Decoding of Individuated Finger Movements Using Surface EMG and Input Optimization Applying a Genetic Algorithm

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Abstract-In this paper we present surface electromyographic (EMG) data collected from 16 channels on five unimpaired subjects and one transradial amputee performing 12 individual finger movements and a rest class. EMG were processed using a traditional Time Domain feature-set and classifiers: a Linear Discriminant Analysis (LDA) a k-Nearest Neighbors (k-NN) and Support Vector Machine (SVM). Using continuous datasets we show that it is possible to achieve an accuracy up to 80% across subjects. Thereafter possibilities to reduce the numbers of channels physically required, as well as the number of features have been investigated by means of a developed Genetic Algorithm (GA) that included a bonus system to reward eliminated features and channels. The classification was performed firstly on the full datasets and in later runs using the GA. The GA demonstrated high redundancy in the recorded 16 channel data as well as the insignificance of certain features. Although the GA optimization yielded to reduce 8 to 11 channels depending on the subject, such reduction had little to no effect on the classification accuracies.

Index Terms— Genetic Algorithm (GA), Myoelectric control, Pattern recognition, Surface electrodes, Upper limb prosthesis

I. INTRODUCTION

The efforts to create a user friendly prosthesis have mainly been limited by electromechanical means in the past. With modern multi-fingered prostheses such as the i-Limb by Touchbionics [1] and the BeBionic hand by RSLSteeper [2], this no longer is the case and the need for a dexterous controller is evident. The most technological advanced and common method employed for prostheses control is the one based on EMG signals processing; to myo-electrically control a dexterous prosthesis it is necessary to map EMG signals corresponding to different muscle contractions to the different existing degrees of freedom available, using a suitable control algorithm. Research on dexterous controllers has been focusing on pattern recognition, as this is the most promising concept in this field. In the past years several classifiers and feature-sets have been exploited. Among these studies only a few investigated the possibility of controlling independent finger movements, or hand gestures [3][4]

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C. Antfolk and F. Sebelius are with the Department of Measurement Technology and Industrial Electrical Engineering, Lund University, 22100 Lund, Sweden. [5][6][7], while most considered wrist movements such as flexion/extension, pronation/supination, abduciont/adduction and sometimes hand closure/opening (all fingers simultaneously). Due to their gross nature, these movements are more reliably detected, with respect to finger postures or specific grips, but surely less intuitive if the aim is to control finger postures or particular grasps. While the final goal of this work is to enable individual finger movements on the newly available and next generation of prostheses, in this paper we present surface EMG data collected from 16 electrodes on six subjects performing 12 individual finger movements and a rest class making up thirteen classes in total. Five able-bodied subjects and one transradial amputee volunteered in the present experiments. EMG were processed using a traditional Time Domain feature-set (as suggested by Englehart et al. [8]) and classifiers; in particular a LDA a k-NN and SVM were employed and compared. Using continuous datasets (i.e. non reorganized or manipulated recordings) we show that it is possible to achieve an excellent accuracy across the five able-bodied subjects and the amputee (up to 80%).

Since such a system should ultimately be clinically viable, the number of physical electrodes and processed features might represent a hindrance toward embedding in an actual prosthesis. In practice, more complex systems tend to be less reliable, and calculating features and computing channels is time consuming. For instance Farrell and Weir [9] showed that linear discriminant classifiers produce statistically similar accuracies to multinomial logistic regression classifiers at a much lower computational cost when using Root Mean Square, Time Domain (TD) and Auto Regression featuresets.

Hence, besides individuated finger movements, this paper investigates the effectiveness of TD features and number of channels on the classification accuracy by means of a GA. The latter was developed for optimizing the classifiers by finding good trade-offs (through a bonus function) between number of features and channels and classification performance. We show that is possible to eliminate the Slope Sign Changes (SSC) feature for all subjects besides the amputee and that for four out of the five able-bodied subjects the Zero Crossings (ZC) features can be discarded.

The outcomes of this work open up interesting insights for the development of clinically viable controllers for dexterous prostheses.

II. MATERIAL & METHODS

In this study, data from five able-bodied subjects (three men and two women, aged 25-34) and one transradial amputee were used. Surface EMG-signals were acquired using an in-house built amplification and acquisition system. The system acquired 16 channels of EMG, sampled at 1.6 kHz per channel and with a bandpassfilter between 0.5 Hz and 800 Hz with 16-bit resolution and a gain of 56 dB per channel. A custom-built LabView application was used to record and store the data.

Red Dot Ag/AgCl (3M Health Care, Germany) electrodes were used in the study. The electrodes were placed on the forearm of the participants as shown in Figure 1. In particular twelve electrodes were placed on the superficial flexor muscles on the volar side of the forearm and four electrodes were placed on the superficial extensor muscles on the dorsal side of the forearm. Electrodes were placed in order to cover as many independent muscles as possible. The optimization of the electrode localization was accomplished by minimizing the cross-talk visually. The participants were seated in front of a screen with their forearm resting on a pillow during the time of the experiment. Thirteen different movements were executed by the subjects in response to a written and pictorial cue on the screen that depicted the movement to be reproduced.



Fig. 1. Location of the 16 electrodes.

The movements consisted of flexions and extensions of all the fingers individually as well as thumb adduction/abduction and a rest class making up thirteen classes in total. These movements would account for individual control of each digit of a multi-fingered prosthesis. During the study after the cue was given the movement was to be held between 4-6 seconds until a rest cue was given. The rest state was of equal length as the movement. Two different datasets each consisting of five repetitions of each movement totaling 60 movements and the rest states were stored on the computer along with the intended class information.

A. Feature extraction and classification

Data were processed employing the Myoelectric control development toolbox [10], the LIBSVM library [11] and custom Matlab scripts. Signals were filtered using a 6th order Butterworth bandpass filter (10-500 Hz) and notchfilter



Fig. 2. Diagram showing the arrangement of the signal processing parts. The dashed section showing where the GA block is introduced, which is skipped when generating the unoptimized results.

(centered at 50 Hz). Thereafter a feature-set composed of four time metrics was computed using a window size of 250 ms with a 25 ms increment. The feature-set consisted of the time domain statistics originally proposed for transient signal classification by Hudgins et al., [12] and lately used as a benchmark by many other studies, namely, the number of Zero Crossings (ZC), the Wavelength (WL), the number of Slope Sign Changes (SSC), and the Mean Absolute Value (MAV) [13] (for a mathematical description refer to [14]).

Data was then used as input for the genetic algorithm (GA) which tried to minimize the number of used inputs, by testing multiple input combinations and their outcomes and selecting solution that is the best according to the result of the fittness function. A Principal Component Analysis (PCA) was performed to further decorrelate (in principal component space) the optimized number of features and inputs found by the GA. The new feature-sets were subsequently used as inputs for the different classifiers.

Three different traditional classifiers as those used in many other studies were tested: LDA, k-NN and the SVM classifier from the LIBSVM [11]. All of the classifiers besides the SVM are available in Matlab. The k-NN classifier used had a k of 16 and the euclidean distance was used as the distance metric. The k value used was empirically found to give the best results for this work. For all the classifiers one dataset was used to train and the other was used for evaluation. The individual processing parts and their arrangements are shown in Figure 2.

B. Genetic Algorithm optimization

A GA is an iterative algorithm frequently used in optimization and search problems that is inspired by the theory of evolution [15]. It starts out with an initial population of possible solutions to the given problem, which are called chromosomes. The algorithm performs a blind search for a solution, by varying the chromosome encoding values and by looking how such variations affect the output of a *fitness function*. The latter allows to determine how good a solution is compared to the others and hence allows to determine the best solution that is generated by the GA. From the initial population, the fittest chromosomes are selected and transferred to the new population. The other chromosomes for the new population are produced by performing crossover pairing among the chromosomes of the current population. Some of these newly created chromosomes are randomly selected to be subject to mutation where the chromosomes are manipulated at random, in order to increase the diversity

TABLE I													
BINARY ENCODED ACTIVITY VECTORS THAT WHERE ISSUED BY THE GA. UNUSED FEATURES ARE NOT LISTED													

Dataset	Features	Features Channels															N _{ch_elim}	
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	
H1	MAV/WL	1	1	1	0	0	1	0	0	0	0	0	1	1	1	0	1	8
H2	MAV/WL	0	1	1	0	0	0	0	0	0	0	0	1	0	1	1	1	10
H3	MAV/WL	0	0	0	0	0	1	0	0	0	1	1	1	1	1	1	0	9
H4	MAV/WL	1	1	0	0	0	0	0	0	1	1	0	1	1	0	0	1	9
H5	MAV/WL/ZC	0	0	0	0	0	0	0	0	0	1	0	1	1	1	1	1	10
A1	MAV/WL/SSC	1	0	0	0	1	1	0	0	0	0	1	0	0	0	0	1	11





Fig. 3. Resulting classification rates for the individual subjects using optimized features and channels, just optimized channels and all features and all the channels and features and hence no GA optimization.

of the population. In the end of each evolutionary step the whole population is evaluated once again by the fitness function. This procedure is then repeated several times in order to find the optimized solution. A detailed description of GA can be found in [15].

In the present work 20 evolutionary steps, each having a population size of 20 chromosomes were computed, allowing the evaluation of 400 possible solutions to the problem. The following rules were used.

- A binary encoding was chosen to encode the chromosomes, where a one was referring to an enabled input and zero to a disabled. Each possible solution consisted of a 20bit chromosome (16 channels and 4 features).
- 2) The misclassification rate of the LDA classifier was used as the **fitness function** to determine the fitness of each chromosome. Furthermore, a bonus system was included to promote the elimination of entire channels or features from the input space.

$$S_i = LDA_{err} - (N_{ch_elim} + N_{feat_elim})$$

Where LDA_{err} refers to the error rate returned by the LDA classifier, N_{feat} is the number of features used (four in this case). $N_{ch.elim}$ is the number of eliminated input channels which denotes the number of channels that are eliminated commonly among all the features used. $N_{feat.elim}$ refers to the number of features that

were eliminated.

The formula applied to the given problem allowed for an deduction of the LDA error rate by 1% for each eliminated channel or feature.

- 3) The parent chromosomes for each pairing were picked among all the population chromosomes by an uniformly distributed random process. After two parents were found, the child was created by combining the channel section from the chromosome of parent one with the feature section from the chromosome of parent two.
- According to a predefined likelihood the child is subject to mutation. For this problem a mutation rate of 50% was used, where either one channel or feature was eliminated.

III. RESULTS & DISCUSSION

The graphs displayed in Figure 3 show the outcomes of the classifiers when using GA optimized features and channels, just optimized channels and all features and all the channels and features and hence no GA optimization. The displayed values for each classifier correspond to the mean of percentages of successful classification among all the 13 classes and the corresponding standard deviation. The reduction in the number of channels and features used for the classifiers in general did not degrade the results of the classifiers and considering subjects H3 and H5 the results of the SVM even improved after channel reduction.

Within the displayed charts the results for the different subjects are grouped according to the classifiers. Table I shows the used inputs for the individual datasets, which correspond to the fittest of chromosomes that was found by the GA. In this table a one corresponds to an activated channel and a zero to an inactive channel. The features used for each dataset are noted in the Features column and channels that were eliminated are counted in the last column($N_{ch.elim}$).

By comparing the outcomes of the different input combinations that are depicted in the three charts in Figure 3, it can be noted that for all subjects the reduction of features or channels had little to no effect. Despite the large amount of channels (≥ 8) that where removed, the ZC and SSC features were as well eliminated by the GA for most subjects. This suggests that the inclusion of these features in these cases did not improve the performance of the classifier by more than 1% per feature and hence they have been voted out.

Finally, the graphs show that even with a greatly reduced number of inputs and features, high mean classification rates (up to 80%) can be achieved over all of the 13 target classes. Hence it can be said that for future works on this problem the number of electrodes can be reduced by great means without having a large impact on the classification outcomes.

IV. CONCLUSION & FUTURE WORK

The provided work showed that a high grade of redundancy is contained within the datasets and hence the amount of input channels that are needed to differentiate among the 13 classes can be reduced. Furthermore, the presented results suggest that the ZC and the SSC features do not increase the performance of the classifiers and in most cases can be omitted and that using multiple redundant channels can degrade classification results.

The use of a GA for the explained optimization task proved a valid approach. Considering the number of possible solutions for this problem being 2^{20} (2^{16} possible combinations of inputs and 2^4 possible combinations of features) the optimization using a GA is too time consuming, as it has to perform a classification on each possible solution. Hence other methods, e.g. based on multivariate statistics, could be applied to further reduce the problem size before applying the GA.

There is no significant difference in classification accuracy, taking into account the standard deviation of the results, when comparing the classifiers, which complies with the results of Farrel [9].

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