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A MECHANOCHEMICAL MODEL FOR SMOOTH MUSCLE CELLS AND ITS FINITE ELEMENT IMPLEMENTATION

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ABSTRACT

Smooth muscle contraction has been studied for several decades but still many phenomena are not well understood. In particular, aspects concerning the mechanochemical and mechanobiological modeling are of crucial interest. To further understand the biomechanical behavior of smooth muscle contraction from the biochemical-initiated activation to the final mechanical contraction point of view, refined coupled mechanochemical models of smooth muscle cells and their appropriate numerical realizations are needed. Mechanochemically-coupled models of smooth muscle cells have been presented prior to this work [1,2], however, very little is known in terms of their finite element implementations (while work [1] considers small deformations, the recent paper [2] proposes a finite strain model by considering the interaction between mechanical and biochemical components of cell function during activation).

When the intracellular calcium concentration in smooth muscle cells is increased, elastic cross-bridges are chemically bound between the thin (actin) and the thick (myosin) filaments, and the two filaments slide towards each other giving rise to contraction. This is also known as the cross-bridge cycle, which in smooth muscle cells has been suggested to follow a four-state latch model, as introduced in the pioneering work by Hai and Murphy [3]. This biochemical model couples calcium concentration to the biochemically and biomechanically-related states of the contractile subunits. It can be combined with a mechanical model to describe the relation between calcium concentration and force distributed by smooth muscle cells.

The present work presents a mechanochemical model of a layer of smooth muscle cells which couples the biochemical four-state latch model by Hai and Murphy [3] with a biomechanical model based on the classical Hill's model [4]. The contractile units are assumed to be arranged together in series constituting long fibres inside the layers of smooth muscle cells. The biomechanical model of the contracting fibers is described through the following strain-energy function

$$\Psi = \frac{n(1-\bar{u}_{\mathrm{s}}(\eta,\kappa))}{2\mu}\left[\lambda^2 - 2(1-2\bar{u}_{\mathrm{s}}(\eta,\kappa))\lambda + 1\right],$$

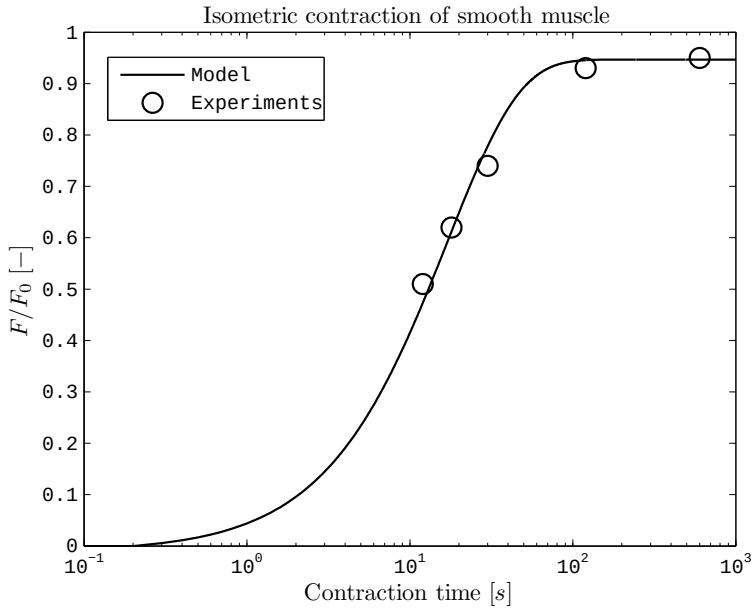

Figure 1: Isometric contraction of smooth muscle cells: Mechanochemical model compared to experimental data of uterine smooth muscle [5].

where λ is the stretch, n is the level of cross-bridge activation, μ is a material parameter and $\bar{u}_{\mathrm{s}}$ describes the relative sliding between the actin and the myosin filaments, which is a function of the material parameters η and κ. The force distributed in these fibers can be divided into an active and a passive part. The active force is due to the increase of intracellular calcium concentration and the passive force is due to the elasticity of cross-bridges. The contractile fibers are assumed to be surrounded by elastin that behaves according to the neo-Hookean model. The unknown material parameters for the model are estimated on the basis of experiments on uterine smooth muscle [5].

The presentation will consist of a short introduction of motivation and theory, followed by the mechanochemical model formulation, and the fitting of the model to experimental data. The implementation of the model into FEAP and the finite element results are shown and discussed (Fig. 1).

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