Gentle Waking System

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Abstract— In this project, we aims at finding relevant feature representations for sleep stage classification which would extract Wake and N1 sleep stages given that the research shows people waking up more refreshingly in these stages. Therefore, we propose a SVM classification model combining with evolutionary algorithms for feature selection. There are three algorithms adopted and compared in our project: Genetic Algorithm (GA), Evolutionary Strategy (ES) and Covariance Matrix Adaptation Evolutionary Strategy (CMAES). The experimental results suggest that even though the best accuracy 90.52% we obtained of three algorithms are the same, CMAES converges fast because of its adaptation which follows a natural gradient approximation of the expected fitness.

Keywords—sleep stage; classification; Genetic Algorithm; Evolutionary Strategy; Covariance Matrix Adaptation Evolutionary Strategy;

I. PROJECT DESCRIPTION AND BACKGROUND

Sleeping conditions affect people's daily lives in different ways. Performance at work, mood or social relationships are few obvious ones, however in medical field, sleep analysis is of great significance in the identification of problems related to sleep, which leads to various psycho-physiological analysis. In the analysis of sleep issues, the very basic problem is the identification of sleep stages. With the help of polysomnographic recording (PSG) during sleep, we can collect data about sleep conditions.

According to R&K rules, each epoch (30-second data) is classified as awake (W); non-rapid eye movement (N-REM stage 1, N-REM stage 2, N-REM stage 3 and N-REM stage 4: from light to deep sleep); and REM.

These days sleep issues have become public concerns. Traditional services offered by sleep technicians are not so convenient and may become strained due to increasing demands. Motivated by these situations, we come up with an idea to automatically distinguish sleep patterns. By distinguishing the sleep stages into 2 categories: one is wake and N1 stages, when people could be waked up without much negative feelings, the other is N2, N3 and REM stages, when people are less willing to be waked, we could create gentle alarm

system to wake people up at proper time, making them feel refreshed and healthy.

Among the physiological signals, the electroencephalogram (EEG) signals are the most frequently used and the most representative way to indicating the sleep problems since they best represent the brain's activity. Our project data is based on the EEG signals. EEG waves (alpha, beta, delta and theta) show different characteristics during different sleep stages, and have highly complicated transformation patterns. These signals are not periodic and their amplitude, phase and frequencies constantly change. Therefore, extended periods are required for the measurements in order to obtain meaningful data.

According to the researches, various models have been raised up for the classification of sleep stages. For these models, the features used by the classification algorithms are of high significant to the accuracy of the model.

This project aims at deciding the best features that are dominant for classifications of sleep stages. By applying evolutionary algorithms to the classification situation, we come up with selected features to help achieve high accuracy for classification.

II. OPTIMIZATION APPLICATION

Our application is a model inference problem. It mainly consists of three stages: feature extraction, feature selection from EEG signals, and classification of these signals which is shown in Figure.1. Each EEG input data of one person is eight hours long and is divided into thirty seconds as an unit which is also called an epoch. Also, an epoch is named with a sleep stage. Then, preprocessing is applied to filter out some noises.

In the feature extraction stage, 37 feature parameters in four different categories are used in our application. Since EEG feature pool is quite large and feature selection is important in the elimination of irrelevant and redundant features, we adopted evolutionary algorithm here. Furthermore, in this manner prediction accuracy may be improved and computational overhead in classification is reduced. In the feature selection stage, three evolutionary algorithms are developed: Genetic

Algorithm(GA), Evolutionary Strategy(ES) and Covariance Matrix Adaptation Evolutionary Strategy(CMAES). Therefore, our optimization object is feature selection. The results, obtained from different evolutionary algorithms are provided so that a comparison can be made between computation times and accuracy rates.

After selecting a set of features which best represent EEG signals, they are used as input parameters for the classification algorithms. We apply Support Vector Machine (SVM) as our classifiers.

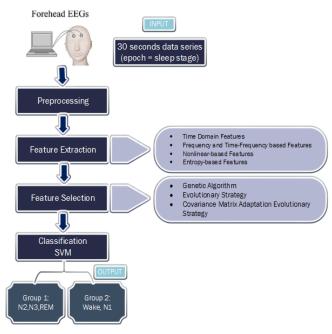


Figure 1. Application flow

III. FEATURE EXTRACTION

A total of 37 feature parameters are used; 10 in the time category, 10 in the frequency based category, 2 in the non-linear category and 1 in the entropy category.[1]

A. Time domain features:

Time domain features are mainly statistical attributes of EEG signals. Mean, Max, Min, STD, and Variance are basic straightforward attributes. Short explanation of the others are provided below.

- Zero-Crossing: it is a point where the sign of a
 mathematical function changes (e.g. from positive to
 negative). It is a commonly used term in electronics,
 mathematics, sound, and image processing. According to
 the researches, we use the number of zero-crossings as a
 feature related to brain activities.
- Skewness: it is a measure of symmetry, or more precisely, the lack of symmetry. A distribution, or a dataset, is symmetric if it looks the same to the left and right of the center point.

 Kurthosis: a measure of whether the data are peaked or flat relative to a normal distribution. Data sets with high kurtosis tend to have a distinct peak near the mean, decline rather rapidly, and have heavy tails.

• Hjorth parameters:

These parameters of mobility and complexity are simple measures of signal complexity based on the second moment of the signal and its first and second difference

Activity (HA)	Mobility (HM)	Complexity (HC)
$HA = \sigma_0^2$	$HM = \sigma_1/\sigma_0$	$HC = \sqrt{(\sigma_2/\sigma_1)}^2 - (\sigma_1/\sigma_0)^2$

 $\sigma 0$ = the variance of the signal

 $\sigma 1$ = the variance of the first derivative of the signal

 σ^2 = the variance of the second derivative of the signal

B. Nonlinear based features

• Hurst index:

The Hurst parameter H is a measure of the extent of longrange dependence in a time series. H takes on values from 0 to 1. The closer H is to 1, the greater the degree of persistence or long-range dependence. Hurst index is defined as:

$$H = \log(R/S)/\log(T) \tag{1}$$

T = the time of the data sample

R/S = the value of the range which was rescaled

Petrosian Fractal Dimension(PFD):

Fractal dimension is a chaotic method calculating the complexity of a signal. The parameter is obtained the following expression:

$$PFD = \log_{10} k / (\log_{10} k + \log_{10} (k / (k + 0.4N_{\delta})))$$
 (2)

k = the number of signal's samples

N = the number of sign changes in the signal derivative

C. Entropy based features

Spectral Entropy:

It is a feature that allows the identification of the degree of regularity in the complex signals. The entropy of the data with regular probability distribution will be higher. On the same line, the entropy of the data with irregular probability distribution will be low. It is calculated by using the probability values of the power spectrum of the signal. It is defined as:

$$H_{sp} = -\sum_{a=f_a}^{f_b} P_i log\left(\frac{1}{P_a}\right) \tag{3}$$

P = the power density over a defined frequency band

fa = the lower frequency

fb = the upper frequency

D. Frequency and time-frequency based features

• Frequency Band-power Ratio:

Frequency Band-power Ratio is a common used feature for describing sleep EEG. Based on different frequency band, EEG can be divided into five classes: delta (0.5~3Hz), theat (3~8Hz), alpha (8~12Hz), sigma(12~16Hz), beta(16~30Hz). We accumulate the power value within specific frequency band and then divide the total value of whole frequency band. This is so-called frequency band-power ratio. Figure 2 is an example to demonstrate how to acquire delta band-power ratio.

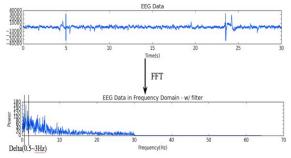


Figure 2. Example of Delta-band-power Ratio

(ex: Delta Ratio = Area Delta Band / Area of Whole Frequency Band)

• Discrete Wavelet Transform (D3, D4, D5, A5):

For time-frequency domain, we utilize Discrete Wavelet Transform to extract features from original time series of EEG. The methodology can be illustrated as Figure 3 shown. It can decompose EEG signal into different time series with specific frequency band. In sleep EEG research, we only concentrate on the signal below 30 Hz. Thus, in this project, we only choose D3, D4, D5 and A5 into our feature pool that is roughly corresponding to delta, theta, alpha, sigma and beta frequency band.

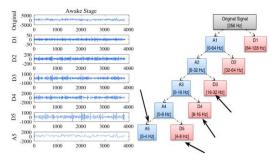


Figure 3. (left) Decomposition by Discrete Wavelet Transform (right) Down sampling tree of Discrete Wavelet Transform

IV. EVOLUTIONARY ALGORITHMS FOR FEATURE SELECTION

The general idea of the 3 evolutionary algorithms are alike. Every individual indicates a kind of feature combination. The features are used in the SVM to classify the sleep stage for each epoch and calculate the classification accuracy. The fitness of the individual is evaluated by the accuracy, and the best features are produced after generations of evolution. The fitness function is described as follows:

$$Fitness = CorrectPredictions/TotalPredictions \times 100\%$$
(4)

And the elements of the three algorithms are described in the following charts:

TABLE I. GENETIC ALGORITHM

Type of EA	Genetic Algorithm
Representation	Binary Representation (37-bit string, each 0/1 denotes whether that feature is used)
Crossover	One-point Crossover with probability being 0.7
Mutation	Bitwise mutation at random point with probability being 0.04
Parent selection	Roulette Wheel Algorithm
Survivor selection	All children replace parents
Termination condition	500 generations

TABLE II. EVOLUTIONARY STRATEGY

Type of EA	Evolutionary Strategy	
Representation	Integer-valued vectors (each feature has corresponding specific number)	
Crossover	Discrete recombination for each object variable Global recombination for each step size	
Mutation	Gaussian permutation	
Parent selection	Uniform random	
Survivor selection	$(\lambda + \mu)$ based on ranked fitness value	
Termination condition	500 generations	

TABLE III. CMA-ES

Type of EA	Covariance Matrix Adaptation Evolutionary Strategy
Representation	Real value as the weights of each feature
Recombination	Intermediate (weighted) recombination to update the mean vector
Mutation	Summation of the mean vector and the Normal distribution which sigma is a covariance matrix.
Parent selection	(μ, λ) ranked based selection
Survivor selection	None
Termination condition	500 generations

V. EXPERIMENTAL RESULT

A. Setup

As for the dataset, it is from Kong-Ning Hospital in Taiwan. There are five people sleep data who don't have any sleep disorder symptoms. Each of them is eight hours long. The sampling rate is 200 Hertz. The ages of them ranges from 25 to 30.

All our codes is written in Python. Because our application has high computation complexity, we chose Amazon EC2 m3.large instances for our experimental environment. In SVM parameter settings, the kernel type is radial basis function (exp (-gamma*|u-v|^2)) and the shrinking heuristic is used to facilitate the process. The number of the training data is 2000 ephoes and the number of the testing data is 1200 ephoes. There are three open source code adopted in our experiment. [2][3][4]

B. Result

1) The Best Fitness Value of Each Generation or Function Evaluation:

The red point in Table IV below indicates the point that they reach the best fitness. The result shows that the ES reaches the best fitness faster than other two. The possible reason is because in ES, the number of features selected is fixed to 10, whereas the number of features is flexible in GA and CMAES. From the result in the CMAES, we found that the average number of selected features is around 6~10.

Therefore, in ES, it first shrinks its search space and the best result lies in that space so that it can reach optimum fast.

2) The Best Fitness in Each Run:

Table V demonstrates the maximum, average and standard deviation of each algorithms throughout the multiple runs. In Figure 4, it shows that with the different seed number the best result of each run in three algorithms.

TABLE V. BEST , AVERAGE AND STD IN 10 RUNS

TIEDED	BEDT , Eluioi	515 11. 101	CIID
	GA	ES	CMAES
Best(%)	90.52	90.86	90.52
Average (%)	90.49	90.78	90.47
Standard deviation	0.04	0.1	0.08

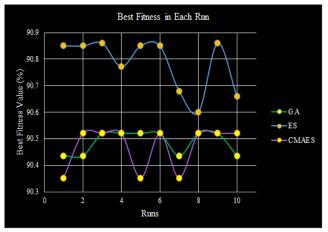
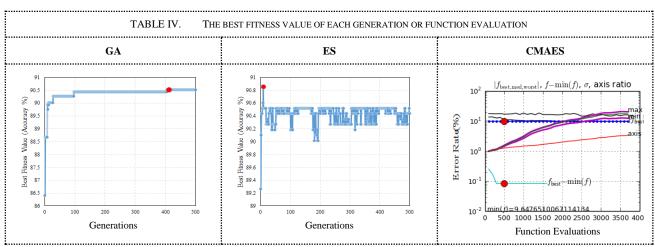
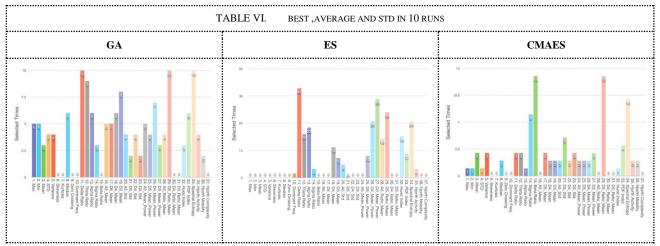


Figure 4. Best fitness in each run

3) The Distribution of the Selected Features of each Algorithms:

From the table VI, with the intersection of three results, the most dominant features are relevant to the category of frequency and time-frequency based features. Overall, Delta Ratio, Beta Ratio, D4 Ratio Mean and Spectral Entropy are representative features for our application. Besides, the range of features selected in ES obviously is smaller than GA and CMAES because it chose 10 out of the feature pool which is a fixed number in each generation.





4) Times of Reaching the Best Result in Each Run:

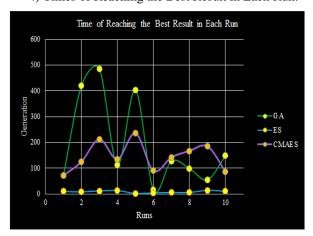


Figure 5. Times of reaching the best result in each run

VI. DISCUSSION AND CONCLUSION

Within the field of sleep stage classification research, the most important and difficult part is to determine which feature is effective for distinguishing sleep stage. Because not all the features are suitable for classifying and some of them will induce computation redundancy. Therefore, in this project, we have implemented three type of evolutionary algorithms to optimize our feature pool: genetic algorithm, evolutionary strategy and covariance matrix adaptation evolutionary strategy for dominant feature selection. According to our results, generated SVM classifier by these three algorithm all can achieve over 90.52% classification accuracy for distinguishing our two stage groups. However, they perform very different in some aspects with the same seed number and the comparison of these three algorithms' result is summarized as the Table VII.

First of all, we have to assume that all environmental settings are the same except for "Individual Length." For Genetic Algorithm and CMA-ES, their individual length is variable for each generation. That is to say, best feature combination can be only one feature or up to 37 feature combinations. Conversely, for Evolutionary Strategy, due to the limitation of the

methodology we choose, we select a fixed number to be its individual length. Therefore, the initial input format of these algorithms in this project is different. Likewise, the final output of feature combinations are totally different as well.

Secondly, based on above assumption, the search space of CMA-ES and GA is bigger than ES. Thus, it is reasonable that they would spend more time (generations) to reach the best fitness value than ES. However, even though CMA-ES has bigger search space, it still has the best performance at run time part. We infer that the function of step-size control of CMA-ES can facilitate fast convergence and computation based on evolution path which make CMA-ES not be trapped into local optimal value.

Lastly, according to the Table VII shown, GA is relatively slow to reach best fitness. We conclude that GA has more parameters that are required to modify than CMA-ES and ES. Thus, it may not yield to good result if the parameters are not best fitted. Tuning GA parameters for this application is also one of the feasible research direction in the future.

TABLE VII. COMPARISON OF THREE ALGORITHMS

	Genetic Algorithm	Evolutionary Strategy	CMA-ES
Best Fitness Value	90.52%	90.86%	90.52%
Run Time (min)	180 min	180 min	30 min
Time to Reach Best Fitness Value	485 generations	10 generations	70 generations
Selected Feature Combination	1, 3, 11, 12, 13, 17, 18, 24, 26, 29, 33, 34	11, 13, 18, 26, 27, 28, 29,32, 34	33, 13, 28, 32, 14, 7
Seed Number	1234	1234	1234
Termination Condition	500	500	500
Population Size	30	30	30
ndividual Length for each Generation	Variable	Fixed (Length = 10)	Variable

VII. FUTURE WORK

In this project, we propose the following attempts to improve our results and make them more reasonable. Simultaneously, we also demonstrate the future research direction and the difficult part of this topic.

1.) Search more feature into our original feature pool

In this project, only 37 features have been chosen to be our original feature data set. However, there are still a lot of other features we can use in this field, such as Hilbert-Huang Transform [8] based or Multi-Scale Entropy [9] based features. Diversify the original feature pool would have chance to enhance classification accuracy.

2.) Collect more data to test and validate our model

Our final result only use 4 people all-night EEG data for training and testing. We should add extra dataset to test the robustness of our model. This will help our research be more convincing.

3.) Accelerate the evolutionary algorithms

At this time the evolution speed may not be quick enough. In order to improve this problem to better suit for larger database, we should find ways for each algorithms to accelerate the selecting process.

4.) Apply this program into real-time system

The original goal of this project is to wake people up at specific sleep stage. Currently we have completed the part of sleep stage classification. Next step we should apply our algorithm into alarm-clock-like system to implement real-time stage classifying and then wake people up.

 Collect data in other age level to establish sleep stage classification model

The dataset of this project is limited age in range $25 \sim 30$. That is to say, the model we generated might be more useful and

suitable in young people than others. For example, the EEG data between elderly and young people might be slightly different. The effective features are thus might be not the same for these two groups.

REFERENCES

- [1] Sen, B., et al., A Comparative Study on Classification of Sleep Stage Based on EEG Signals Using Feature Selection and Classification Algorithms. *Journal of medical systems* 38(3):1–21, 2014.
- 2] Feature Extraction (pyEEG): http://code.google.com/p/pyeeg/
- [3] CMAES: https://www.lri.fr/~hansen/cmaes_inmatlab.html
- [4] libsvm: http://www.csie.ntu.edu.tw/~cjlin/libsvm/
- [5] B. Y. Kim and K. S. Park. Automatic sleep stage scoring systems using genetic algorithms and neural network. In J. D. Enderle, editor, Proceedings of the 2000 Annual International Conference of the IEEE Engineering in Medicine and Biological Society, volume 2, pages 849– 850, Chigaco, IL, USA, 23.-28.July 2000. IEEE, Piscataway, NJ. * www/IEEE ga00aBYKim
- [6] Corralejo R, Hornero R, Alvarez D (2011) Feature selection using a genetic algorithm in a motor imagery-based Brain Computer Interface. In: Proceedings of the 2011 annual international conference of the IEEE engineering in medicine and biology society, EMBC, Boston, MA, pp 7703–7706. doi:10.1109/IEMBS.2011.6091898
- [7] S. Gudmundsson, T. P. Runarsson, S. Sigurdsson. Automatic Sleep Staging using Support Vector Machines with Posterior Probability Estimates. Proceedings of the 2005 International Conference on Computational Intelligence for Modelling, Control and Automation, and International Conference Intelligent Agents, Web Technologies and Internet Commerce IEEE computer society.
- [8] Fan Yingle, Li Gu, Tong Qinye, Sleep stage classification based on EEG Hilbert-Huang transform, Industrial Electronics and Applications, 2009. ICIEA 2009. 4th IEEE Conference on, pp 3676 - 3681.
- [9] Madalena Costa, Ary L. Goldberger, C.-K. Peng, Multiscale entropy analysis of biological signals, physics review, 2005