2018 CMBEC41 Conference
Charlottetown PEI
May 8–11, 2018

MYOSIM 2.0: ENHANCING AND VALIDATING AN EMG SIMULATION TOOL

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ABSTRACT

In 2006, we presented a MATLAB tool called Myosim, which allows users simulate signals measured through surface electromyography (SEMG) [1]. Based on user input, the tool sets generative model parameter values such as the geometry of each fibre in each motor unit relative to the electrode location, the number of motor units, the number of fibres per motor unit, conduction velocity and firing statistics. Using the parameter values, the tool then outputs an SEMG signal based on a finite length model of muscle and a convolution between action potential source and tissue filter. Recently we have made updates to the tool which improve the underlying model used to generate the signal, and allow users to add instrumentation effects associated with the data capture process including baseline noise, band-pass filtering, and quantization. We have also used a genetic algorithm to select generative model parameter values which optimize matching between real and simulated signals, to validate that the tool produces output representative of EMG.

INTRODUCTION

Myosim is a user friendly SEMG simulation tool developed by MacIsaac, Rogers and Bhandarkar using MATLAB [1]. In short, the tool uses a finite length model of muscle proposed by González-Cueto and Parker [2] to model a single fibre action potential (SFAP) as observed at the surface of the skin. The model convolves a double layer differential source, originally proposed by Plonsey [3], with a tissue filter that considers various geometric and physiological parameters of the fibre to produce SFAP. The SFAP are then summated to form motor unit action potentials (MUAPs) which can be convolved with impulse trains and summed to form SEMG signals.

The original tool (Myosim 1.0) had a few limitations: 1) it produced signals with normalized amplitudes (ie scaled from 0 to 1), 2) because of random variation built into parameter settings, it was difficult to explicitly and completely control model parameters (for example, in reproducing identical signals), and 3) it ignored the influence of data capture in the output. Also, besides informal observation by SEMG experts, output from the simulation tool had never been directly compared with measured recordings to validate that it matched signals measured through SEMG. In this work, we made improvements to Myosim 1.0 to overcome the limitations. To test the validity of the upgraded tool (Myosim 2.0), we used a genetic algorithm to optimise the generative parameter values to match a particular signal, measured *in vivo* (ie. recorded). We then compared features of the recorded signal to the features of the simulated signal.

METHODS

Tool improvements

Adjusting Internal Model Parameters

In Myosim 1.0, the amplitude of the SFAPs were normalised and a few other internal model parameters were nominally set. Thus, the amplitude of the generated SEMG signals could not be easily compared to records. Previous studies that used this tool mostly focussed on metrics that did not depend on the amplitude of the signal, such as conduction velocity (CV) or mean frequency (MF). However, several other features, such as the mean absolute value (MAV) and waveform length (WL) rely on amplitude values. To account for this, we surveyed the literature to establish values for the model

parameters set nominally and for expected SFAP amplitudes.

The internal model parameter values were adjusted based on values used by Van Veen and Rijkhoff in [4] for a similar model. The source was left unadjusted from what was originally reported in [1]. However, the tissue filter:

$$h(t) = K \cdot \frac{t}{\left[\frac{\sigma_l}{\sigma_t}\left(\frac{r}{v}\right)^2 + t^2\right]^{3/2}} \qquad (1)$$

where

$$K = k \cdot {\sigma_i \theta^2}\Big/{8\sigma_e} \text{ and } \theta = {a}/{v}$$

was adjusted as delineated in Table 1. In the table, k represents an amplitude scaling factor, σ_l/σ_t represents anisotropy, σ_i and σ_e represent intracellular and extracellular conductivities, and θ represents a constant ratio between fibre radius to conduction velocity.

Table 1: Adjusted Model Parameters

Parameter	Myosim 1.0	Myosim 2.0
k	1	500
${\sigma_l}/{\sigma_t}$	1	5
σ_i	1	$0.45\ s/m$
σ_e	1	$2.5\ s/m$
θ	1	$6.25\ usec$

To adjust the SEMG signal amplitude, the scaling factor (k) was introduced to scale SFAP amplitudes. To establish this factor, we simulated a single motor unit close to the surface and compared the MUAP amplitude to the values measured with indwelling electrodes close to a motor unit as reported by Buchtal et al in [5].

Incorporating Instrumentation Effects

Data captured through SEMG are subject to several instrumentation effects, including noise from the instrumentation, bandpass filtering, and quantisation. Though these effects are expected to be minimal for a proper setup, including these effects as part of the simulation model may provide useful insight into the effects of improper instrumentation setup on SEMG signal features. Thus, we included options to add baseline noise modeled as a piecewise linear combination of pink and white noise as expected from instrumentation [6], to bandpass filter the signal based on low and high cut-off frequencies set by a user, and to quantize the signal based on a bit resolution provided by a user.

Regenerating SEMG signals

While Myosim 1.0 had the option to save output signals, its generative parameter values, and its summed components (SFAPS, MUAPs, impulse trains etc), it did not provide any means to load components back into Myosim for reuse. It was therefore difficult to recreate setups for comparison since the tool randomises several generative parameter values based on ranges specified by a user. Since such comparisons may be useful, for example in studies looking to ascertain the effects of generative parameters on signal features, we added the option to load signal components back into Myosim 2.0 for reuse. Now the tool provides the option to regenerate signals with a subset of components (eg. the impulse trains, half of the MUAPS etc.) from another simulated signal.

Output Validation

Because of the random nature of SEMG signals, it is difficult to verify that an SEMG simulator is producing signals representative of those collected through SEMG. Since the values of the generative parameters driving a real signal are unknown, it is impossible to know what generative parameter values to set when comparing a simulated output to a real signal. To offer some support for the validity of Myosim, we used a genetic algorithm (GA) to provide a set of generative parameter values optimized to match a simulation output with a recorded signal.

A canonical GA was used with a fitness function defined as the mean absolute error (MAE) between the power spectral densities (PSDs) of the simulated and recorded signals. A roulette wheel selector was used to select the fittest chromosomes for continued searching. Each chromosome was made up of four generative parameters, namely number of fibres, number of motor units, depth, and conduction velocity and the search space was

limited to include values within reasonable physiological limits. A nominal population of 100 chromosomes was initially generated, and each search iteration included crossover at 1 point at a rate of 10%, and mutation at rate of 5%. Search continued until a solution was found with a fitness score which indicated that the MAE was within the variation expected among power spectra of SEMG signals assumed to come from the same contraction. To determine the expected variation, a long signal was simulated and split into segments. The first segment was used as a template and the remaining segments were used to determine the mean MAE and standard deviation. The fitness threshold was then set to 1.15 times the mean + 3 standard deviations, which yielded a threshold of about 0.0075.

The GA was used to match a total of 22 recordings taken from 11 subjects at 2 contraction levels. These signals were collected as part of another SEMG study aimed at investigating variability in SEMG signal features. Signals were measured from the biceps brachii, with electrodes in bipolar configuration, and amplifiers set to bandpass the signal from 20-500Hz. An instrumentation amplifier with CMRR>100dB was used. Signals were sampled at 5000Hz.

Comparing the power spectral densities of the records and simulated output signals provides a good indication of fitness, but it compares only a partial representation of the signals. To more completely evaluate how well an output signal matches a recorded one, several other output signal features were also inspected. These features were chosen based on their widespread use in SEMG studies and include Mean Absolute Value (MAV), Mean Frequency (MeanFreq), Slope Sign Changes (SSC), Waveform Length (WL), and zero Crossings (ZC). All of the features were calculated via the methods provided be Chan and Green [7].

RESULTS

Figure 1 compares feature values calculated from a recorded signal (solid dot markers) with feature values calculated from a simulated signal with generative parameters set to match the recorded signal (x markers). Each of the recorded signal data points comes from a 1 sec segment of a 5-sec record. Each of the simulated signal data points come from a 1-sec segment of the matching simulated signal. Each data point has been normalized to the mean value of the recorded features for visual clarity. This example is representative of the results across all 22 matches. In all cases, feature values extracted from the simulated signal fell within the same range as values extracted from different segments of the same recorded signal.

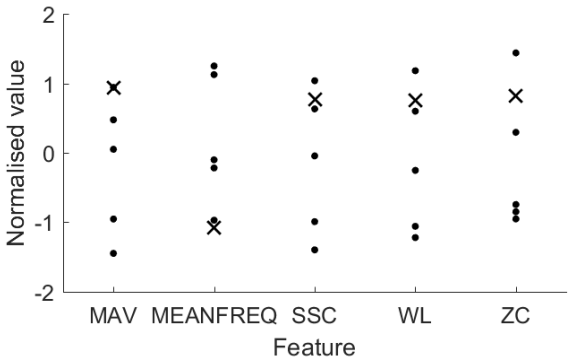

Figure 1: Feature values calculated from Recorded Signal (solid dot markers) and matching simulated signal (x markers)

CONCLUSION

When tool parameters are set appropriately, Myosim 2.0 will produce simulated SEMG signals with features within the same range as recorded data. This result supports the validity of Myosim as an automated solution for simulating signals representative of SEMG recordings.

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