sEMG-based Endpoint Stiffness Estimation of Human Arm using Gene Expression Programming

To cite this article: Jiang Zainan et al 2019 J. Phys.: Conf. Ser. 1267 012016

View the article online for updates and enhancements.
sEMG-based Endpoint Stiffness Estimation of Human Arm using Gene Expression Programming

Jiang Zainan*, Yang Fan, Li Chongyang, Liu Daxiang, Wang Chenliang, Li Tianhui and Liu Hong

State Key Laboratory of Robotics and Systems, Harbin Institute of Technology Harbin 150001 China

*E-mail: yangfan_hit@163.com

Abstract. The endpoint stiffness of the human arm has been long recognized as a key factor in the smooth contact between humans and environment. And the endpoint stiffness of the human arm is highly correlated with the surface electromyography (sEMG) produced by the contraction of the muscles. In this paper, the Gene Expression Programming (GEP) Algorithm is proposed to estimate the endpoint stiffness of human arm based on sEMG. This paper improves the traditional decoding method of GEP. Instead of generating an expression tree, it is directly decoded by looking for the effective length of the gene. And experimental results show that nonlinear models such as GEP models in this paper have higher correlation and lower RMSE (root mean square error) than regression stiffness using linear regression models. Selecting different feature of EMG signals, the correlation coefficient and the root mean square error of the model is very different. For the GEP model in this paper, WPTSVD (Wavelet Package Transform Singular Value Decomposition) and WTSVD (Wavelet Transform Singular Value Decomposition) are selected as the feature of sEMG signals have high performances and the correlation can reach 57% ± 12.1%.

1 Introduction

Facing the non-deterministic and unknown environment such as post-earthquake, traditional initiative compliant control had shown insufficient performance in terms of adaptive ability and robustness [1]. But on the other hand, humans arm demonstrate versatile and stable interactions with the uncertain environment. This is achieved through the modulation of the mechanical properties of the limb, and as a consequence, task-related restoring forces are applied in response to the environmental displacements [2]. Therefore, in order to realize the transmission of the dynamic characteristics of the human arm to the robot, how to quantitatively measure the dynamic characteristics of the human arm endpoint is particularly important for Human-Robot Interaction (HRI).

Surface electromyography (sEMG) is a human body's own resource, which contains rich information about human body motion [3]. The frequency and amplitude value of the sEMG signal depend on the motion of the human arm. Currently, sEMG has become an important parameter for studying the characteristics of human arm.

One way to quantify the stability of the contact between the limb and the environment is through the estimation of the endpoint stiffness. The research of sEMG-based estimation of human arm endpoint stiffness has been discussed in many papers. The models based on sEMG to estimate the human arm endpoint stiffness are mainly divided into two types, one is linear and the other is nonlinear. R.Osu and
H. Gomi proposed an algorithm for estimating the human arm stiffness which relies on identifying the map between muscular activities (as coded by sEMG) and joint torques [4]. R. Osu also propose an index of contraction around the joint (IMCJ) calculated from EMG and joint torques as well as confirmed that IMCJ was correlated well with joint stiffness [4]. M. Maehara et al. propose a first-order least squares method based on the existing data to obtain the relationship between EMG signal and stiffness, and the accuracy is higher, but only on a single joint [5]. Liang et al. proposed a discrete-time algorithm for stiffness extraction from sEMG and obtained the accurate value by integrating the increment [6]. Ze Cui et al. estimated upper limb muscle stiffness based on artificial neural network (ANN) but the performances was poor [7]. In addition, Catherine et al. confirmed that several factors were connected with the sEMG force relationship like muscle length, joint angle and arm posture [8]. In our experiments, subjects kept in the same posture while performing the operation, trying to avoid these influential factors.

In this paper, section 2 presents the GEP methods, including performance evaluation index of the method. Section 3 describes the experiment apparatus, the experiment procedures, data processing and the Cartesian impedance model at the end of the human arm. Section 4 presents results and discussion. Section 5 presents conclusions and the future work.

2 Methods

2.1 Gene Expression Programming Algorithm

According to the previous studies, the nonlinear model based on sEMG to estimate the human arm endpoint stiffness is more accurate and closer to the actual situation. In this paper, sEMG-based Stiffness is estimated by the model of Gene Expression Programming (GEP).

GEP is a function mining algorithm proposed by Ferreira, which combines the advantages of Genetic Algorithm (GA) and Genetic Programming (GP) [9]. Compared with GAs that solve simple problems with simple coding and GPs that solve complex problems with complex coding, GEP responds to complex problems with simple coding by using a linear string of a certain length to correspond to a flexible nonlinear tree structure of variable length. The calculation speed is 2~4 orders of magnitude faster than the traditional algorithm. This section improves the traditional GEP algorithm and establishes a mapping relationship between the sEMG signal and the stiffness in different directions of the Cartesian space.

In order to improve the efficiency of the GEP algorithm, this paper improves the traditional decoding method with reference to Xie's research. Instead of generating an expression tree, it is directly decoded by looking for the effective length of the gene.

Algorithm 1: Chromosome Decoding Algorithm

**Input:** Effective length of gene: len, Genotype: gene

**Output:** Gene expression: gene(1)

```plaintext
for i=len-1:1
    if gene(i)== function symbol
        judging the number of parameters of the function: num
        switch num
            case 1
                perform the corresponding calculation on gene(len) and assign it to gene(i);
                len=len-1;break;
            case 2
                perform corresponding calculations on gene(len) and gene(len-1) and assign them to gene(i);
                len=len-2;break;
        end
    end
end
```
In order to integrate more closely with the research object and subsequent data processing of this paper, this section designs a fitness function based on root mean square error, which is represented by (1).

\[ f = M \left[ \frac{1}{n} \sum_{k=1}^{n} (e_k - m_k)^2 \right]^{1/2} \]  

(1)

Where \( M \) is a constant indicating that the bandwidth is selected, \( e_k \) is the value calculated by the function, \( m_k \) is the value obtained by the experiment, \( f \) is the fitness value. In addition, a suitable \( M \) value can improve the quality of evolution. The greater the fitness value, the stronger the ability of the individual to adapt to the environment and the better the performance.

Through the use of simple elite strategy, roulette selection operator, mutation, interpolation and two-point reorganization, the population is updated. While maintaining the diversity of the population, it is ensured that the optimal individual is not eliminated and the organizational structure of the new population is consistent with the original population. Table 1 lists the parameters of the GEP algorithm in this section.

### Table 1. Parameter of GEP algorithm

| Experimental Parameters | GEP algorithm | Experimental Parameters | GEP algorithm |
|-------------------------|---------------|-------------------------|---------------|
| Number of runs          | 100           | Population size         | 20            |
| Max number of times     | 100           | Gene head length        | 4             |
| Function set            | +,-*/^qcls    | Gene tail length        | 5             |
| Variable set            | X             | Number of genes         | 4             |
| Constant candidate set  | --            | Chromosome length       | 36            |
| Terminator set          | X             | Mutation rate           | 0.044         |
| Random constant array length | 10        | IS displacement rate    | 0.1           |
| Random constant value range | [-10,10]  | IS element length       | 1.2           |
| Connection function     | +             | Two-point recombination rate | 0.3 |

Note: The function set ‘\(^q\)’ represents an exponential function, q denotes the square root, c denotes a trigonometric function, l denotes a logarithmic function, s denotes a square, and the variable set X is \{'x1', 'x2', 'x3', 'x4', 'x5', 'x6', 'X7', 'x8'\}.

#### 2.2 Performance Evaluation Criteria

After the model is established, the root mean square error (RMSE) and the correlation coefficient (CC) are used as the evaluation indicators of the model. RMSE represents the deviation between the predicted and experimental values, which can be calculated as follows:

\[ \text{RMSE} = \sqrt{\frac{1}{n} \sum_{k=1}^{n} (p_k - m_k)^2} \]  

(2)

Where \( p_k \) indicates the predicted value, \( m_k \) indicates the experimental value. And the CC can be calculated by:

\[ \text{CC} = \frac{\text{cov}(p,m)}{\sigma_p \sigma_m} \]  

(3)
Where $\text{cov}(p,m)$ represents the covariance of the predicted and measured values, $\sigma_p$ indicates the expectation of the predicted value, $\sigma_m$ indicates the expectation of the measured value. In general, the closer the RMSE is to 0, the closer the CC is to 1, the better the performance of the model.

3 Experiment

3.1 Experiment Apparatus

The purpose of this experimental platform is to verify the mapping between sEMG and the endpoint stiffness of the human arm. It is mainly composed of three modules: Robot System, Force Measurement System, sEMG Acquisition System. Among them, the robot system is used to provide the random disturbance displacement of the upper limb and obtain the end displacement of the human arm in real time. The force measurement system uses a six-dimensional force/torque sensor (JR3 Inc., USA) to detect the force generated at the end of the upper limb during the experiment. sEMG electrode (TrignoTM Wireless system, Delsys Inc., USA) is used to detect muscle electrical signals of human upper limbs. The platform also supporting the corresponding interface and data synchronization collection, storage and other software programs.

In the upper limb stiffness measurement experiment, 6 wireless electrodes are evenly arranged around the forearm at 1/3 of the elbow joint, 2 wireless electrodes are evenly arranged around the upper arm at 1/2 of the elbow joint, as shown in Figure 1(a). 6 wireless electrodes of the forearm mainly measure the activity of the muscles such as the radial wrist long extensor, ulnarextensor, the extensor digitorum, flexor carpi radialis muscle, flexor carpi ulnaris and the pronator teres. 2 wireless electrodes of the upper limb mainly measure the activity of the muscles such as the musculus biceps brachii and the musculus triceps brachii. The data acquisition system consists of three control computers, a KUKA manipulator, an F/T sensor and a wireless electrode. The force signal and the displacement signal are sent to the master control computer through the TCP and UDP protocols respectively, so that it can control the connection, disconnection, simultaneous acquisition, display and save of multi-modal data of each sub-computer as shown in Figure 1(b).

![Figure 1](image1.png)

**Figure 1** Electrode distribution and data acquisition system

3.2 Experiment Procedures

Five subjects (22-28 years old, 4 male and 1 female, respectively, A, B, C, D, E) were volunteered to participate in the experiment. Subjects knew the procedure before the experiment and agreed to participate in the experiment.

The robot was adjusted before the experiment to enable the subject to maintain the level of the forearm and the upper arm and the forearm at an angle of about 130-150°. We applied continuous stochastic perturbations to the subject’s hand through the handle in a three-dimensional. The amplitude
of the applied perturbations had the peak-to-peak value of 20mm. Data were collected from subjects at three different levels (relax, 30-50% MVC, 70-90% MVC), three experiments per muscle state, each disturbance lasting 30s. Each subject performed a total of 9 experiments (3 muscle states * 3 repetitions), and rested at any time during the experimental to avoid muscle fatigue. Including preparation time, each person takes about 40 minutes. The experimental device for predicting upper limb stiffness is shown in Figure 2.

![Experimental device](image)

**Figure 2** The schematic diagram of the experimental device

### 3.3 Data Processing

As described above, sEMG data were sampled at the frequency of 2000Hz and stored for offline analysis. F/T data and position data were also sampled at the frequency of 200Hz synchronously. Data preprocessing, parameter estimation, and model training were all done in MATLAB. The sEMG signal is filtered by a 4th-order Butterworth 20–500Hz bandpass filter and passed through a 50Hz notch filter to eliminate the influence of the power frequency. And the force signal and the position signal are filtered by a 4th order Butterworth 5–50Hz bandpass filter. Then according to the label of the displacement signal, find the corresponding force signal and the sEMG signal. Around this label, the mean value (MV) of force and position were extracted with the window of 250ms. The TDPSD, WPTSVD, WTSVD, WL, MDA, DASDV, RMS and MAV characteristics of sEMG were extracted with the window of 250ms. In the experiment, the horizontal grip data and the vertical grip data of the subject E are shown in Figure 3. It can be seen from Figure 3 that different levels of muscle contraction can produce different degrees of restoring force under random displacement sequences, whether horizontal or vertical.

![Graphs](image)

**Figure 3** Partial experimental data of subject E
### 3.4 Modeling arm impedance

The Cartesian impedance model at the end of the human arm can be expressed by equation (4):

$$M_e \ddot{X} + B_e \dot{X} + K_e (X - X_u) = F$$  \hspace{1cm} (4)

Where $M_e$, $B_e$, $K_e \in \mathbb{R}^{3 \times 3}$ represented the Inertia, damping, stiffness matrices respectively. $X, F \in \mathbb{R}^{3 \times 1}$ are the end-point position and force vectors with respect to the human reference system. While $X_u$ represented the virtual equilibrium position of the stiffness component. Equation (5) is expressed in the form of a matrix:

$$Y \pi = F$$  \hspace{1cm} (5)

Where $\pi \in \mathbb{R}^{27}$ was the parameter vector to be identified, given by

$$\pi = [M^T_{ex}, B^T_{ex}, K^T_{ex}, M^T_{ey}, B^T_{ey}, K^T_{ey}, M^T_{ez}, B^T_{ez}, K^T_{ez}]^T$$  \hspace{1cm} (6)

$Y$ was a $(3 \times 27)$ matrix defined by

$$Y = \begin{bmatrix} L^T & 0_{1 \times 9} & 0_{1 \times 9} \\ 0_{1 \times 9} & L^T & 0_{1 \times 9} \\ 0_{1 \times 9} & 0_{1 \times 9} & L^T \end{bmatrix}$$  \hspace{1cm} (7)

Where $L = \begin{bmatrix} \dot{X}^T & \dot{X}^T & (X - X_u)^T \end{bmatrix}^T$.

By formula (5), we could get:

$$\pi = Y^+ F$$  \hspace{1cm} (8)

So according to the acquired characteristic values of the force signal and the displacement signal, the endpoint stiffness of the human arm during the experiment can be obtained. Table 2 shows the impedance characteristics of the subject E when it is gripped vertically.

|       | M     | B     | K     |
|-------|-------|-------|-------|
| Relaxed | 5.81  | 0.30  | 4.91  | 32.21 | 7.34  | 28.27 | 151.07 | 188.42 | 34.43 |
|       | 0.13  | 7.14  | 6.20  | 3.17  | 1.89  | 1.33  | 151.40 | 472.57 | 199.86 |
|       | 2.96  | 0.02  | 2.73  | 10.95 | 1.80  | 1.81  | 85.50  | 29.02  | 42.74 |
| 30-50%MVC | 16.88 | 22.01 | 20.65 | 61.65 | 2.25  | 46.68 | 265.4  | 312.5  | 120.6 |
|       | 18.24 | 32.83 | 16.74 | 90.39 | 41.66 | 8.13  | 316.2  | 238.6  | 353.6 |
|       | 20.65 | 5.61  | 16.18 | 22.71 | 11.69 | 20.77 | 85.71  | 47.60  | 70.14 |
| 70-90%MVC | 139.9 | 41.48 | 121.97 | 175.54 | 48.26 | 46.25 | 150.40 | 548.29 | 179.0 |
|       | 34.33 | 49.01 | 27.46 | 28.96 | 44.67 | 22.67 | 191.47 | 460.86 | 380.01 |
|       | 53.71 | 19.48 | 38.59 | 84.12 | 21.46 | 62.61 | 194.52 | 57.67  | 69.03 |

Taking the characteristics of the sEMG signal as input, the vector formed by the calculated diagonal value of the stiffness matrix $K$ is output, and the regression training and testing are performed using the GEP algorithm described in the second part.

### 4 Results and Discussions

#### 4.1 Results

First divide training set data and test set data, Four-fold cross-validation was used. In each subject, 3/4 of the data set was randomly selected as the training set, and 1/4 of the data set was used as the test set. The GEP algorithm is used to train and test the sEMG features and the calculated stiffness data. The experimental results are shown in Figure 4.
4.2 Discussion

Among the eight selected sEMG features, the two characteristics WPTSVD and WTSVD based on singular value decomposition are the best. It can be seen that the singular value decomposition can effectively extract the differential mode information in the EMG signal to characterize the muscle stiffness. Secondly, the TDPSD feature is better because it reflects the complexity of the changes in myoelectric signals. The prediction effects of time domain features DASDV, MAV, MDA, RMS and WL are basically the same, and the performance is very stable and relatively low.

5 Conclusion

In this paper, sEMG-based stiffness is estimated by the model of Gene Expression Programming (GEP). According to the experimental results, the following conclusions can be obtained. First, nonlinear models such as GEP models have higher correlation and lower RMSE than regression stiffness using linear regression models. Secondly, selecting different feature of EMG signals, the correlation coefficient and the root mean square error of the model is very different. For the GEP model in this paper, WPTSVD and WTSVD are selected as the feature of sEMG signals, and the correlation can reach $57\% \pm 12.1\%$. In the future, we mainly focus on real-time human arm impedance estimation and more accurate estimation of human arm impedance after considering factors such as human arm configuration.

Acknowledgment

The authors gratefully acknowledge the financial supports by National Natural Science Foundation of China (No. 61803124 and No. 91848202) and Heilongjiang Provincial Postdoctoral Research Startup Fund.
References

[1] Ajoudani, A. (2016). Transferring human impedance regulation skills to robots. *Springer Tracts in Advanced Robotics*, 110.

[2] Tsuji T, Morasso P G, Goto K, et al. Human hand impedance characteristics during maintained posture. *Biological Cybernetics*, 1995, 72(6):475-85.

[3] Kinnaird, C. R., Ferris, D. P. (2009). Medial gastrocnemius myoelectric control of a robotic ankle exoskeleton. *IEEE Transactions on Neural Systems & Rehabilitation Engineering A Publication of the IEEE Engineering in Medicine & Biology Society*, 17(1), 31.

[4] Osu, R. (2002). Short- and long-term changes in joint co-contraction associated with motor learning as revealed from surface emg. *J. Neurophysiol*, 88.

[5] Maehara, M., Tanaka, D., Maeda, H., Nakamura, T. (2010). Estimation of joint stiffness using EMG and application to master-slave system with an artificial muscle manipulator. *International Symposium in Robot & Human Interactive Communication*. IEEE.

[6] P. Liang, C. Yang, N. Wang, Z. Li, R. Li and E. Burdet. “Implementation and Test of Human-Operated and Human-Like Adaptive Impedance Controls on Baxter Robot,” *Taros*. 2014, pp. 109-119.

[7] Cui, Ze, Han, Wangyang, Qian, Donghai. Estimation of upper limb muscle stiffness based on artificial neural network. 2069-2074. 10.1109/ROBIO.2017.8324724.

[8] Disselhorst-Klug, C., Schmitz-Rode, T., & Günter Rau. (2009). Surface electromyography and muscle force: limits in semg–force relationship and new approaches for applications. *Clinical Biomechanics*, 24(3), 0-235.

[9] Ferreira, C. (2002). Gene expression programming: mathematical modeling by an artificial intelligence. *Engineering Applications of Artificial Intelligence*, 1(3), 223–225.