, standard deviation of all NN interval within one epoch.
- RMSSD, square root of the mean of the squares of differences between adjacent NN interval.
- PNN, percentage of differences between adjacent NN intervals that are greater than 50 ms.

The frequency domain features are,

- TOTPWR, total spectral power of all NN intervals up to 0.04 Hz
- ULF, total spectral power of all NN intervals up to 0.003 Hz
- VLF, total spectral power of all NN intervals between 0.003 and 0.04 Hz
- LF, total spectral power of all NN intervals between 0.04 and 0.15 Hz
- HF, total spectral power of all NN intervals between 0.15 and 0.4 Hz
- LF/HF, ratio of low to high frequency power

We also incorporate the result of Yilmaz et al. [6] who used additional features from HRV features which are,

- Median, the median of RR interval.
- IQR (Inter Quartile Range), the difference between 75^{th} and 25^{th} percentiles of the RR interval value distribution.
- MAD (Mean Absolute Deviation), the mean of absolute values obtained by the subtraction of the

mean RR interval values from all the RR interval values in an epoch.

Fig. 1 shows example diagram of ECG signal. It shows the important segment of ECG which labelled as QRS complex and distance between two QRS Complex (or its R peak) as RR interval.

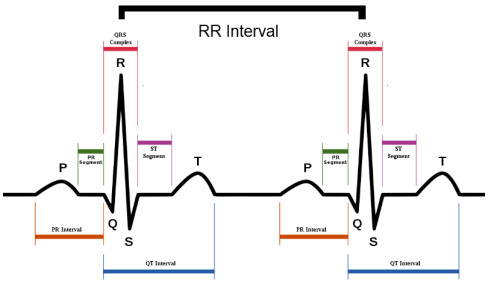

Fig. 1. The illustration of QRS complex

For the HRV features of EDR, we adopted research from Chazal et al. [4]. During the breathing phase, as the lung is filled and emptied with air, the body-ECG is influenced by electrode motion relative to the heart and by changes in thoracic electrical impedance. We filtered the ECG signal twice with median filter of 200-ms and 600-ms to produce the baseline of the ECG signal. The original ECG signal is then subtracted with the resulted signal to produce baseline-corrected ECG signal. Then we calculated the area under each QRS complex up to 100 ms before and after the R peak to generate EDR signal. After that we can extract the same HRV features from this signal as explained above.

For the third set of features, we calculated directly the raw signal with features that had been proposed in another research [23] [24]. The list is as follows.

- Energy, $\sum_i x_i^2$
- 4^{th} Power, $\sum_i x_i^2$
- Curve Length, $\sum_i ||x_i - x_{i-1}||$
- Non linear Energy, $\sum_i -x_i * x_{i-2} + x_{i-1}^2$
- Peak Power, $max(PSD)$
- Peak Frequency, $index(max(PSD))$
- Mean PSD, $mean(PSD)$
- Median PSD, $median(PSD)$
- Spectral Entropy, $\sum_i PSD_j * logPSD_j$
- Katz Fractal Dimension, $\frac{logN}{logN+log\frac{max(\sqrt{(x_i-x_0)^2+i^2})}{\sum_i \sqrt{(x_i-x_{i+1})^2+1}}}$
- Detrended Fluctuation Analysis, the slope of the line relating log of root-mean-square fluctuation to log N
- Higuchi Fractal Dimension, based on Higuchi algorithm
- Hjorth Mobility, $\sqrt{\frac{\sum_i \frac{x_i - x_{i-1}}{N}}{\sum_i \frac{x_i}{N}}}$
- Hjorth Complexity, $\sqrt{\frac{\sum_i \frac{(x_i - 2x_{i-1} + x_{i-2})^2}{N}}{\sum_i \frac{x_i - x_{i-1}}{N}}}$
- Petrosian Fractal Dimension, $\frac{logN}{logN+log(\frac{N}{N+0.4N_\sigma})}$

III. Generalized Learning Vector Quantization

A. Learning Methodology

To ensure the reference vectors or codebooks to continue to approximate the class distributions, GLVQ is using a new learning method different than LVQ based on minimizing the cost function. Let x be the input vector with class C. Let w_1 be the nearest reference vector that belongs to the same class of x ($C_1 = C$), and likewise let w_2 be the nearest reference vector that belongs to a different class from x ($C_2 \neq C$). Let us consider the relative distance difference $\mu(x)$ defined as follows:

$$\mu(x) = \frac{d_1 - d_2}{d_1 + d_2}, \tag{1}$$

where d_1 and d_2 are the distance of x from w_1 and w_2, respectively. $\mu(x)$ ranges between -1 and +1, and if $\mu(x)$ is negative, x is classified correctly; otherwise, x is classified incorrectly. In order to improve error rates, $\mu(x)$ should decrease for all input vectors. Thus, a criterion for learning is formulated as the minimizing of a cost function S defined by

$$S = \sum_{i=1}^{N} f(\mu(x_i)), \tag{2}$$

where N is the number of input vectors for training, and $f(\mu)$ is a monotonically increasing function. To minimize S, w_1 and w_2 are updated based on the steepest descent method with a small positive constant α as follows:

$$w_1 \leftarrow w_1 - \alpha \frac{\partial S}{\partial w_1}, i = 1, 2 \tag{3}$$

If squared Euclid distance, $d_i = |x - w_i|^2$, is used, we can obtain the following.

$$\frac{\partial S}{\partial w_1} = \frac{\partial S}{\partial \mu}\frac{\partial \mu}{\partial d_1}\frac{\partial d_1}{\partial w_1} = -\frac{\partial f}{\partial \mu}\frac{4d_2}{(d_1+d_2)^2}(x - w_1) \tag{4}$$

$$\frac{\partial S}{\partial w_2} = \frac{\partial S}{\partial \mu}\frac{\partial \mu}{\partial d_2}\frac{\partial d_2}{\partial w_2} = -\frac{\partial f}{\partial \mu}\frac{4d_1}{(d_1+d_2)^2}(x - w_2) \tag{5}$$

Therefore, the GLVQ's learning rule can be described as follows:

$$w_1 \leftarrow w_1 + \alpha\frac{\partial f}{\partial \mu}\frac{d_2}{(d_1+d_2)^2}(x - w_1) \tag{6}$$

$$w_2 \leftarrow w_2 + \alpha\frac{\partial f}{\partial \mu}\frac{d_1}{(d_1+d_2)^2}(x - w_2) \tag{7}$$

B. Multi Codebook GLVQ

LVQ is designed with multi codebook. As GLVQ is derived from LVQ, it is supposed to be capable to works with many prototype. However, the effectiveness of GLVQ when worked in multi codebook for sleep stages data remain to be seen. Surprisingly, Ghosh et al. in their research pointed out that original LVQ shows best performance in terms of stability, asymptotic generalization ability, and robustness of initializations. The comparison included comparison with minimizing cost function based LVQ [15]. GLVQ with single codebook per class may not be adequate for data which has diverse and separate distribution as shown in Fig. 2.

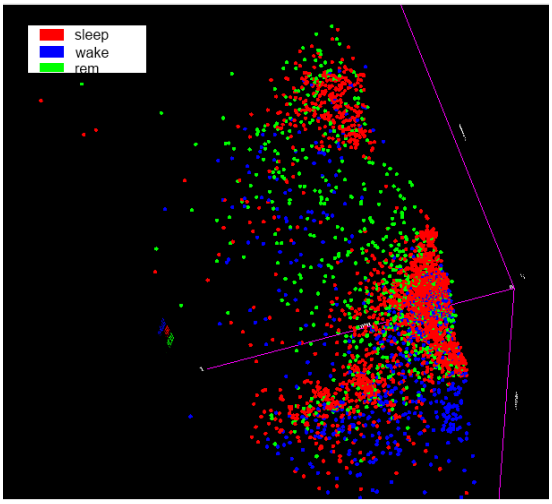

Fig. 2. Sleep class distribution from rMSSD, SDNN, and AVNN features

Therefore, we used MPGLVQ instead of only standard GLVQ to handle this kind of data. Another characteristic of sleep stages data is the imbalanced distribution between each class. This situation is even worse for some data patient that only has 2 or 3 instances from 1 class. One way we used to alleviate this situation is by combining data from all patient. This lessen the problem but still leave the imbalanced distribution for overall data. Fig. 3 and Fig. 4 show the proportion of the MIT and Mitra dataset, respectively. With that consideration in mind, the number of codebooks is designed to be proportional with the number of data in each class.

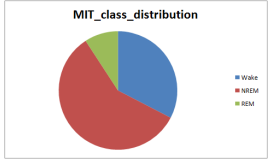

Fig. 3. MIT class proportion

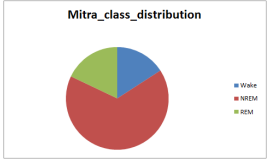

Fig. 4. Mitra class proportion

IV. Experiment and Result

We used all the features we extracted on the previous steps. For experimenting, we customize open source tools Weka Data Mining Software [25] to implement our pre-processing filter and the developed classifier. In this experiment, we experimented with 3 class of sleep stages data namely Wake, Sleep (NREM), and REM from MIT and Mitra database. Full dataset record from merging all individual records is created to see the generalization capability of the classifier aside from subject dependent test. The accuracy is calculated using five fold cross validations method. Kappa statistic is also calculated to prove the robustness of the algorithm in measuring the correctness per class.

A. Full Record Test

In this scenario, the classifier is performed against full record set of MIT and Mitra database. The classifier is benchmarked to run at specific epoch (30) while the learning rate and codebooks number are changed throughout the experiment to find the best possible combination. The resulting classifier performance is shown in Fig. 5 for MIT data and Fig. 6 for Mitra data. Both figure show constant improvement of the classifier performance after the number of codebooks are increased. Incorporating small learning rate, typically below 0.1, also give best performance with relatively short training time at 30 epoch.

The performance comparison of MIT data in Fig. 5 with Mitra data in Fig. 6 indicates MPGLVQ work best for Mitra data which consisted only of healthy patients. This holds true based on general accuracy performance and kappa value. As comparison, the standard GLVQ with single codebook performance is capped with 45% accuracy and kappa value of 0.05 for MIT data.

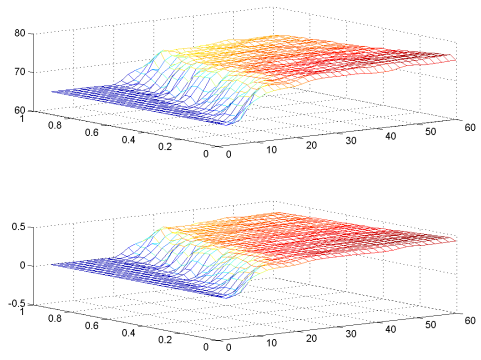

Fig. 5. Top and bottom image shows the accuracy and kappa statistic for mit data

B. Record Specific Test

In the second experiment, the classifier is tested against each data record. The result for MIT data with classifier accuracy and kappa value is shown in Fig. 7 and Fig. 8, respectively. The x axis is the number of codebooks while the y axis is the accuracy value. In terms of accuracy, 11 out of 18 records have steady performance gain until the codebooks are increased to

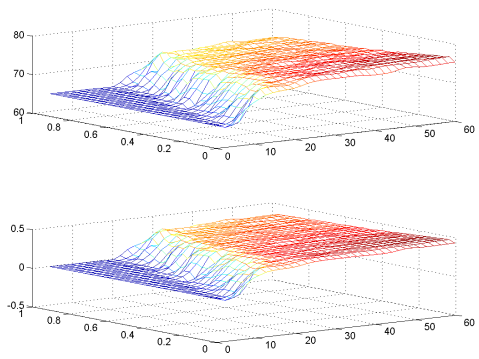

Fig. 6. Top and bottom image shows the accuracy and kappa statistic for mitra data

192. Length of record in MIT data is varied by much. For 6 hours of recording, there are ± 700 instances. Henceforth, for short record, appropriate codebooks should be at most $\frac{1}{10}$ of maximum instances and around 7 time of class number. This holds true for complex data such as sleep records.

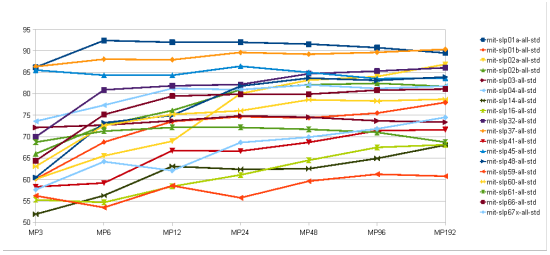

Fig. 7. The classifier accuracy for MIT record specific test.

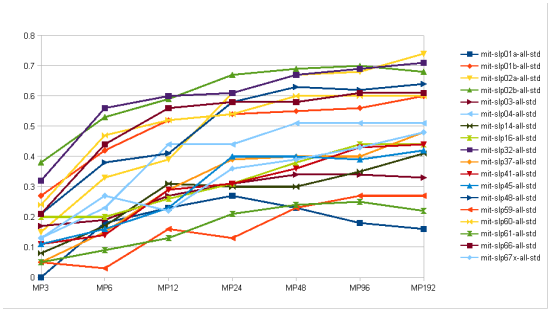

Fig. 8. The classifier kappa for MIT record specific test

The experiment result on Mitra data as shown in Fig. 9 and Fig. 10 showed that more codebooks made the classifier performs better, both in accuracy (5 - 10%) and kappa statistic (0.2 - 0.4). The x axis indicates the number of codebooks while the y axis indicates the kappa statistic value.

C. Visualization of Multi Codebooks Placement

In order to understand the impact of many codebooks in enhancing appropriately classified data, its important for us to visualize codebooks placement as

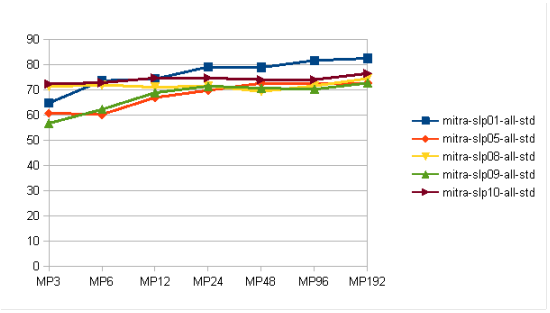

Fig. 9. The classifier accuracy for Mitra record specific data

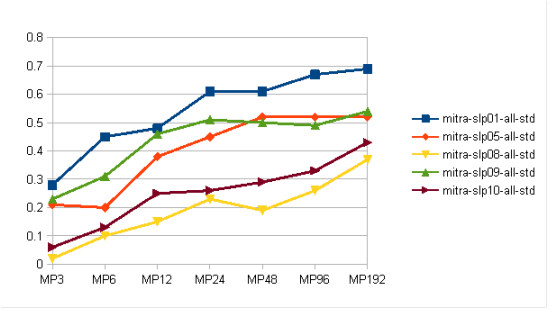

Fig. 10. The classifier kappa for Mitra record specific data

model between data and class target. The visualization for single codebooks is shown in Fig. 11 and multi codebooks is shown in Fig. 12. From the Fig. 11, NREM data vector is separated into three local cluster. Hence, after training is finished, the codebook is placed in the appropriate position for modelling class NREM where its placed in heavily populated NREM vectors. This made minor clusters being ignored at all.

By placing many codebooks, relationship between NREM data with its class target can be more appropriately modelled. As can be seen in Fig. 12, four codebooks for representing NREM stages create better model for representing the class hence no minor clusters was ignored impacting better classification performance.

V. Conclusions

The usage of multi codebooks GLVQ is analysed where it shows promising result in discriminating sleep stages data, better than GLVQ with single codebook. It leads us to conclude that the sleep stages data is diverse and scattered which makes a single codebook to be insufficient to cover the whole distribution of data. To further improve the accuracy of sleep stage detection, we plan to apply this method to FNGLVQ which proposed by Setiawan et al. [26] in later research.

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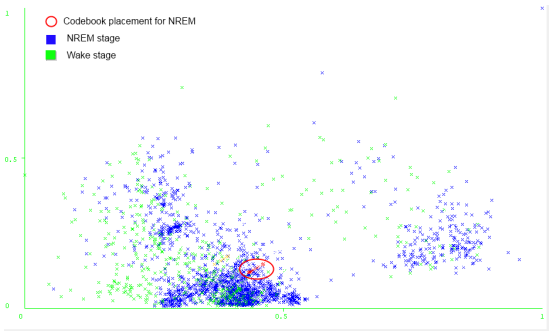

Fig. 11. Single codebooks model for NREM stage

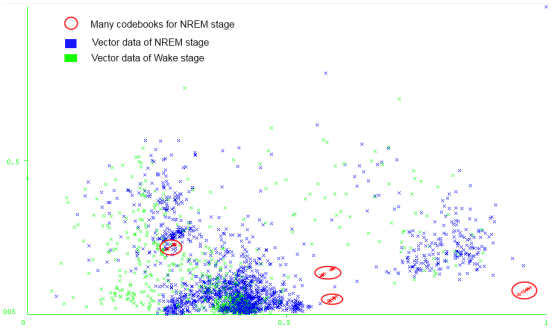

Fig. 12. Many codebooks model for NREM stage

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