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## Supplemental information

## FiberSim: A flexible open-source model

## of myofilament-level contraction

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# FiberSim: a flexible open-source model of myofilamentlevel contraction

### *Supporting Material*

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*cell (1).*

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#### **ISOMETRIC TWITCH**

Fig. S1 shows an isometric twitch simulation similar to the one presented in https://campbell-muscle-

lab.github.io/FiberSim/pages/demos/getting\_started/isometric\_twitch/isometric\_twitch.ht ml, except that the number of thick filaments is increased from 16 to 196. The simulation takes approximatively 30 minutes to run on a standard Windows laptop, using 3 of the 4 processors (meaning that other tasks still can be performed during the FiberSim simulations). As a comparison, an equivalent simulation performed with MUSICO (with 200 thick filaments) takes approximatively 10 hours on a system with 192 processors (2).



#### **TIME-STEP**

Fig. S2 shows four isometric activations similar to the one presented in https://campbellmuscle-lab.github.io/FiberSim/pages/demos/getting\_started/isometric\_activation/isometr ic\_activation.html. Each simulation is run with a different (constant) time-step.

Since the thin filament kinetics model is associated with the fastest rates, this will determine the maximal time-step we should use. The probability for a regulatory unit to activate is calculated using  $k_{on}$  . [Ca<sup>2+</sup>], where in the model files from the presented demos  $k_{on}$  is equal to 3.10<sup>7</sup> M<sup>-1</sup> s<sup>-1</sup>. Thus, for an isometric activation such as the one presented in Fig. S2, the activation rate is given by  $3.10^7.10^{-4} = 3000 \text{ s}^{-1}$ . The chosen time-step  $\Delta t$ should be small enough so that Δt <  $\frac{1}{3000}$  ~ 3.10<sup>-4</sup> s. We chose to work with Δt = 10<sup>-4</sup> s in all the simulations presented in this paper. According to Fig. S2, this step size is enough to accurately describe thin and thick filaments activation while keeping a reasonable computational time.



#### **THIN FILAMENT ACTIVATION CURVES**

Fig. S3 shows two thin filament activation curves. The active binding sites proportion is calculated at different calcium concentrations in the absence of cross-bridges. When cooperativity is turned off ( $y_{coop} = 0$ ), the Hill coefficient is close to 1. When cooperativity is turned on ( $y_{coop}$  = 10), the Hill coefficient increases to ~4. This last curve is in good agreement with the experimental data from (3).



#### **SUPPORTING REFERENCES**

- 1. ten Tusscher, K. H., and A. V. Panfilov. 2006. Alternans and spiral breakup in a human ventricular tissue model. *Am J Physiol Heart Circ Physiol*. 291(3):H1088- 1100, doi: 10.1152/ajpheart.00109.2006.
- 2. Mijailovich, S. M., M. Prodanovic, C. Poggesi, M. A. Geeves, and M. Regnier. 2021. Multiscale modeling of twitch contractions in cardiac trabeculae. *J Gen Physiol*. 153(3):e202012604, doi: 10.1085/JGP.202012604.
- 3. Kampourakis, T., Y. B. Sun, and M. Irving. 2016. Myosin light chain phosphorylation enhances contraction of heart muscle via structural changes in both thick and thin filaments. *Proc Natl Acad Sci U S A*. 113:E3039-E3047, doi: 10.1073/pnas.1602776113.