

Bacterial Memetic Algorithm based Feature Selection for Surface EMG based Hand Motion Recognition in Long-term Use

Dalin Zhou*, Yinfeng Fang*, János Botzheim[†], Naoyuki Kubota[†] and Honghai Liu*

*Intelligent Systems & Biomedical Robotics Group, School of Computing
University of Portsmouth
Portsmouth PO1 3HE, UK

Email: dalin.zhou@port.ac.uk, yinfeng.fang@port.ac.uk, honghai.liu@port.ac.uk

[†]Graduate School of System Design
Tokyo Metropolitan University

6-6 Asahigaoka, Hino, Tokyo, 191-0065, Japan
Email: botzheim@tmu.ac.jp, kubota@tmu.ac.jp

Abstract—Pattern recognition algorithms have been applied in the surface electromyography (sEMG) based hand motion recognition for their promising accuracy. Research on proposing new features, improving classifiers and their combinations has been extensively conducted in the past decade. Meanwhile, the feature projection methodology, has been routinely exploited between the phases of feature extraction and classification. Meanwhile, limited publications have been seen addressing the feature selection, which is a vital alternative in dimensionality reduction for pattern recognition. Recent development of sEMG acquisition devices have contributed to more signal capturing sites or even detection arrays of high density in the application. In this paper, the memetic evolutionary method named bacterial memetic algorithm (BMA) has been adopted as the feature selection strategy for sEMG based hand motion recognition. A case study of 4 subjects in long-term use has been conducted to demonstrate the feasibility of the proposed strategy, that comparable recognition accuracy with reduced computation cost has been achieved. A further discussion on the feature redundancy and inter-subject use has also been demonstrated based on the experimental results derived from BMA based feature selection.

Index Terms—Electromyography, Hand Motion, Pattern Recognition, Feature Selection, Bacterial Memetic Algorithm

I. INTRODUCTION

The human-machine interfaces (HMIs) of prosthetic hand control have been extensively researched in the past few decades. For prosthesis users, intuitiveness, higher success rate, low latency and less adaptation cost are the prior concerns to be fulfilled [1]. In details, the premise of an ideal control is crafted by the accurate recognition of users' intention, the imperceptible delay between the execution of mechanical extremity and the employment of users' residual limb, and the consistent feasibility for long-term use. Among various feasible approaches, surface electromyography (sEMG) based pattern recognition for prosthetic hand control has been widely investigated for its most promising performance to meet the mentioned criteria [2]. The aim of such methodology is

to distinguish users' intention of hand movement through classifying the sEMG signals exerted from forearm muscle contractions. Let alone the emphasis on preprocessing of captured physiological signals [3] or the post-processing of decision stream generated by the classifier [4], increasing high accuracy and improved feasibility have been frequently published and witnessed within the framework of pattern recognition in academia [5].

Among all the progress, most of intensive research and improvement are reported in typical pattern recognition strategies regarding the combination of new feature descriptions and evolved classifiers. Similar to other pattern recognition based problems, the application in sEMG based hand motion recognition is highly dependent on the feature extraction phase and would be essentially improved when appropriate feature representations are adopted [6]. Recent studies have also urged the interests towards the clinical scenario, especially the robust usability [7], to which a selected group of distinguishable and repeatable features might be a potentially elementary solution for the purpose of long-term use. However, despite the elaborate comparisons among features extracted in different domains like time (TD), frequency (FD) and time-frequency (TFD) [8], limited publications have addressed the issue on feature selection.

Oskoei et al. [9] considered the feature subset selection instead of exploiting the ensemble for a 4-channel and a 6-channel system respectively, in which the limited number of channels has constrained the redundancy to overcome, and furthermore the research was targeting at improving the inferior classifier for repeated sessions. Much as the inspiring consideration of feature selection a decade ago, it is now more essential to be combined with recently developed sEMG acquisition device design, which has contributed to more equipped channels in application. Thus intuitively, more physiological information could be captured by the system with an increased number of available channels. Despite the informative patterns

brought in by extra signal sources, the extraction of more features could be time-consuming, and a redundant pooled feature set sometimes degrades the recognition performance with imported outliers. Retrieving the most discriminating feature subset while keeping the computation complexity and the loss of information balanced has become an emerging topic. Phinyomark et al. [10] evaluated a group of candidate features captured by 5 electrodes and stated the superfluity and redundancy of TD features. In spite of the constructive discussion, the selection part was neither focusing on the capturing system with multiple detection sites nor long-term use targeted. Thus a further investigation on the selection and utilization of optimal feature subset for desired scenarios still remains an open topic.

In order to exploit the most of feature selection, proper methodology is required to cope with the natural complexity of the sEMG patterns. The weighted sum of electrical quantity of motor units (MUs) forms the captured EMG signal, which is influenced by various biological factors like the size of MUs with their corresponding patterns of employment, activation and firing rate, and muscle fibers' type, size and state within it [11]. Because of either revealed or unknown physiological contributions, nonlinearity and multimodality are brought to sEMG related problems, which is also the case for feature selection in sEMG based hand motion recognition. Nature inspired evolutionary optimization algorithms are suitable for such searching problems with proven global optimization capabilities. This paper underlies the feature selection problem in sEMG based hand motion recognition for long-term use utilizing the evolutionary technique of bacterial memetic algorithm (BMA). A case study of 4 subjects has been conducted to demonstrate the effectiveness of the incorporated strategy.

The remaining of the paper is organized as follows. Section II presents the details of the BMA. Section III describes the applied scenario of hand motion recognition with testing settings. Section IV presents the experimental results with corresponding discussion and finally Section V concludes the paper.

II. BACTERIAL MEMETIC ALGORITHM

The BMA is a memetic evolutionary technique inspired by the nature of microbial evolution[12]. This heuristic algorithm combines the evolutionary method and the local search strategy to make the best of both concepts. It has been applied to solve various multimodal problems like path planning and flow shop scheduling problem [13]. An early study on the adopted bacterial evolutionary algorithm has been applied in the feature selection on the fitting problem, in exclusion of the memetic approach [14]. However conventional evolutionary algorithms, in most cases, suffer from the low convergence rate. To alleviate this situation, the memetic algorithm (MA) [15] is adopted to apply local search procedure within each evolutionary cycle. Bacterial mutation, gene transfer and the application dependent local search routinely constitute the main operators of the BMA process. After initialization, the operators function iteratively in searching of the global

optimum. In feature selection of sEMG based hand motion recognition, the goal is to find the optimal or at least quasi-optimal combination of different features from each individual channel.

A. Encoding and Evaluation

The optimization problem is essentially encoded in the evolutionary form of candidate solutions. And every candidate solution is represented by a bacterium (chromosome) to be optimized. In the initialization operation, a total of N_{ind} individual bacteria are created as the whole population to be processed in the following stages. The chromosome length of each bacterium is first randomly initialized within a predefined interval and filled with a trial of non-negative integers. In our case of feature selection, each integer in the chromosome represents the index of an individual from the pooled sEMG features of all channels. Features denoted by chromosomes will be retrieved for the performance evaluation (routinely named with the terminology *fitness function*) in each evolutionary memetic cycle. The chromosome with the best evaluation result in the last cycle is exported as the optimal feature set. In our feature selection problem, the recognition accuracy obtained from the retrieved features and the predefined classifiers stands for the fitness.

Inspired by previously mentioned publications, in our application the chromosome length is variable and modified with fixed probability P_{bm} in each bacterial mutation and gene transfer operation to explore a broader search space. Referring to the prior knowledge of the scenario, the size of a constrained search space is controlled by lower and upper boundaries of chromosome length.

$$S = \sum_{i=n_L}^{n_U} \binom{N}{i} \quad (1)$$

where N is the total number of candidate features, and n_U and n_L represent the upper boundary and lower boundary of the chromosome length.

An alternative constraint is to combine the penalty function (regularizer) on the chromosome length in the evaluation. To constraint the complexity of the model, the regularized fitness function is adopted [16]. The evaluation is closely related to the application and will be explained in details in Section III.

$$\sigma_{\epsilon_i} = \frac{1}{N} \sum_{(x,t) \in T} \delta[f(x) - t] + \lambda \frac{l_b}{n_U} \quad (2)$$

$$\delta(x) = \begin{cases} 1, & x = 0 \\ 0, & x \neq 0 \end{cases}$$

where σ_{ϵ_i} is the fitness of i-th bacterium ϵ_i , N is the size of testing data, $f(x)$ is the classification function which outputs the category, (x, t) is the sample from the testing domain T , l_b is the chromosome length, n_U is the upper boundary of chromosome length, λ is the regularization parameter and $\delta(x)$ is the Kronecker delta function.

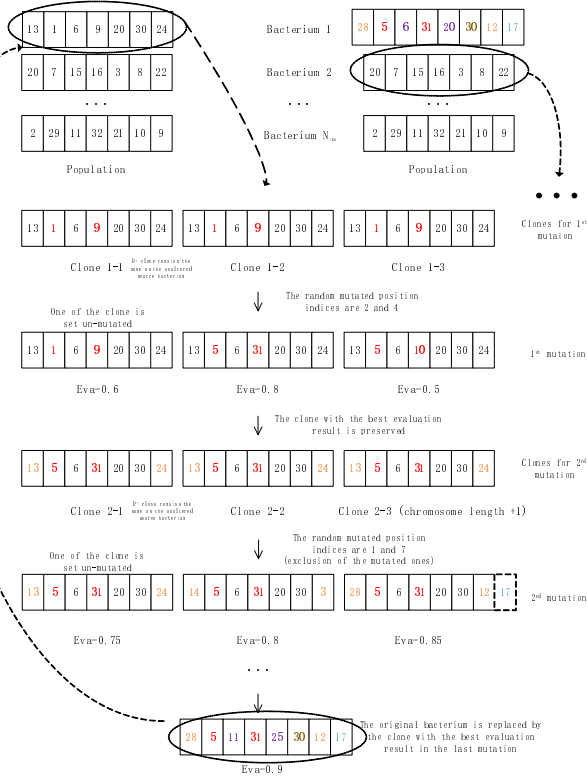


Fig. 1. Mutation in BMA

B. Bacterial Mutation

BMA searches for the global optimum through mutation in the chromosome, which imports new information in a randomly selected space. Similar to other evolutionary algorithms, individuals from the population are mutated, evaluated and replaced (preserved).

The mutation operation is performed for all N_{ind} chromosomes one by one in each cycle. The mutation starts with the duplication of the objective chromosome for N_{Clone} times. Then a random length of l_{bm} is generated to indicate the segments to be mutated in the chromosome. Despite the mutation in the clones, the 1-st clone remains the same as the unaltered source chromosome in this stage. The evaluation operation is conducted on each chromosome and the source one is replaced by the one with the best result whereas the inferior ones are waived. In our application, the mutation epoch of one bacterium is set as adaptive to its length to guarantee that all the segments are mutated at least and only once in every generation. During the mutation process, the length of each chromosome varies by l_{cl} or remains unchanged according to the predefined probability P_{bm} . The mutation operation and length modification is illustrated in Fig. 1, where $N_{Clone} = 3$, $l_{bm} = 2$, $l_{cl} = 1$, Eva is the fitness function of accuracy and a larger Eva is preferred in the selection.

C. Local Search

After the mutation, the local search operators will randomly function on the individuals from mutated population

with a probability of P_{ls} . A predefined local search space is explored to find the best neighboring solution of one or grouped segments. Memetic algorithms incorporate the local search operation to accelerate the whole searching process. The chance of local search needs to be carefully designed to balance the acceleration of the convergence and the avoidance of the local optimum.

In our case, the prior knowledge is the physiological factors influencing the exerted sEMG signals and the anatomical deformation of the forearm muscles for certain hand gestures. For each feature in the searching space, its index possess two properties of sEMG acquisition site and the extraction strategy. Naturally the local space is defined with either fixed channel or fixed extraction domain. Depending on the design of signal acquisition system, which is either muscle targeted or muscle untargeted, two different views can be generalized in the local search protocol. For a fixed channel in untargeted sEMG capturing system, only features extracted from the same signal source can be viewed as the candidates. It is intuitively understandable that certain hand gestures only involve the contraction of certain muscles, and it is more reasonable to compare the acquired information for the same motion intention. While the muscle untargeted detection normally cover an overlapped area with muscle synergies, a muscle targeted way only gathers the sEMG signals from certain muscles with negligible influence by others. In this situation, the candidate group of channels will be enlarged by those who are responsible for the same motions. For a fixed domain only the features computed in the same domain like FD or others are included for the selection because of their own characteristics to facilitate different physiological conditions. As indicated in previous research, spectral features are good indicators for muscle fatigue and the entropy based indices perform robustly under circumstances where small contraction and noise are included [8]. In the end of each local search, the chromosome is replaced by the alternative with the best evaluation performance in its defined neighborhood.

D. Gene Transfer

Mutation and local search are followed by the operation of gene transfer, which allows the segment flow between two bacteria. The goal of the mutation and local search is to explore the unknown searching space and bring in new beneficial information while gene transfer aims to preserve the incorporated features instead of introducing new features through passing them to multiple bacteria within the population.

First the population is divided into two sorted halves, a superior set and an inferior set, according to the evaluation results. Then one bacterium is randomly picked from both superior and inferior halves as the transfer candidates. A group of segments with predefined length of l_{gt} from the source bacterium are assigned to pointwise matches in the destination bacterium. This process mimics the *infections* of the bacteria and will be repeated for N_{inf} times in each generation. During the gene transfer, the chromosome length is

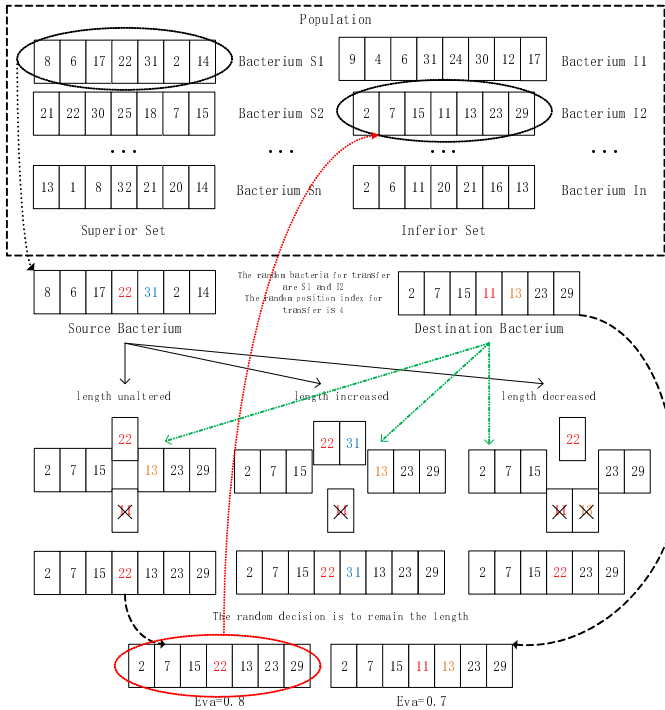


Fig. 2. Transfer in BMA

also modified with the fixed probability, however in a different way from the mutation operation. The difference between the two modifications lies on the concept that gene transfer only preserves the existing information without incorporating unseen features. To preserve the improvement of the destination bacterium, the updated population will be divided again according to another evaluation after each transfer. The gene transfer process including the length modifications is shown in Fig. 2, where $l_{gt} = 1$, $l_{cl} = 1$ and the chromosome length randomly remains the same.

III. FEATURE SELECTION IN SEMG BASED HAND MOTION RECOGNITION

A. Hand Motion Recognition

A typical process of sEMG based hand motion recognition is illustrated in Fig. 3. The sEMG signals are first acquired by electrodes covering the forearm muscles. After the preprocessing of raw input, segmentation is conducted over the signal stream to provide either separate or overlapped windows for further process. Features are then extracted from the data and dimensionally reduced by principal component analysis (PCA), later fed to the classifier to generate the decision streams of the consecutive windows. Consequently the hand motions are executed by prosthetic devices based on the recognition results. In this research, we focused on the phase between feature extraction and classification. Despite the feasibility of PCA in the dimensionality reduction, it still requires the calculation of all named features to exploit the most of the information. However, with the increase in the number of detection sites, the computation cost would heavily

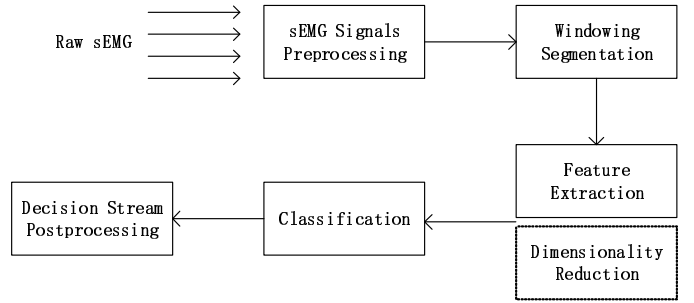


Fig. 3. sEMG based hand motion recognition flowchart

hinder the real-time performance in clinical use. An alternative is to use the feature selection strategy instead of the feature projection, which could be done in offline environment. The best trade-off is to achieve a comparable recognition accuracy with reduced computation complexity to a certain extent.

B. Testing Scenarios

The sEMG signal acquisition system proposed in [17] was utilized in this research. The specification of the system includes 16 bi-polar sEMG sites embedded in the sleeve, with the gain of 3000 and the ADC resolution of 12 bits. The sEMG signals are captured with the sampling frequency of 1kHz and common mode noises removed first, then Butterworth band-pass filtered between 10Hz and 500Hz, and filtered by the notch filter to remove the power line noises.

Four healthy subjects were employed in the experiment to carry out the capturing paradigm in 7 days out of consecutive 14 days comprising multiple trials for day of trial. A total of nine motions (hand at rest, hand open, hand close, index finger point, fine pinch, wrist flexion, wrist extension, supination, pronation) were identified in the recognition problem. During the capturing stage, the subjects were instructed to repeat a random displayed sequence of motions as shown in Fig. 4. Each of the motion was conducted and lasted 10 seconds in a steady contraction. The everyday donning/doffing, which leads to electrode shift, is considered not only in inter-day trials but also the intra-day trials. To preliminarily consider the influence of muscle fatigue, one of the subjects was instructed to exhaust his strength between consequent session without donning and doffing of the sleeve.

In the experiments we exclude the transient phase between two motions and only evaluate the feature selection of stationary signals during hand motion conduction. The overlapped windowing strategy was adopted to segment the sEMG signal stream with a window length of 250ms and an increment of 50ms. The most prevalent Hudgins' TD features [18] in combination with 4-th order autoregressive (AR) coefficients were adopted as the baseline feature options, the total number of which is 128. The detailed definition of other included features can be referred to in the review paper on sEMG feature [8]. The multi-class linear discriminant analysis (LDA) was adopted as the classifier for its simplicity.



Fig. 4. From left to right, top to bottom: a. sEMG acquisition hardware including electrodes embedded sleeve and processing circuit b. 9 motions to be recognized c. display of 16 channels' sEMG samples [17]

The current research mainly focuses on the long-term use, thus the evaluation result in BMA is obtained from inter-day trials of the same subject. Here the source domain and the target domain are two disjoint set which consist of labeled sEMG signals captured on separate days. Besides the inter-day test, the test on fatigue, which is another physiological issue affecting the recognition accuracy in long-term application. To fulfill the fatigue simulation, the subject for fatigue test was informed to exhaust the strength as much as possible between each trial within the same day.

IV. EXPERIMENTS AND DISCUSSION

A. Experimental Results

The evaluation results (convergence) of the same subject with different parameter settings are depicted in Fig. 5. It can be seen that the evaluation has reached a quasi-optimal performance with around the 10 generations of evolution and searching in both settings. The number of evaluation times is 177278 and 191046 respectively. No obvious differences in convergence or accuracy are witnessed in the comparison, which indicates that the application of BMA in this specific sEMG based feature selection is not sensitive to the parameter settings.

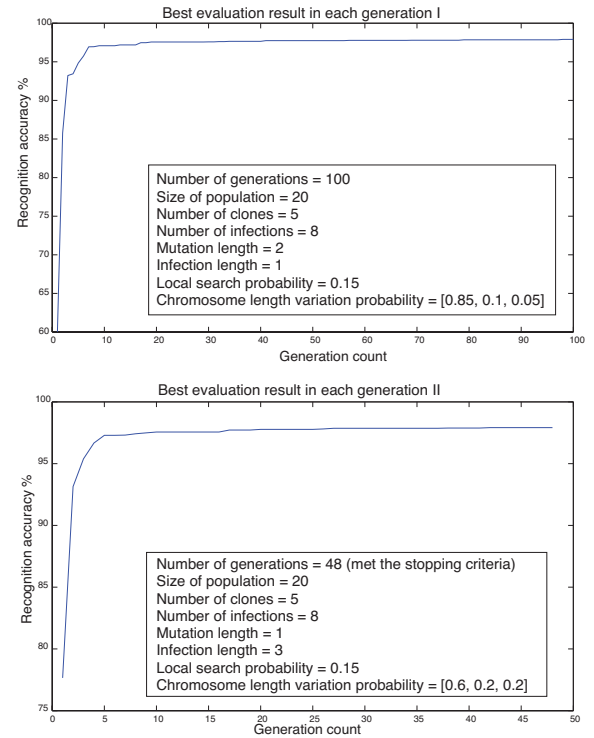


Fig. 5. Evaluation in BMA with different parameter settings

The detailed properties of all bacteria after the entire evolutionary process are illustrated in the Table I. It should be noted that the average evaluation result for all bacteria including the omitted ones is $97.0922 \pm 0.6028\%$ that almost every individual would perform comparable results to each other. It can be inferred that the redundancy or overlapping exists among the candidate features to be exploited.

A further enumeration of corresponding channels of selected features is shown in Fig. 6. Here the statistics is based on the pooled subset selection of the whole population, where each of the bacteria has reached a promising evaluation result. An approximately similar chance of involvement for all the channels is observed, which implies the feasibility in adopting all the detection sites, but with limited features from each of them for computation reduction.

The experiments for inter-day feasibility were conducted in comparison with PCA based dimensionality reduction, as shown in Fig. 7. In BMA feature selection, first two days' labeled data were utilized in the feature selection stage as the training set and evaluation set respectively. The LDA classifier was later trained by the labeled selected features extracted from the sEMG signals on the first day and adopted for pseudo (offline) inter-day application. The PCA based solution calculated the projection matrix on the first two days' data and tested for the same domain. The test on the fatigue data captured from one of our subjects was following a similar routine but in inter-trial instead of inter-day way. Between each trial, the subject was informed to exhaust the strength

TABLE I
SELECTED FEATURE SUBSET EXAMPLES

Indices of selected features	Number	Evaluation accuracy %
5 10 13 18 20 22 25 33 41 44 45 49 56 57 63 66 76 82 84 91 92 96 113 122 123	25	97.5249
3 6 10 13 18 20 25 26 37 44 53 58 59 63 71 72 83 91 92 96 110 112 122	23	97.0442
5 6 10 11 13 16 17 19 20 22 25 27 29 31 33 34 35 41 44 45 49 52 55 58 63 65 76 82 84 87 88 91 92 103 104 111 113 122 123 124 128	41	97.8989
5 6 8 11 13 15 16 17 18 19 20 22 24 26 27 29 43 44 53 56 58 76 82 84 91 92 97 101 105 119 121 123	32	97.0976
1 2 11 13 18 20 22 26 30 37 44 53 58 63 71 76 83 92 96 99 110 118 122 123 128	25	96.2785

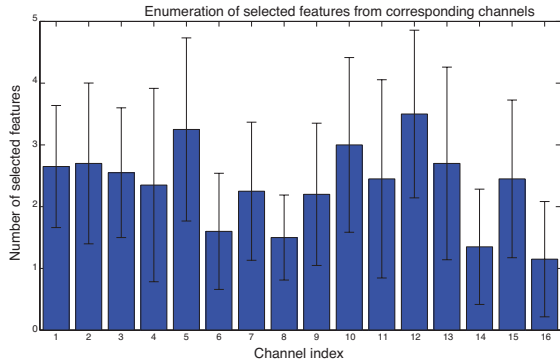


Fig. 6. Enumeration of adopted features for each individual channel

as much as possible to cause muscle fatigue, which would be another critical issue to impede the recognition accuracy in long-term use. It can be seen that the BMA based method leads to an increase of near 1% in the error rate for inter-day experiments, which is rather small when compared to the $\frac{2}{3}$ reduction at least in the number of extracted features shown in Table II, which would largely reduce the computation. A further reduction is expected because only limited 128 candidates were adopted in the experiments. However, the result already revealed the efficiency of the BMA based feature selection. When considered the fatigue test, the reduced extracted features through BMA even outperformed the whole feature set PCA based method in both computation cost and average accuracy, shown as the last error bars in Fig. 7, despite the large degradation by both methods in this scenario.

The last but not the least, the inter-subject test was preliminarily conducted to investigate the feasibility of the transfer of

TABLE II
TRADE-OFF BETWEEN FEATURE REDUCTION AND AVERAGE ACCURACY ON INTER-DAY TEST AND FATIGUE TEST

Subject No.	Number of extracted features		Average accuracy %	
	BMA	PCA	BMA	PCA
1	41	128	90.9900	92.0355
2	33	128	98.7061	98.8129
3	37	128	92.5389	93.7976
4 (fatigue)	30	128	63.8651	62.9725

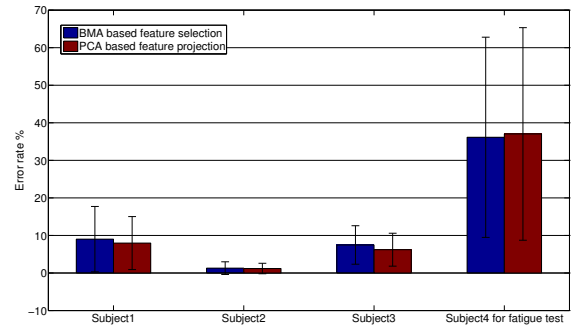


Fig. 7. Comparison of 4 subjects between BMA and PCA

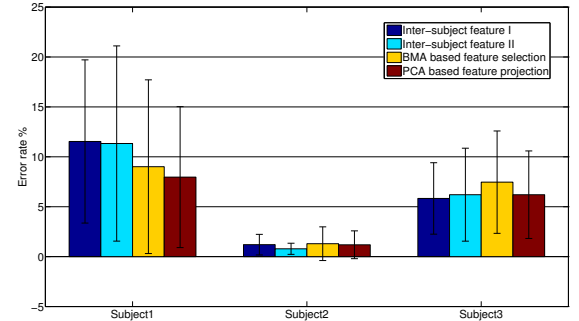


Fig. 8. Comparison of selected features for inter-subject use

feature selection between different subjects. The best subset of candidate feature from each subject was applied to the other two subjects. A comparable and even improved performance of the inter-subject feature set transfer could be seen in Fig. 8 utilizing the feature subset selected from other subjects.

B. Discussion

The development of sEMG capturing device will inevitably bring more deployed capturing electrodes, and moreover the utilization of high-density sEMG sensing array. The computation cost for feature extraction will largely increase with the scale of detection sites. In this research, we addressed the importance of feature selection and the feasibility of BMA

as the implementation method. The experimental results have demonstrated the quick convergence of BMA in our application, which would be beneficial with the inclusion of a lot more features extracted in FD or TFD. The redundancy exists in the TD features as indicated in the demonstrated selected feature sets, which is in accordance with the published result from [19]. It has been pointed out that features with maximum class separability, robustness and less computational complexity are desirable in the real-time clinical use. Regarding the evaluation results of our selected feature set, another property should be considered in the future is less redundancy.

The long-term usability is always demanded in clinical environment. In our application, the inter-day test achieved a computation reduction in the feature extraction stage while preserving a comparable performance. Specifically, the subject 2 had a superior performance over others as seen in Fig. 7, because this subject had more experience in the sEMG capturing. Besides the inter-day changes, the intra-day performance is also a critical metric for long-term use. The preliminary test result on the intra-day fatigue data has shown the plausible improvement of BMA based feature selection over PCA based feature projection. A possible explanation for the improved recognition accuracy might be the variety of severe physiological changes. Some selected features instead of the whole feature pool might be more robust to such inconsistency lead by muscle fatigue. However, because of the single subject employed, it remains to be determined whether the assumption holds when a more reasonable group of subjects are involved under a dedicated experimental protocol.

Feasible feature transfer between subjects is naturally desired to reduce the burden of extra computation. Our experimental results have shown that the selected feature subset could be shared in common between different individuals. In our experimental protocol, all the subjects were informed to place the electrodes with a rough reference, which provided the similar region of muscles for sEMG extraction. In that case, the electrode shift became less important in impeding the recognition rate when compared to muscle fatigue. It can be expected that, feature selection would function better, in combination with more standard capturing paradigm. As a promising result, the feature subsets selected from other subjects can be incorporated in the population initialization phase to obtain an extra neighborhood for the optimum or at least the quasi-optimum.

V. CONCLUSION AND FUTURE WORKS

In this paper, the BMA based feature selection in sEMG based hand motion recognition is investigated to achieve a comparable recognition accuracy with a reduced cost of feature extraction. A promising trade-off between the reduction of computation cost and the comprising in recognition rate has been seen in the experiments for long-term use. The potential of feature selection in inter-subject use is also shown at an early stage.

In our future work, we will focus on the utilization of selected feature subset to improve the recognition accuracy

in real-time scenario. Structure extraction strategies would be applied to enhance the efficiency of local search. The potential of feature selection for inter-subject use will be further investigated as well.

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