

Features extraction and multi-classification of sEMG using a GPU-Accelerated GA/MLP hybrid algorithm

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Abstract.

BACKGROUND: Surface electromyography (sEMG) signal is the combined effect of superficial muscle EMG and neural electrical activity. In recent years, researchers did large amount of human-machine system studies by using the physiological signals as control signals.

OBJECTIVE: To develop and test a new multi-classification method to improve performance of analyzing sEMG signals based on public sEMG dataset.

METHODS: First, ten features were selected as candidate features. Second, a genetic algorithm (GA) was applied to select representative features from the initial ten candidates. Third, a multi-layer perceptron (MLP) classifier was trained by the selected optimal features. Last, the trained classifier was used to predict the classes of sEMG signals. A special graphics processing unit (GPU) was used to speed up the learning process.

RESULTS: Experimental results show that the classification accuracy of the new method reached higher than 90%. Comparing to other previously reported results, using the new method yielded higher performance.

CONCLUSIONS: The proposed features selection method is effective and the classification result is accurate. In addition, our method could have practical application value in medical prosthetics and the potential to improve robustness of myoelectric pattern recognition.

Keywords: Surface electromyography signal, features selection, genetic algorithm, multi-layer perception, biological signal processing, GPU acceleration

1. Introduction

Surface electromyography (sEMG) signal, which is recorded by electrodes on skin, is a kind of biological signal produced by neuromuscular activities. There exist different correlations among sEMG changes, muscle states and functional status. sEMG can objectively reflect the activities of neuromuscular in real time. Therefore, sEMG has great theoretic significance and engineering value in neuromuscular disease diagnosis in clinical medicine, rehabilitation medicine, fatigue evaluation in sports medicine and ergonomic analysis of muscle in human ergonomic [1]. It is possible to control prosthesis by recognizing sEMG signals [2, 3]. For example, the signals from upper limb musculature can be used to identify motion commands for the control of an externally powered prosthesis hand [4].

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Besides, sEMG signals reflect neuromuscular activities. It has important reference value for judging muscle fatigues and analyzing sport technologies. Scientific analysis and quantitative detection of sEMG signals can be used to evaluate the ability of athletes. And it has great significance in guiding and improving athletes' training effect [5, 6].

EMG is unstable and nonlinear. More and more researchers pay more and more attention to the feature extraction and classification of sEMG. Similar to many medical imaging and signal processing tasks [7, 8], feature extraction and optimal selection is also the basis of highly performed and robust sEMG analysis. Features in time domain were extracted based on raw EMG time series in literature [9, 10]. Wavelet transform-based features was used in literature [2]. Discrete wavelet transform (DWT) was a common used time-scale feature extraction method [11–15]. Besides, Chu et al. [16] used wavelet packet transform (WPT) to extract feature vector and used linear discriminant analysis (LDA) to reduce and cluster the WPT features. Phinyomark et al. [17] concluded the feature extraction methods in time domain and frequency domain. They discussed 24 different methods in time domain, such as mean absolute value, log detector, auto-aggressive coefficients, and 9 methods in frequency domain, such as mean frequency, mean power, frequency ratio, and power spectrum ratio.

In recent years, some feature selection methods were proposed, such as simulated annealing (SA) algorithm, tabu search (TS) algorithm, genetic algorithm (GA) [18, 19]. Boostani et al. [20] selected the best features from three points of view: classification of motion, noise tolerance and calculation complexity. GA is a kind of combinatorial optimization method to evaluate a feature subset, not a single feature. This can ensure the optimal combination in the feature subset, without considering features' correlation. In addition, GA is parallel, self-adaption and field independence. It can treat high-dimensional feature set very well and can be used for feature selection effectively [21].

The classification of signal features can recognize sEMG produced by different movements. Some algorithms were proposed for sEMG classification, such as particle swarm optimization (PSO) [11], neural network [22–24], support vector machine (SVM) [25, 26]. Subasi [11] used PSO optimized SVM to classify sEMG signals while Lucas et al. [12] used discrete wavelet transform and SVM. Alkan et al. [26] used discriminant analysis and SVM to classify sEMG signals. Naik et al. [26] used SVM for gesture classification. And Huang et al. [27] improved classification accuracy by spatial filtering. Nagata et al. [28] used Euclidean distance to classify the sEMG of 12 movements of hands. Bu et al. [29] classified EMG signals by a probabilistic neural network and combined it with the Bayesian network motion prediction to generate motion commands for controlling. Wang et al. [30] implemented the classification by optimal wavelet packet method based on Davies-Bouldin criterion.

The paper is organized as follows. In Section 2, we describe the methods used for sEMG signal classification. It includes feature extraction, genetic algorithm (GA) and multi-layer perceptron (MLP). Section III presents how the proposed method is applied for classification of sEMG signals and the results comparison. Finally, we conclude the paper in Section IV.

2. Methodology

The sEMG dataset published by researchers from University of Technology, Sydney and University of Baghdad, Iraq [2] has a large number of raw sEMG signals corresponding to six different hand movements. And because the original sEMG signal is noisy and high-dimensional, we need to extract features from the signals first. For feature extraction methods, we select the methods in time domain and frequency domain. Time domain methods are classical sEMG analysis methods which can get some statistical features of the signals. Frequency domain methods transform time domain signals into frequency domain signals in order to analyze the frequency spectrum and power spectrum of signals. There exist many feature extraction methods, but we want less optimal features to express the data.

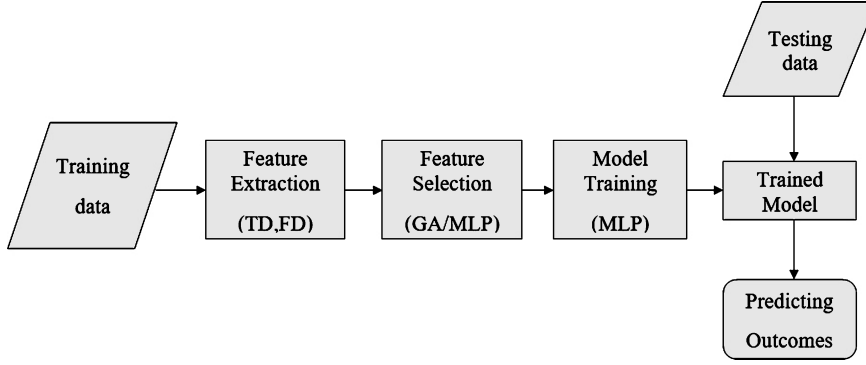


Fig. 1. The process of sEMG multi-classification.

So, we use GA to select features. After feature selection, every movement of the collected signal is converted into a sample consisting of several features. And the selected features are used to train the classifier based on MLP. Finally, the trained classifier is used to predict testing signals. The process is shown in Fig. 1.

2.1. Feature extraction

For the original signal, we need to find a set of features. To extract specific features of the signals and improve classification accuracy, we extract ten features $\{f_1, f_2, f_3, f_4, f_5, f_6, f_7, f_8, f_9, f_{10}\}$. The ten features contain seven time domain features and three frequency domain features. Because the extraction of time domain features is relatively simple, it is widely used in EMG field.

Assume that $x_t (t = 1, 2, \dots, n)$ is a time serial with the length of n .

The first feature f_1 : Root mean square (RMS) [31]. RMS reflects energy of the signal. The definition of RMS is shown in Equation (1).

$$f_1 = \sqrt{\frac{1}{n} \sum_{t=1}^n x_t^2} \quad (1)$$

The second feature f_2 : Waveform length (WL) [31]. The waveform complexity of each EMG data segment can be represented with wave length, which is defined as Equation (2).

$$f_2 = \sum_{t=2}^n |x_t - x_{t-1}| \quad (2)$$

The third feature f_3 : Integral absolute value (IAV) [31]. IAV shows the integral absolute value of EMG signals, defined as Equation (3).

$$f_3 = \sum_{t=1}^n |x_t| \quad (3)$$

The fourth feature f_4 : Mean absolute value (MAV) [31]. Because EMG signal is approximately random signal with zero mean, the feature will be close to zero and cannot represent the difference among signals if mean is treated as a feature directly. But, if we use the absolute value, the mean of the signal is greater than zero, constantly. So, the mean absolute value is selected. Equation (4) defines MAV.

$$f_4 = \frac{1}{n} \sum_{t=1}^n |x_t| \quad (4)$$

The fifth feature f_5 : Mean absolute value slope (MAVS) [32]. It is the mean of the difference between absolute values of the adjacent segments in a signal. The definition is shown in Equation (5).

$$f_5 = \frac{1}{n-1} \sum_{t=1}^{n-1} (|x_{t+1}| - |x_t|) \quad (5)$$

The sixth feature f_6 : Zero crossing (ZC) [31]. The EMG signal comes from electric pulse sent by nervous centrals and its intensity is related to the frequency of electric pulse. So, we chose ZC as a feature:

$$f_6 = \sum_{t=1}^{n-1} \text{sgn}(-x_t \cdot x_{t+1})$$

$$\text{Subject to : } \text{sgn}(x) = \begin{cases} 1, & \text{if } x > 0 \\ 0, & \text{other} \end{cases} \quad (6)$$

The seventh feature f_7 : Slope sign changes (SSC) [31]. A feature that may provide another measure of frequency content is the number of times the slope changes sign. The feature is defined as Equation (7).

$$f_7 = \sum_{t=2}^{n-1} \text{ssc}((x_t - x_{t-1}) \times (x_t - x_{t+1}))$$

$$\text{Subject to : } \text{ssc}(x) = \begin{cases} 1, & \text{if } x > 0 \\ 0, & \text{other} \end{cases} \quad (7)$$

The above seven features are time domain features. Because for some signals, it is difficult to get characteristics in time domain, we use fast Fourier transform (FFT) algorithm to extract features in frequency domain. Assuming that there are n sampling points, x_k ($1 \leq k \leq n$) is the value of the k^{th} point. Applying FFT to these sampling points could also get a set of n points and y_k ($1 \leq k \leq n$) is the transforming result of x_k . The modulus of y_k is the amplitude feature under the frequency.

We select three points with the largest values of modulus as the three features f_8 , f_9 , f_{10} in frequency domain, as shown in Fig. 2.

2.2. GA based MLP classification model

Genetic algorithm was proposed by Holland et al. [32] in 1975. It is an optimization method based on the genetic and evolution mechanism of biology and can be applied to adaptive probability of complex system optimization. Different from classical searching algorithm, GA is not based on evaluation function and Gaussian statistics but searching global optimal solution by simulating natural evolution procedures. In this paper, the feature selection process and the number of selected features are optimized by GA.

In GA, we use binary encoding to code searching space, which is called chromosome encoding. The chromosome encoding is composed of a series of certain elements corresponding to features. The encoding result is shown in Fig. 3. C is a binary chromosome encoding and C_k^i represents the value of the k -th element of the i -th segment. If C_k^i is 1, it represents the corresponding feature is selected by GA. Otherwise, the feature is not selected.

GA has three operators: selection, crossover and mutation [32]. The selection operator adopts roulette method. This method can ensure that the chromosome with high fitness value has high selected probability while the chromosome with low fitness value also has certain selected probability so that to avoid falling into local optimal solution. The crossover operator selects two chromosomes in the group with high probability and exchange one or some points of these chromosomes which embodies information

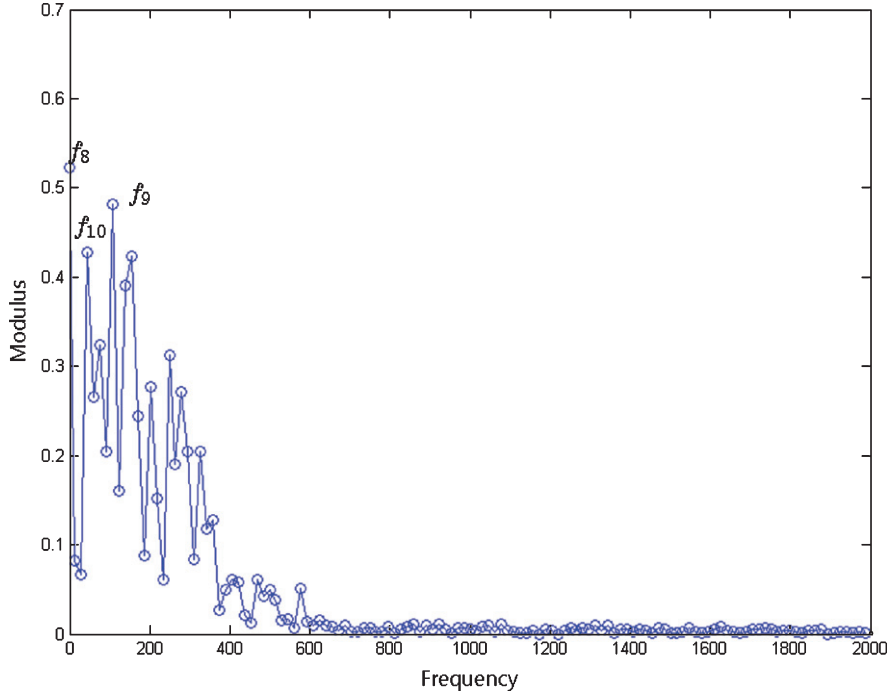


Fig. 2. Example of feature f_8 , f_9 , f_{10} in frequency domain.

C				
C^1	...	C^i	...	C^n
		C_1^i		
		C_2^i		
		C_3^i		
...
		C_k^i		
		...		
		C_m^i		

Fig. 3. The structure of a chromosome encoding.

exchange idea. There are many crossover methods. We adopt multi-points crossover which is also called generalized crossover. It means to randomly set some crossover points on the chromosomes and exchange them. The mutation operator means mutating on a chromosome's point based on the mutation probability. When mutation, the corresponding bit of the mutation point is negated.

The fitness function of GA, which is confirmed by the objective function, is the standard to distinguish good individual and bad individual. It is the only selection standard and the selection result will directly influence the performance of the algorithm. In this paper, we define fitness function as Equation (8).

$$\text{fitness}(C) = \alpha - \phi \times \sum_{i=1}^n \sum_{k=1}^m C_k^i \quad (8)$$

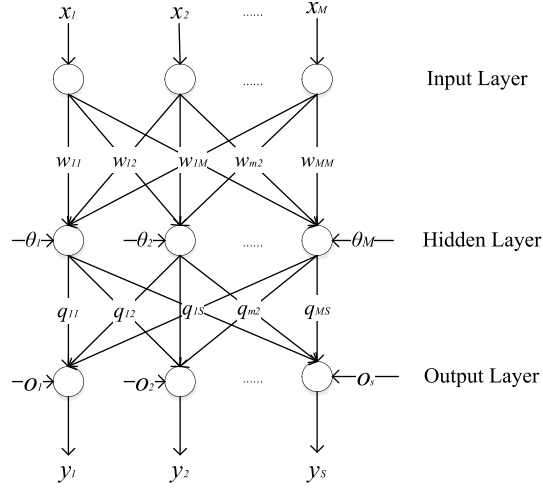


Fig. 4. The structure of MLP.

In Equation (8), α is classification accuracy and ϕ is a non-negative coefficient. $\sum_{i=1}^n \sum_{k=1}^m C_k^i$ is the total number of selected features. The optimization aims at increasing the classification accuracy with less selected features.

Multi-layer perceptron (MLP) is an artificial neural network with forward structure which maps a set of input vectors into a set of output vectors. MLP can be seen as a directed graph which is composed of multiple node layers and each layer fully connects to the next layer. MLP is described as being fully connected, with each node connected to every node in the next and previous layer [33]. Except input nodes, each node is a neuron (or processing unit) with nonlinear activation function. And the nodes are connected by weights and each node's output is a function of the sum of its inputs. A supervised learning method called back propagation algorithm is often used to train MLP. MLP is the extension of perceptron and it overcomes perceptron's disadvantage which cannot recognize linear inseparable data.

MLP often adopts classical three-layer network: input layer, hidden layer and output layer (as shown in Fig. 4). The network does not have either the connection between neurons in the same layer or feedback connection between layers. So, MLP is also called feed forward neural network (FFNN). Network with this structure is mainly applied to pattern recognition, function approximation, logical function and so on.

In this paper, we use GA to select features. Then, the selected features are used to train MLP classifier. The flow chart of the classification model is shown in Fig. 5.

3. Experiments and results

3.1. Data description and preprocessing

The experimental data is from literature [2]. There're six different movements: hand close (A), hand open (B), wrist extension (C), wrist flexion (D), wrist ulnar deviation (E), and wrist radial deviation (F), as shown in Fig. 6. In the experiments, as shown in Fig. 7, we considered three forearm orientations: wrist fully supinated, at rest, and fully pronated. Each orientation includes three force levels: low, medium and high. At each orientation, the six movements were repeated for 3 trials under each force level.

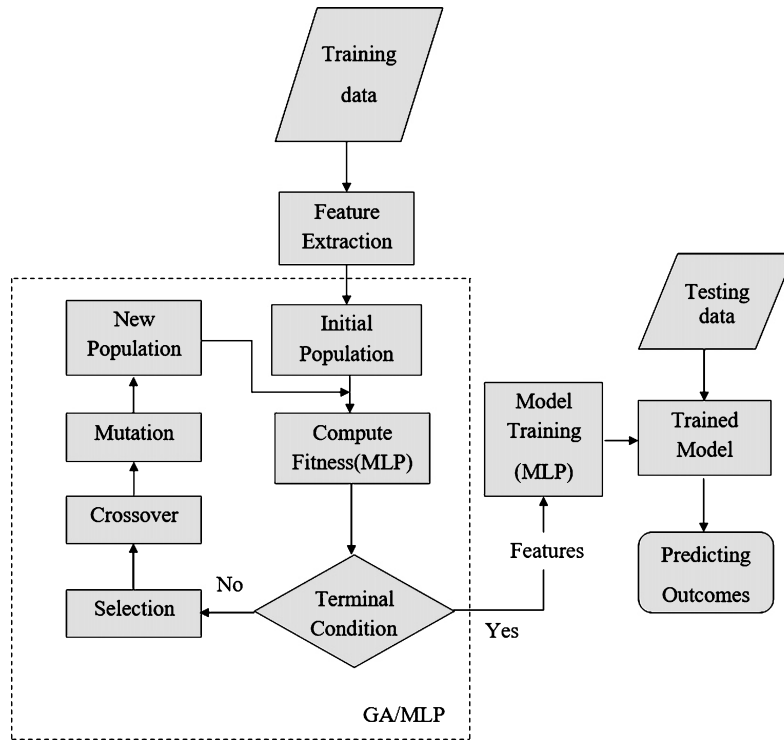


Fig. 5. GA based MLP classification model.

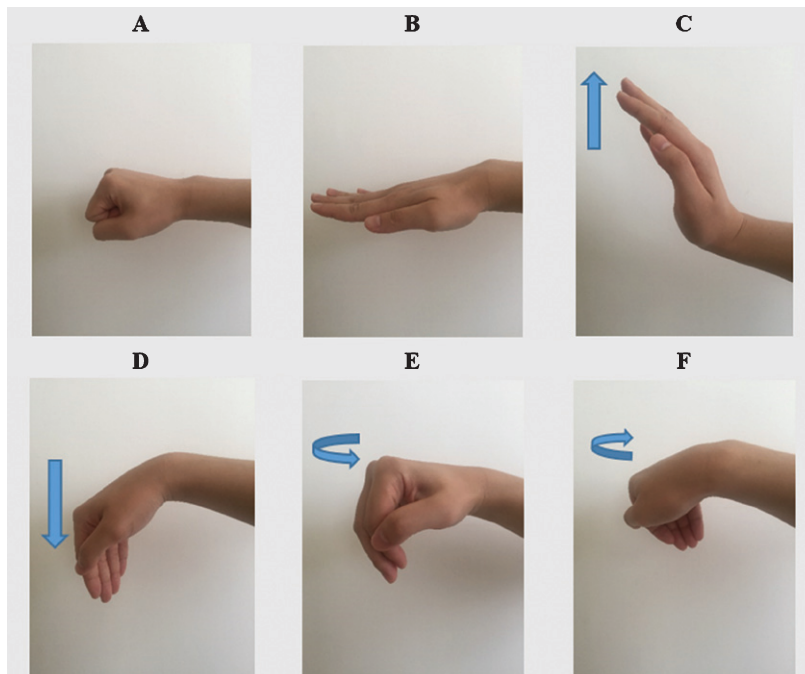


Fig. 6. Six different movements.

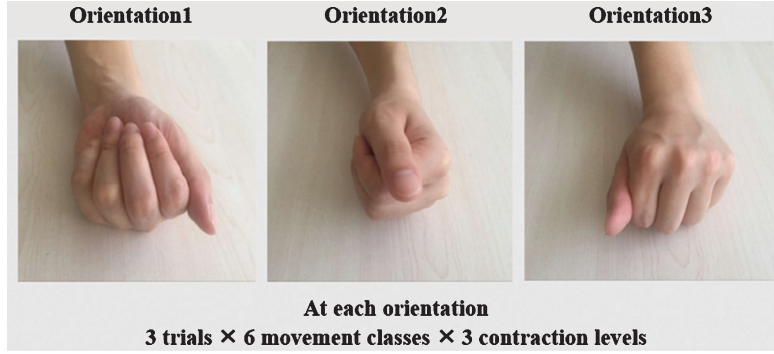


Fig. 7. Three forearm orientations performed the six classes of movements, each at three muscular contraction levels.

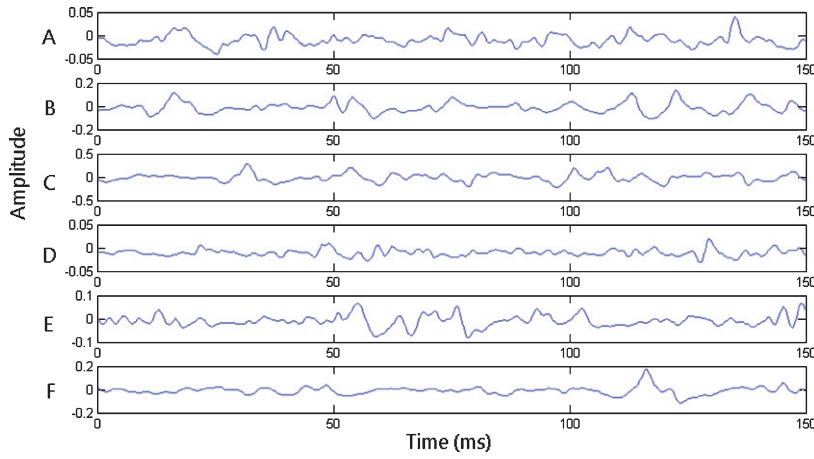


Fig. 8. Six class movements of sEMG signal samples.

In each trial, the sEMG data were collected at a frequency of 4000 values/sec and for 5 sec for each trial, therefore we ended up with 20000 values in each trial. We used an overlapping window size of 150 ms with 75 ms increments (50% overlap) to sample. So, for each sample we got 600 values and for each movement we could get 4680 samples. The six classes of samples are shown in Fig. 8.

Each sample has six sEMG channels and we used above feature extraction method to extract 10 features for each channel. So each sample finally got $6 \times 10 = 60$ features, as shown in Fig. 9. f_k^i is the k -th feature of the i -th channel. A chromosome encoding C could be used to represent all these features and each segment of C represents the features of one channel. If the value of C_k^i is 1, it represents feature f_k^i is selected by GA. Otherwise, the feature is not selected.

3.2. Environment and parameters

The experiment was implemented in python running on CentOS 7 with an Intel Core i7-6850k CPU server and 128 GB RAM. In addition, the training process was accelerated by GPU. In this study, the parameters of GA based MLP classifier were set as Table 1. In the table, the first four lines are the parameters of GA: population size, max generation, crossover operator and mutation operator. The fifth line is the parameter for MLP which means that there are two hidden layers and the first hidden layer has 100 neurons while the second hidden layer has 60 neurons. And the last line is the parameter for Equation (8).

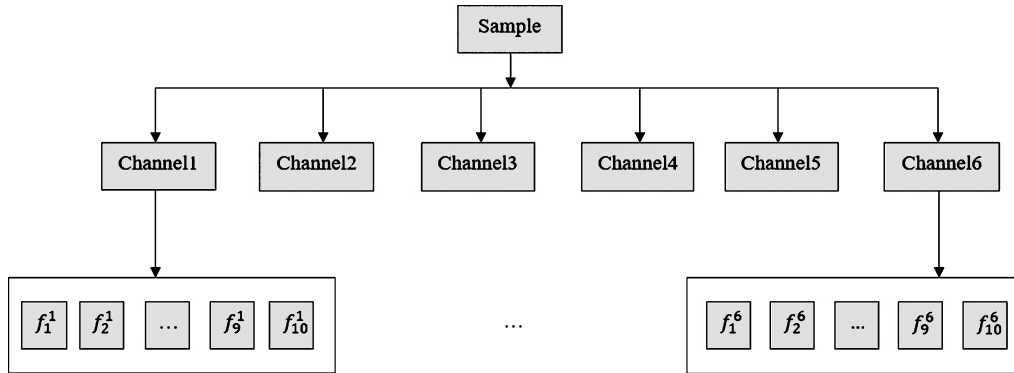


Fig. 9. The composition of each sample's features.

Table 1
Parameters for GA and MLP in sEMG multi-classification

N	Description	Value
1	Population size	200
2	Maximum of generations	1000
3	Crossover probability	0.9
4	Mutation probability	0.02
5	Hidden layer sizes	100,60
6	ϕ	0.005

Table 2
The selected features of GA

C_k^i	1	2	3	4	5	6
C_1^i	0	0	0	1	1	0
C_2^i	0	0	0	0	1	0
C_3^i	1	0	0	0	0	0
C_4^i	1	0	0	0	1	1
C_5^i	0	0	0	0	0	1
C_6^i	1	1	1	1	1	0
C_7^i	1	1	0	1	1	0
C_8^i	1	1	1	0	1	1
C_9^i	0	0	0	0	1	0
C_{10}^i	0	1	1	0	0	0

3.3. Results

After the optimization of GA, 25 features were selected, and the corresponding chromosome encoding is shown in Table 2.

We input the selected features to MLP classifier. The results are shown in Tables 3–5 which correspond to orientation 1, orientation 2 and orientation 3, respectively. Using the results of orientation 1 as the example, we had done three trials and each trial had different ratios of training set to testing set. From Table 3, we could know that our method has high accuracy when the ratio of training set

Table 3
Multi-classification results of orientation 1 sEMG signals

Input	Sample Size (every movement)	Train:Test (every movement)	Sensitivity (%)	Specificity (%)	Accuracy (%)
6 movements of orientation 1	4680	9 : 1	63.61	99.67	91.13
		8 : 2	85.90	99.52	97.67
		7 : 3	67.80	98.48	92.20

Table 4
Multi-classification results of orientation 2 sEMG signals

Input	Sample Size (every movement)	Train:Test (every movement)	Sensitivity (%)	Specificity (%)	Accuracy (%)
6 movements of orientation 2	4680	9 : 1	83.02	99.60	96.44
		8 : 2	71.71	99.94	95.59
		7 : 3	42.37	99.07	89.94

Table 5
Multi-classification results of orientation 3 sEMG signals

Input	Sample Size (every movement)	Train:Test (every movement)	Sensitivity (%)	Specificity (%)	Accuracy (%)
6 movements of orientation 3	4680	9 : 1	43.11	98.12	88.57
		8 : 2	59.65	96.76	90.91
		7 : 3	50.10	99.40	86.57

to testing set was 8 : 2. Accuracies with other ratios are a little lower, but they are also stable. So, we could conclude that our method has high accuracy and stability for different orientations with different ratios of training set to testing set.

Using the second experimental result of orientation 1 as example, the fitness value of GA and the experimental accuracy are shown in Fig. 10. The blue line represents the tendency of fitness value, and the green line is the tendency of accuracy. The larger the fitness value is, the better the features selected. Otherwise, the smaller, the worse. From Fig. 10 we could see that the fitness value becomes larger with the increase of the number of iterations. Even if there is variability, the fitness value increases generally. At the same time, accuracy also increases. It means that the features GA got became better and better.

Receiver operating characteristic (ROC) curve is the aggregate indicator of sensitivity and specificity. It uses the composition method to reveal the relation between sensitivity and specificity. The method can calculate a serial of sensitivity and specificity by setting many critical values for continuous variables and set sensitivity (true positive rate, TPR) as vertical coordinate, 1-specificity (false positive rate, FPR) as horizontal ordinate to draw the curve. The larger the area under the curve is, the higher the classification accuracy is. On ROC curve, the points nearest to top left corner are the critical values with higher sensitivity and specificity. Figure 11 illustrates the ROC curves of the dataset of orientation 1 whose ratio of training set to testing set is 8 : 2. There are 6 ROC curves in the Fig. 11 in total, representing six classes. Area Under Curve (AUC) could be a quantitative evaluation for the effect of the model. The larger the AUC is, the better the model is. Moreover, the value of AUC will

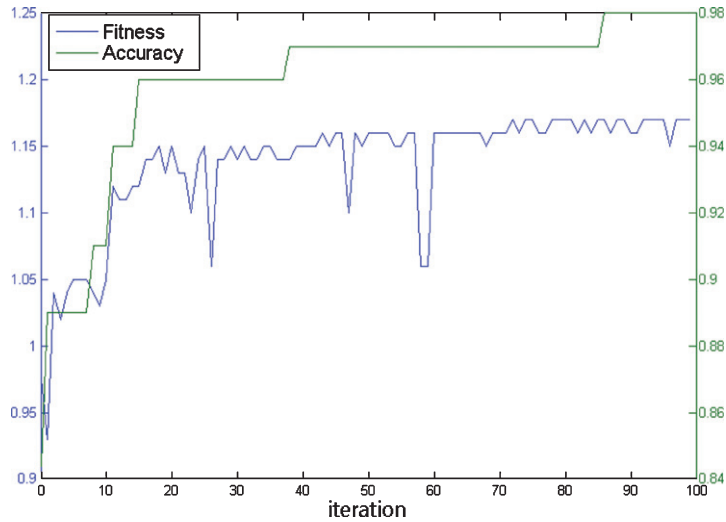


Fig. 10. Tendency of fitness value and accuracy (the blue line is fitness value while the green line is accuracy).

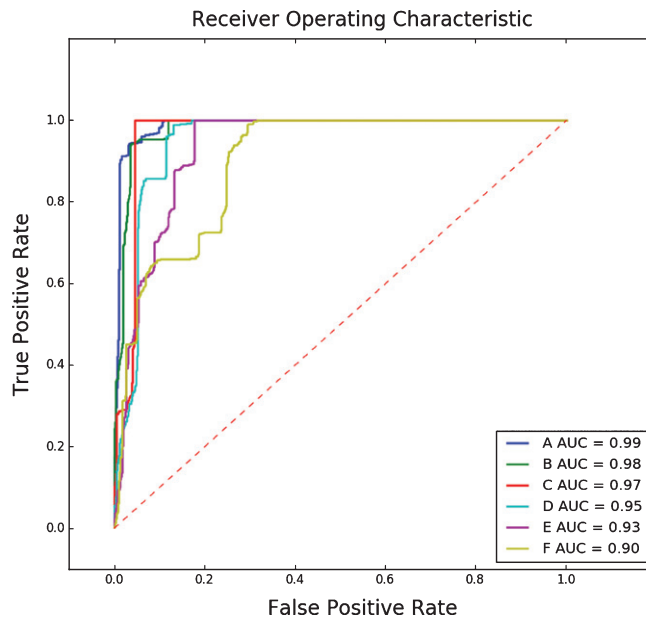


Fig. 11. ROC curves of six classes.

not exceed 1. The values of AUC of A, B, C, D, E, F are 0.99, 0.98, 0.97, 0.95, 0.93, 0.90. It means that in this classification model, the accuracy of A is the highest and E is the lowest. Although the values of AUC of the other classes are smaller than the first class, their values are all above 0.9. So it can be explained that this model is very effective.

A representative classification confusion matrix is shown in Fig. 12. We still use the second experiment results of orientation 1 as example. A, B, C, D, E, F in the horizontal coordinates represent the target classes. A, B, C, D, E, F in the vertical coordinate represent the predicted classes. From Fig. 12, we could see that the accuracies of six classes are all greater than 90%. Among all classes, F has the

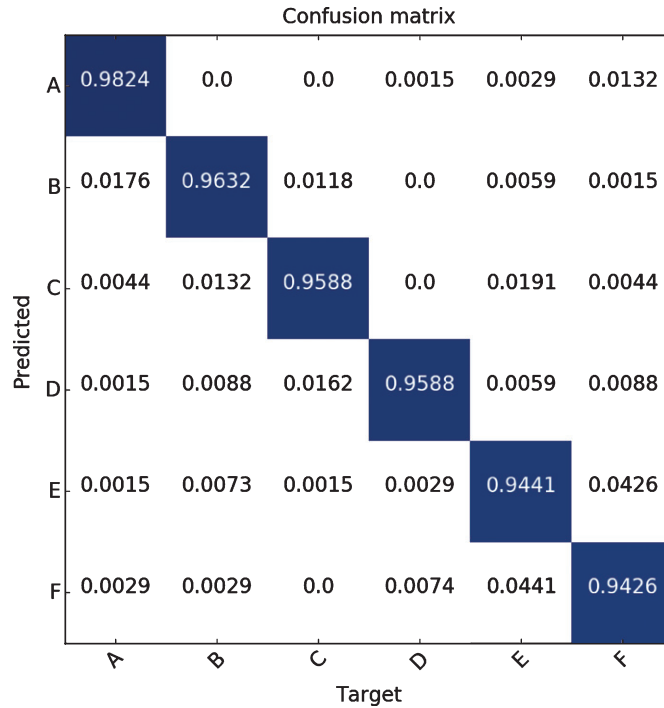


Fig. 12. A representative classification confusion matrix.

largest error and A has the minimum error. In general, it is more determined that our method could achieve a higher accuracy rate.

3.4. Comparison

Many researchers had worked on sEMG multi-classification. Table 6 shows the comparison between our work and a previous work when using the same dataset. The difference is that we adopt GA based MLP classifier, but SVM was used as the classifier in the previous work [2]. The average accuracies of previous work for three orientations were 91%, 93% and 90%. However, our classification accuracy is improved. Moreover, MLP is more effective than SVM for multi-classification problem. Because the classical SVM algorithm only support binary classification, even though it can solve the multi-classification problem through the combination of multiple SVMs, it is still more direct and effective to use MLP rather than SVM.

Table 6
Comparison of results between our method and other's method for sEMG multi-classification problem

Researches	Year	Feature Extraction	Classification	Dataset	Accuracy (%)
Rami N. Khushaba et al. [2]	2016	Wavelet transform-based features, TD,TDAR1,TDAR2,DFT,TD-PSD	Support vector machine	Orientation 1	91
				Orientation 2	93
				Orientation 3	90
This work		Time domain (RMS,WL,IAV,MAV,MAVS,ZC,SSC), Frequency domain (FFT)	GA based MLP classifier	Orientation 1	97.67
				Orientation 2	95.59
				Orientation 3	90.91

4. Conclusions

This paper proposes a GA based MLP multi-classification method using GPU acceleration to classify sEMG signals which can be used in the medical prosthetic field. GA can effectively optimize feature selection to reduce the number of features and the use of GA enables less features to represent samples. Besides, GA can improve the global convergence of MLP. Experimental results show that our model has high accuracy and the feature optimization method is effective. Moreover, we compare our method with other method. The results show that our method has high accuracy and it can be used in many applications. In addition, future work is needed to verify the effectiveness of our method. In this paper we only perform experiments within three orientations, so we will do some experiments between orientations in the future. Finally, sEMG signals can be applied to medicine. There needs not only theoretical study in biology and hardware, but also engineering researches.

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