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In vivo MRI-validation of a micromechanics-based active contraction model of healthy and diseased human hearts

Martin Genet^{1,2}, Lik Chuan Lee¹, Ellen Kuhl³, Sebastian Kozerke⁴ and Julius Guccione¹

¹ *Surgery Department, School of Medicine, University of California at San Francisco, USA*

² *Marie-Curie International Outgoing Fellow*

³ *Mechanical Engineering Department, Stanford University, USA*

⁴ *Institute of Biomedical Engineering, ETH Zurich, Switzerland*

ABSTRACT

Active contraction of cardiac muscle is a complex phenomenon that involves multi-physics across several scales at or below the cellular level. Many constitutive models, from the very basic to the extremely complex ones, have been formulated to describe this phenomenon. In this presentation, we will focus on the micromechanics-based constitutive model formulated by Guccione et al. [1]. Although this constitutive model is rather simple, it has strong physical meaning and incorporates most of the key aspects of cardiac muscle contraction. In this presentation, we will briefly review the model's mechanical foundations and focus on its calibration, specifically, the personalization of this model to a given animal-subject and/or patient.

A common issue associated with model identification is that some parameters are not easily accessible in classical experimental setups because of their physical scale (e.g., cellular or sub-cellular parameters) or their physical location (e.g., within the human body). Thus, we will first discuss the definition of each model parameter based on physiological considerations. Following that, we will discuss the personalization of one model parameter (T_{max}) that scales the magnitude of the tissue contraction based on computational modeling.

The active contraction law is incorporated into organ scale subject/patient-specific heart models based on continuum mechanics. Personalized ventricular geometries, myocardial strain and chamber volumes are obtained from Magnetic Resonance Imaging (MRI) whereas a rule-based fiber orientation field based on previous histological studies is prescribed to the heart models. A transversely isotropic Fung constitutive model is used to describe the passive cardiac mechanics. A rule-based fiber orientation field is used. The models are solved using the Finite Element Method (FEM). These models form the bases of an inverse problem which we then solve to personalize the model parameter (T_{max}) of the active contraction law for each subject by

matching the measured volume changes. The last point we will discuss is the model validation, particularly, the estimation of the modeling error and associated validity domain, for which we use the measured strains.

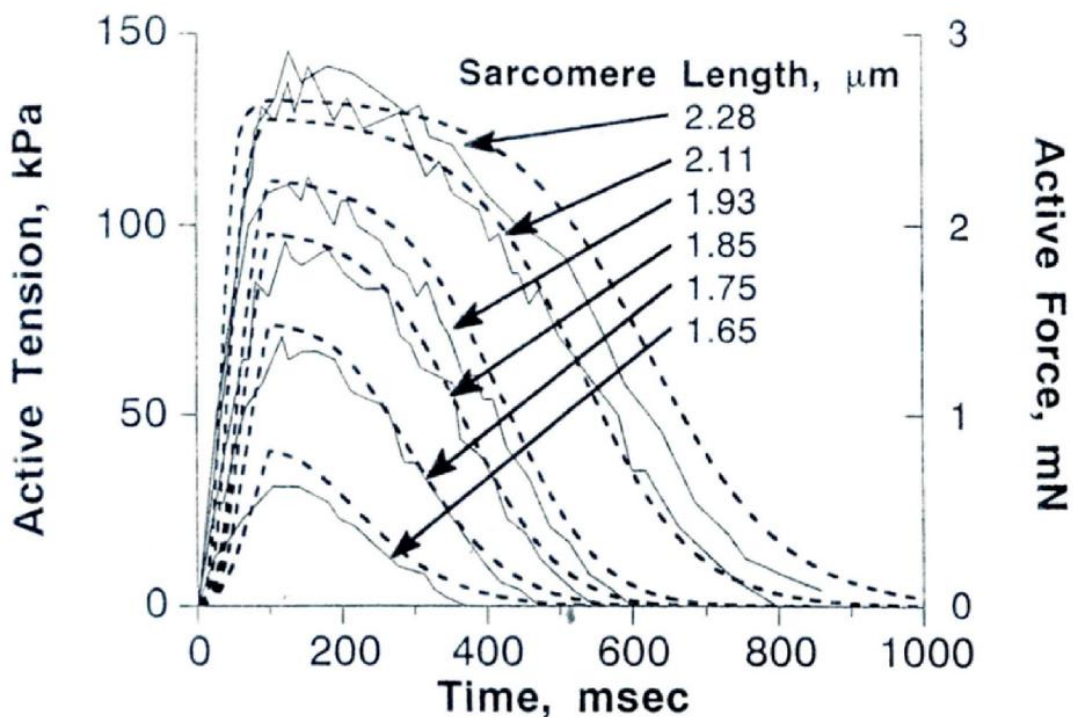
In conclusion, we will discuss in this presentation how modern imaging and computational modeling techniques can be used in a robust and validated way to non-invasively personalize cardiac active contraction models in vivo.

Words = 358

Key Reference

- [1] J. M. Guccione and A. D. McCulloch, "Mechanics of Active Contraction in Cardiac Muscle: Part I—Constitutive Relations for Fiber Stress that describe Deactivation," *J. Biomech. Eng.*, vol. 115, no. 1, pp. 72–81, Feb. 1993.

Figure



Time course of isometric tension development. Reproduced from [1].