System identification of a motor unit pool using a realistic neuromusculoskeletal model

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Abstract-The synaptic input to the motoneurons cannot be measured in humans due to ethical and technical difficulties. For these reasons realistic computational models of a motoneuron pool and the innervated muscle fibers (a "motor unit pool") have an important role in the study of the human control of muscles. However such models are complex and their mathematical analysis is difficult. We present a system identification approach of a realistic motor unit pool model with the objective of obtaining a simpler model capable of representing the transduction of the motoneuron pool inputs into the force generated by the respective muscle. The system identification was based on an orthogonal least squares algorithm to find a NARMAX model, the input being the net dendritic excitatory synaptic conductance of the motoneurons and the output being the force produced by the muscle. The identified model output reproduced the mean behavior of the output from the realistic computational model even for input-output signals not used in the identification process, such as sinusoidally modulated output force signals.

I. INTRODUCTION

The motor units are transducers of the premotoneuronal input into force [1]. As the synaptic input to the motoneurons (MN) cannot be directly measured in humans, due to both technical and ethical issues, the usage of computational models to estimate the relationship between synaptic currents and muscle force becomes very important [2]. Recently, some realistic neuromuskuloskeletal computational models capable of simulating motor behaviors have been developed [3]–[5]. Although these models achieved great success in reproducing and explaining some motor behaviors and the transduction of the premotoneuronal input into force, they are usually so complex that performing any mathematical analysis would be very difficult and the ability of generalization is practically inexistent.

This high complexity of the system motivates the use of system identification techniques as a means of achieving model complexity reduction. System identification consists of a set of methods to find a mathematical description of a system based solely on its observed inputs and outputs [6]. Although experimental input-output data are not available, the necessary data can be obtained using a realistic computational model. In this work the adopted realistic neuromusculoskeletal model was that described and validated in [4], [7], [8] for the *Triceps Surae* (TS).

Therefore, the objective of this work was to find a dynamic model simpler than those complex biologically-realistic models mentioned above, that could reproduce the transduction of the MNs' synaptic inputs into the force signal with the same characteristics of the realistic models.

The paper is organized as follows: Section II describes the neuromusculosketal model and the simulation protocol used for the data acquisition to the identification of the model. The system identification method used is explained afterwards. Finally the validation methods of the identified model is explained. Section III shows the identified model and its validation. Section IV discusses the validity of the motor unit pool identified model and its possible uses.

II. METHODS

A. Neuromusculoskeletal model

A previously reported model [4], [7], [8], hereafter referred to as the original model, was used as the neuromusculoskeletal model for the acquisition of the premotoneuronal inputs and the force signals. Briefly, each MN pool of the TS - for the Soleus (SOL), Medial Gastrocnemius (MG) and Lateral Gastrocnemius (LG) - encompasses conductance-based MN models arranged according to the available physiological and anatomical data (all the parameter values were the same used in [8]). The main difference between each MN pool is its number of MNs: SOL has 900, MG has 600 and LG has 260. Each spike generated by a MN produces a twitch in the muscle unit following the impulse response of a second-order critically-damped system [4], [9]. Descending axons were represented by 400 independent renewal point processes. A 30% connectivity was adopted between the descending axons and MNs, i.e. each descending axon connects to approximately 30% of the MNs randomly [8] to account for the inter-subject variability. For each performed simulation the contacts of the descending axons with the MNs is randomized. A diagram of the neuromusculoskeletal model is depicted in Fig. 1.

B. Data acquisition

Differential equations describing the neuromusculoskeletal model were solved by a fixed-step (0.05 ms) fourth-order Runge-Kutta integration method. Ten statistically independent simulations using the neuromusculoskeletal model described in the previous section were performed to simulate isometric contractions equivalent to 10% maximal voluntary contraction. Each descending axon conducted a spike-train modeled as a Poisson point process with a mean inter spike

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Fig. 1. Structure of the neuromuscular model used in this study. (a) schematic view of the *Triceps Surae* (TS) muscle group and the three TS muscles: Soleus (SOL), Medial Gastrocnemius (MG) and Lateral Gastrocnemius (LG). The motor unit pool of each muscle encompasses motoneurons (MN) and the respective muscle units (MU); (b) schematic representation of muscle-specific motor units (MNs and MUs). Each of the 400 renewal point processes representing the descending axons connects to approximately 30% of the MNs. Each MU receives a train of action potentials from the respective MN and generates twitches that are summed with the contributions from the other MUs to produce the muscle force F(t). (c) train of renewal point-process representing a train of spikes of a descending axon; (d) equivalent circuit used to represent each MN model. g_{syn_1} to g_{syn_M} :synaptic conductances for synapse 1 to M, respectively; g_c : coupling conductance; g_{Ld} and g_{Ls} : dendritic and somatic leakage conductances, respectively; g_{Na} , g_{Kf} and g_{Ks} : conductances of Na⁺, fast K⁺ and slow K⁺, respectively; E_L : leakage Nernst potential; E_{Na} : and E_K : Na⁺ and K⁺ equilibrium potentials, respectively; E_{syn_1} to E_{syn_M} : reversal potentials for synapses 1 to M, respectively; C_s and C_D : somatic and dendritic capacitances, respectively; V_S and V_D : somatic and dendritic membrane potentials, respectively. (e) force produced by a single MU.

interval (ISI) equal to 11.2 ms, as in [8]. Each simulation had an equivalent duration of 15 s.

Four additional simulations were performed for the purpose of evaluating the performance of the identified model during a sinusoidal modulation of the ISIs of the descending axons point processes. The modulation of the point processes produced a simulated rhythmic voluntary contraction. In these simulations, the ISIs mean of the point processes varied sinusoidally with mean of 11.2 ms, amplitude of 0.5 ms (*i.e.* ISIs varying from 10.7 ms to 11.7 ms) and frequencies of 0.5 Hz, 1 Hz, 2 Hz and 3 Hz.

C. System identification

The type of model used in the motor unit pool identification was the polynomial representation of the nonlinear autoregressive moving average with exogenous input (NAR-MAX) model [10]:

$$y(k) = \theta_0 + \sum_{i_1=1}^n \theta_{i_1} x_{i_1}(k) + \sum_{i_1=1}^n \sum_{i_2=i_1}^n \theta_{i_1 i_2} x_{i_1}(k) x_{i_2}(k) + \dots + \sum_{i_1=1}^n \dots \sum_{i_l=i_{l-1}}^n \theta_{i_1 i_2 \dots i_l} x_{i_1} x_{i_2} \dots x_{i_l} + \xi(k)$$
(1)

where $\theta_{i_1i_2...i_m}$ are the respective model coefficients and

$$x_m(k) = \begin{cases} u(k-m) & 1 \le m \le m_u \\ y(k-(m-m_u)) & mu+1 \le m \le m_u + m_y \\ \xi(k-(m-m_u-m_y)) & m_u + m_y + 1 \le m \le m_u + m_y + m_\xi \end{cases}$$
(2)

with m_u, m_y and m_{ξ} being the maximal lags for, respectively, u, y and ξ . $\xi(k)$ is computed by using:

$$\xi(k) = y(k) - \hat{y}(k|k-1)$$
(3)

The signal chosen as the input signal u(t) in the identification of the motor unit pool system should contain the ensemble information of the activations from all the presynaptic inputs. The most natural choice to be used as the input signal is the net dendritic excitatory synaptic conductance of

the MNs. As the connectivity between the descending axons and the MNs is approximately 30% (see Fig. 1), each MN receives a different combination (mean 120) out of the 400 independent input Poisson spike trains. As each conductance is generated by the same linear system dynamics and the overall input is composed by the 400 sample functions of the same Poisson point process (*i.e.*, with a pre-established parameter value), we adopted as an overall input signal for the identification process a conductance which is activated by all the 400 Poisson spike trains. This is equivalent to measure the conductance signal from a MN as the connectivity were 100%. The choice of this signal as the input guarantees that the signal u(t) contains the information from all presynaptic inputs of all MNs.

The choice of Poisson point processes models for the spike trains in the descending axons facilitates the identification process because the power spectrum of the net dendritic excitatory synaptic conductance is flat until 100 Hz [8].

The force F(t) (see Fig. 1) was chosen as the output signal y(t). Fig. 2 shows an example of the input signal u(t) (Fig. 2(a)) and the corresponding output signal y(t) (Fig. 2(b)).



Fig. 2. Examples of (a) input signal u; (b) output signal y

The model identification of the motor unit pool was performed using the NARMAX technique of system identification based on the multiple forward regression orthogonal least squares algorithm (MFROLS) using the error reduction ratio (ERR) to select the model terms (see page 81 in [10]). This technique was chosen because the structure that the identified model should have was not known *a priori*. While most of the identification techniques require previous knowledge of the model structure [11], [12], the MFROLS algorithm conducts an exhaustive search in a set of candidate terms and selects the most important terms of this set according to the ERR [10].

Given the above, five of the ten input/output pairs obtained in the simulations (see Section II-B) were used to identify a model by using the MFROLS algorithm. The original data set was first low-pass filtered by an eighth-order lowpass Chebyshev zero-phase filter with a cutoff frequency of 160 Hz and then downsampled to 400 Hz. This sampling frequency was chosen based on the autocorrelation of the squared output criterion explained in [13]. The set of candidate terms was built with all possible combinations of the signals u and y with the maximal order of a polynomial term in Eq. (1) being seven (l = 7). By using the sum of the error reduction error criterion [10], the values of $m_u = 10$ and $m_y = 4$ were obtained. After the selection of the model terms, the values of the coefficients $\theta_{i_1i_2...i_m}$ were found by using least squares.

The estimation of the values of $\theta_{i_1i_2...i_m}$ previously found are biased since it is necessary to identify a model of the residue of the estimation [6]. Therefore, the MFROLS algorithm is used once again to find a model for the signal $\xi(k)$, computed as in Eq. (3). In this phase of the system identification all combinations of u(t), y(t) and $\xi(t)$ up to the seventh order polynomial (l = 7) were used as the set of candidate terms to model the signal ξ and the value $m_{\xi} = 10$ was adopted.

After the selection of all the model terms (including the residue model) it was necessary to reestimate the values of $\theta_{i_1i_2...i_m}$. This was performed by using the extended least squares algorithm of parameter estimation [10].

D. Model validation

The estimation of the values of $\theta_{i_1i_2...i_m}$ will be unbiased only if the residue ξ is uncorrelated from the selected model terms. It has been shown [14] that ξ will be uncorrelated from the selected model terms if the following correlation tests are obeyed:

$$\Phi_{\xi\xi}(k) = \delta(k), \forall k$$

$$\Phi_{u\xi}(k) = 0, \forall k$$

$$\Phi_{\xi(\xi u)}(k) = 0, k \ge 0$$
(4)

where Φ_{wz} is the normalized cross-correlation between w and z, $\delta(k)$ is the unitary impulse (assumes the value of 1 when k = 0 and the value 0 otherwise) and $(\xi u)(k) = \xi(k+1)u(k+1)$.

The five simulation signal pairs that were not used during the identification procedure, were used to evaluate the identified model output. The predicted output signals were obtained during a completely free simulation of the identified system, *i.e.* the output y(t) from the original model was not used during the prediction. To compute the contribution to y(t) of the terms that depend on past values of y(t), the values of the estimated output $\hat{y}(t)$ were used instead.

Since the identified system has a stochastic nature (mainly due to the random connections of the descending axons with the MNs), the comparison between the output signals from the original model and from the identified models was done by means of a frequency domain analysis. For this purpose the power spectra of both output signals and the cross-spectra between the input and the output signals from both models were computed. To evaluate the spectra only when a steady state was reached, the spectra were computed using the last 12 s of each of the five signals using Welch's method [15]. The spectra and cross-spectra from both the original and the identified model were estimated by averaging the values from each of the five trials. To test the similarity of the curves from both models, the following statistic having a chi-square distribution was used [15]:

$$X^{2} = \left(\frac{1}{n_{d_{\text{orig}}}} + \frac{1}{n_{d_{\text{ident}}}}\right)^{-1} \sum_{i=1}^{n} \left[\log_{10}\left(\frac{|\hat{S}_{\text{orig}}(f_{i})|}{|\hat{S}_{\text{ident}}(f_{i})|}\right)\right]^{2}$$
(5)

where \hat{S} is spectra or cross-spectra estimation, n_d is the number of averages used for each estimation using the Welch's method, and the subscripts orig and ident are used to the original and the identified models, respectively.

III. RESULTS

The model terms selected by using the MFROLS algorithm [10] are shown in Table I. The same table shows the final values of the respective $\theta_{i_1i_2...i_m}$ coefficients of the three motor unit pools of the TS.

TABLE I Selected model terms and final values of the $\theta_{i_1i_2...i_m}$ coefficients

Model term	SOL	MG	LG
y(k-1)	2.08e+00	2.06e+00	1.86e+00
y(k-2)	-1.22e+00	-1.28e+00	-8.85e-01
y(k-3)	1.87e-01	3.41e-01	1.55e-01
y(k-4)	-4.56e-02	-1.21e-01	-1.29e-01
u(k-6)	-1.31e-04	-1.31e-04	7.97e-05
u(k-7)	1.68e-06	-5.92e-05	-2.70e-05
u(k-8)	2.77e-04	1.37e-04	1.07e-04
u(k-9)	6.60e-05	3.77e-05	-6.23e-06
u(k-10)	3.17e-06	6.97e-06	9.44e-06
u(k-6)u(k-6)u(k-7)	-8.82e-11	9.60e-11	-2.05e-10
u(k-6)u(k-7)u(k-8)	-2.15e-09	-9.87e-10	-5.38e-10
u(k-6)u(k-7)u(k-7)	1.45e-10	2.80e-10	-1.71e-10
u(k-6)u(k-7)u(k-7)y(k-1)	-7.95e-13	-4.14e-12	1.19e-11
u(k-7)u(k-7)u(k-7)u(k-8)u(k-9)	2.57e-16	1.41e-16	8.21e-17
u(k-8)u(k-8)u(k-9)u(k-9)	-1.57e-16	-6.59e-17	-8.16e-18
u(k-6)u(k-6)u(k-7)u(k-7)u(k-8)	4.60e-15	1.75e-15	1.31e-15
u(k-6)u(k-7)u(k-7)u(k-8)y(k-1)	-2.92e-13	1.49e-14	7.86e-13
u(k-6)u(k-7)u(k-7)u(k-8)y(k-3)	-2.23e-13	1.12e-13	8.68e-13
u(k-6)u(k-7)u(k-7)u(k-8)y(k-2)	5.14e-13	-1.28e-13	-1.66e-12
u(k-6)u(k-8)u(k-8)u(k-8)y(k-3)	4.40e-16	1.12e-15	3.39e-16
u(k-6)u(k-6)u(k-7)u(k-7)u(k-7)y(k-1)	1.19e-15	7.93e-16	4.08e-16
u(k-6)u(k-6)u(k-7)u(k-7)u(k-7)y(k-2)	-2.38e-15	-1.56e-15	-8.41e-16
u(k-6)u(k-6)u(k-7)u(k-7)u(k-7)y(k-3)	1.19e-15	7.71e-16	4.24e-16
u(k-6)u(k-6)u(k-7)u(k-7)u(k-7)u(k-8)	-1.54e-21	-6.11e-22	-2.11e-22
u(k-6)u(k-6)u(k-6)u(k-6)u(k-7)u(k-8)	1.05e-21	7.55e-22	2.90e-22
u(k-6)u(k-6)u(k-7)u(k-7)u(k-8)u(k-8)	-1.41e-21	-6.98e-22	-4.90e-22
u(k-6)u(k-6)u(k-6)u(k-7)u(k-7)u(k-7)	-3.91e-22	-3.40e-22	6.48e-23
u(k-6)u(k-6)u(k-6)u(k-6)u(k-6)y(k-1)	-3.88e-22	-1.82e-21	-1.76e-21

Fig. 3 shows the results of the cross-correlation tests of Eq. (4) computing ξ (Eq. (3)) from the estimation of the output of the identified model (Table I) to one input/output pair used in the identification process (Fig. 3(a) shows $\Phi_{\xi\xi}$, Fig. 3(b) shows $\Phi_{u\xi}$ and Fig. 3(c) shows $\Phi_{\xi(\xi u)}$). The three figures show that all values that should be zero are inside the 95% confidence interval.

The results in Fig. 4 and Fig. 5 were computed using the five simulation signals not used during the identification process. Only the results from SOL pool are shown. The results from the other pools are similar.

Fig. 4 shows the output signal of the original model and the output signal of the identified model, using the same signal u(t) as input. It is worth noting that, since the motoneuron pool is a stochastic system, it is not expected that both signals should have exactly the same time course.

Fig. 5 shows the results of the frequency domain analysis. Fig. 5(a) shows the power spectra of the output signals from



Fig. 3. Correlation tests (a) $\Phi_{\xi\xi}$; (b) $\Phi_{u\xi}$; (c) $\Phi_{\xi(\xi u)}$. The dashed blue lines indicate the 95% confidence interval.



Fig. 4. Output example of the original model (blue line) and the identified model (red line). Only the last 12 seconds are shown.

the original model and from the identified model. Fig. 5(b) shows the cross-spectra between the input signal and the output signals from the original model and from the identified model. By using the statistics in Eq. (5) to test the similarity of the power spectra and cross-spectra from the original and identified model, the hypothesis that the curves are equal between 0 and 10 Hz is accepted with a significance level of 0.05.

Fig. 6 shows the output signals corresponding to the input signals (descending axons' point processes) being produced with ISIs modulated sinusoidally (see Section II-B). Four modulation frequencies were used: 0.5 Hz (Fig. 6(a)), 1 Hz (Fig. 6(b)), 2 Hz (Fig. 6(c)) and 3 Hz (Fig. 6(d)). Mean



Fig. 5. (a) Power spectra of the output signals. (b) Cross-spectra between the input signal and the output signals of the original model and the identified model.

square error measures present no difference for the different modulation frequencies.



Fig. 6. Output force sinusoidally modulated with frequencies of (a) 0.5 Hz, (b) 1 Hz, (c) 2 Hz, (d) 3 Hz. Only 5 s are shown.

IV. DISCUSSION

In this paper we identified a model that has as input a signal originated from all the premotoneuronal inputs and its output is the force produced by the muscle. Both input and output signals used in the identification process were acquired from a realistic neuromusculoskeletal model of the TS muscles.

The output signal from the identified model (see Fig. 4) has the same mean and approximately the same time course as the output signal from the original model. As mentioned before, since the original system (the complex biologically realistic model) has a stochastic behavior the two output signals need not have exactly the same time course. The origins of the stochastic behavior of the original system are mainly due to: for each simulation there are small random variations around the means of the original model parameters; the random connectivity (30%) from the input

spike trains to the motor unit pool each time a simulation is performed.

This random connection of the descending axons imposes difficulties in the system identification of the motor unit pool. That was the reason to use five signal pairs from different simulations to perform the identification of the pool. The use of five signal pairs tries to capture the mean behavior of the motor unit pool, which can be assessed by means of a spectral analysis. The power spectra and the cross-spectra from both the original and the identified model (see Fig. 5) have similar values at all frequencies, suggesting that the dynamical behaviors from both models are similar.

Probably some of the terms found in the identification process (see Table I) are spurious and could be removed from the model. This is a known issue of the MFROLS algorithm [10] and requires an extra analysis to find the spurious model terms. Besides the existence of spurious terms, some tests other than that shown in Fig. 3 can indicate the necessity of some additional term to represent a particular dynamical behavior. The small deviation of the output power spectra (see Fig. 5(a)) around 1 Hz also indicates the possibility that there may be some missing terms.

Nevertheless, the dynamic model found in this work was able to replicate force signals having different characteristics from those used during the identification process. The force curves from the identified model shown in Fig. 6, simulating voluntary rhythmic contractions (produced by a sinusoidal modulation imposed to the descending axons), common in multiple daily tasks as postural control or gait, have the same frequency as the force curves of the original model. The differences between the signals generated by both models are, as noted before, due to the stochastic nature of the involved systems and their magnitudes have no statistic differences for the different modulation frequencies. Regardless of the signal differences, the force signal from the identified model follows the frequency of the force signal from the original model in all the four cases.

Besides the mathematical simplicity, when compared to the original model, the identified model has the advantage to produce the force signal significantly faster than the original model. For example, to produce the force signal from Fig. 4 the realistic neuromusculoskeletal model takes around 40 minutes (using an Intel®) 3.4 GHz processor and 24 Gb RAM memory). The identified model produced the force signal generated by the same input signal (Fig. 4) in less than 5 s, using the same processor and memory. Indeed, the original realistic model, focusing only on the SOL pool, is composed of 900 MNs, each having: fast and slow, sodium and potassium, ionic channels; a one-compartment dendrite modeled by an RC circuit and as many synaptically-activated conductances (with exponential time courses) in parallel at the dendrite as the number of presynaptic inputs. Each of the 900 motor units activates a second order linear model to produce a force twitch. In comparison, the identified model is a difference equation with only 28 model terms.

The output of the identified model can be used as the activation signal of a Hill-type muscle model [16] and be

coupled to proprioceptors sending input signals to the MNs, as in the original neuromusculoskeletal model in [17], [18]. This coupling would allow the study of physiological questions that would be difficult to tackle either by experiments or using the realistic neuromusculoskeletal model.

Besides the study of neurophysiological questions, a system like that described in the last paragraph could be used to control a robotic leg. A much studied approach for human leg rehabilitation has been the interface between muscle EMG and robotic legs [1], [19], [20]. A more advanced approach, that would require either EEG signals or some more invasive signal acquisitions, could benefit from the identified system developed here. Its output would serve as the activation signal for Hill-type muscle models which would serve as model for the robotic dynamics. Additionally, the proprioceptor models would produce realistic reflexes in the robotic leg. This system could be used not only in amputees but also in subjects with spinal cord injury. Clearly, this is just a conceptual proposal, much science and technology still need to be created to realize such an approach.

In sum, the preceding results show that the identified model of the motor unit pool can transduce the MNs inputs into a force signal with the same dynamic characteristics as the generated by the realistic neuromusculosketal model.

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