

Do coupling activation and contraction dynamics improve the accuracy of Hill-type models?

Andrea Sgarzi^{1,2}, Théo Meranger¹, Bart Bolsterlee^{1,2}, Arnault Caillet³, Dario Farina³, Nigel H. Lovell¹, Luca Modenese¹

¹Graduate School of Biomedical Engineering, UNSW, Sydney, NSW

²Neuroscience Research Australia (NeuRA), Sydney, NSW

³Dept of Bioengineering, Imperial College London, UK

Email: a.sgarzi@unsw.edu.au

Summary

Current Hill-type models neglect the physiological dependence of contraction dynamics on the active state. This study evaluates the accuracy of two muscle models with non-linear coupling between activation and contraction dynamics using a publicly available biological benchmark of muscle forces measured in various contractile conditions. At maximal activation, we observed a significant improvement in predictions compared to uncoupled models when considering a motor-unit-level model. Predicted forces, however, were less accurate with larger displacement amplitudes for all models and only minimally improved in sub-maximal activation conditions. Overall, the study suggests that models with coupled contraction and activation dynamics offer slightly better accuracy than standard Hill-type models.

Introduction

Hill-type muscle models are based on a phenomenological characterization of muscle contraction dynamics [1]. Models consistent with the framework described by Zajac [2] neglect the physiological dependence of contraction dynamics on the active state. While they show good accuracy in slow, nearly maximally activated contractions, they are less accurate in faster, submaximal contractions that better represent in vivo muscle conditions [3]. This study aims to quantify the accuracy of two muscle models considering the non-linear coupling between activation and contraction dynamics by predicting experimental force measurements in maximally [4] and sub-maximally [5] stimulated muscles. The results are evaluated against those of a muscle model without activation-contraction coupling [3] for the same benchmarks.

Methods

We considered two muscle models: the Hatze model (HA) [6], incorporating active state dependency on fiber length [7], and a modified version of the motor-unit-level model by Caillet et al. (CA) [8], accounting for motor unit (MU) types, the force-length and force-velocity relationships dependency on fiber length and active state, and a time-dependent effect of muscle yielding [9] for slow-twitch MUs. Models were benchmarked against force measurements from a maximally activated rat soleus [4] and a sub-maximally activated cat soleus [5]

undergoing various displacement amplitudes. For the maximal benchmark, the curvature of the force-velocity relationship and maximum isometric force F_{iso} of both models were calibrated through a least-squared fit to the maximal-displacement trial [3]. For the sub-maximal benchmark, the control parameters of HA were calibrated through a least-squared fit in each trial, while CA model activation dynamics were calibrated using a single isometric trial. The agreement with experimental data was assessed in terms of maximum and mean absolute errors (MAE, mAE), and two-sample t-test were performed for the results of each model against results from Millard et al. [3] (MI model).

Results and Discussion

The results obtained are shown in Table 1. In the maximal benchmark, both models' errors increased with the displacement amplitude, reaching a maximum MAE of 67% (HA) (vs 45% for [3]). MAEs, however, improved significantly for the CA model compared to [3]. As for the sub-maximal benchmark, no significant improvement was observed compared to [3], except for CA's mAE at maximum displacement and random frequency due to the inclusion of yielding which seems determinant at high displacements.

Conclusions

Muscle models with coupled contraction and activation dynamics and MU-level muscle dynamics can predict muscle force slightly more accurately than standard Hill-type models in maximally and sub-maximally stimulated muscles. The inclusion of time-dependent effects may enhance model accuracy in future developments.

References

- [1] Hill AV. (1938) *Proc Royal Soc B*. **126**:136-195.
- [2] Zajac FE. (1989) *Crit Rev Biom Eng*. **17**:359-411.
- [3] Millard M et al. (2013) *J Biomech Eng*. **135**: 021005.
- [4] Krylow AM et al. (1997) *J Biomech*. **30**:27-33.
- [5] Perreault EJ et al. (2003) *J Biomech*. **36**(2): 211-218.
- [6] Hatze H. (1978) *Biol Cyber*. **28**:143-157.
- [7] Rockenfeller et al. (2016) *J Theor Biol*. **454**:240-252.
- [8] Caillet AH et al. (2023) *PLOS Comp Biol*. **19** e1011606.
- [9] Brown IE et al. (1999) *J Muscle Res Cell M*. **20**: 627-643.

Table 1: predicted vs exp. force MAEs / MAEs [% F_{iso}] at different displacements (Orange: max., Blue: sub-max., C: const. freq, R: rand. freq).

	±0.05mm	±0.25mm	±1.0mm	±2.0mm	±1mm, C	±1mm, R	±8mm, C	±8mm, R
HA	4 / 18	4 / 14	4 / 29	7 / 67	4 / 15	3 / 14	8 / 30	10 / 48
CA	1 / 9	3 / 13	5 / 21	6 / 31	3 / 10	4 / 15	7 / 35	6 / 40
MI	3 / 29	4 / 22	6 / 33	8 / 45	3 / 7	3 / 9	11 / 37	10 / 41