

## Modeling the spatial distribution of surface electromyogram amplitudes

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### Summary

Muscle excitations are distributed heterogeneously within the muscle, resulting in local differences in the amplitude of surface electromyograms. The functional significance of regionalized muscle excitation may be studied with high-density recordings, but these data are high-dimensional, making them difficult to analyze and interpret. Thus, we assessed the ability of two analytical approaches, Gaussian and sinusoidal functional forms, to represent uni- and bimodally (one or two peaks) distributed surface electromyography (sEMG) amplitudes. In the unimodal case, Gaussian functions fit the data well and had physically meaningful parameter estimates; sinusoidal fits were poor. In the bimodal case, neither Gaussian nor sinusoidal fits accurately represented the underlying amplitude distributions.

### Introduction

Single bipolar electrodes are typically used to measure and represent the excitation of entire muscles, based on the assumption that muscles are homogeneously excited. However, sEMG amplitudes are non-uniformly spatially distributed [1], suggesting that more information about muscle excitation can be gleaned from sEMG recordings over a large areas of muscle as opposed to a single bipolar electrode.

Grid electrodes have been increasingly used to study spatial distributions of sEMG amplitudes [1]; however, an analysis problem is introduced: how can high-dimensional data be analyzed so that empirical data are accurately represented and easily interpretable? One approach is to model sEMG amplitudes as function of space. For instance, Gaussian functions provide intuitive parameter estimates; mean, variance, and amplitude are interpretable [1]. However, pilot data suggest that the number of peaks may be task-dependent, to which sine waves fit well. While Gaussians may fit data with one peak [1], they may fail if data have more than one peak. Therefore, we sought to evaluate the ability of both Gaussian and sinusoidal functions to represent simulated sEMG amplitudes that have either one or two peaks.

### Methods

The medial gastrocnemius was modeled as a volume containing fibers [1, 2]. Single-fiber action potentials (SFAP) were simulated to obtain raw sEMG signals across 70 monopolar electrodes (5 mm inter-electrode distance). The average rectified value (ARV) of the sEMG amplitude was computed for each electrode. Unimodal distributions for a range of mean

locations, spreads, fiber densities, and signal-to-noise ratios were simulated. Bimodal distributions were obtained by summing raw sEMG amplitudes from the unimodal simulations with the smallest and greatest mean locations, resulting in peaks at either end of the sEMG array.

Simulated data were fit to Gaussian (uni- and bimodal) and sine waves using nonlinear least squares (MATLAB). Regression related each curve's parameters (Gaussian:  $\mu$ ,  $\sigma$ , and amplitude  $\beta$ ; sinusoid:  $\phi$ ,  $f$ , and amplitude  $\beta$ ) with the parameters of the underlying excitation distribution (location, size, and degree of excitation).

### Results and Discussion

In the unimodal condition, Gaussian fits outperformed sinusoidal fits for all parameters (Table 1) and representation of the underlying signal ( $R^2 = 0.85 \pm 0.06$  vs.  $0.6 \pm 0.2$ ). The superiority of the Gaussian can likely be attributed to bias arising from the inability of a sine wave to fit flat regions.

In the bimodal condition, neither Gaussian nor sinusoidal fits accurately represented the underlying signals (Table 1;  $R^2 = 0.5 \pm 0.3$  and  $0.01 \pm 0.01$  for Gaussian and sinusoidal fits, respectively). This could be due to the sharp peaks in the data, which leads to bias in both the Gaussian and sinusoidal fits.

These data provide insight into what Gaussian and sine fits can and cannot represent. These analytical approaches may perform differently in different muscles or with empirical data.

### Conclusions

In agreement with previous work [1], Gaussian functions can be used to reduce the dimensionality of sEMG data that have one peak. Functional forms other than Gaussian and sine waves may be needed to reduce the dimensionality of sEMG distributions with more than one peak.

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### References

- [1] Vieira et al. (2011) *J. Physiol.* **589**: 431-43.
- [2] Mesin et al. (2004) *IEEE Trans. Biomed. Eng.* **51**: 1521-9.

**Table 1:** Coefficients of determination ( $R^2$ ) of model parameter with the location, size, and degree of simulated regions of excitation.

Parameter	Gaussian $\mu_1$	Gaussian $\sigma_1$	Gaussian $\beta_1$	Gaussian $\mu_2$	Gaussian $\sigma_2$	Gaussian $\beta_2$	Sine $\phi$	Sine $f$	Sine $\beta$
Unimodal $R^2$	> 0.99	0.98	0.76				< 0.01	< 0.01	0.11
Bimodal $R^2$	0.5	< 0.01	0.06	0.5	0.01	< 0.01	< 0.01	< 0.01	0.11