A Data-Driven Constitutive Framework for Soft Biological Tissues

Computational biomechanics is a valuable tool to successfully model and understand physiological function. Constitutive material models for soft biological tissues lie in the center of these biomechanical simulations. However, different tissue types in living organisms have different mechanical characteristics that need to be reflected at the constitutive level which poses a challenge from modeling perspective. Constitutive models can be divided into two categories: classical analytical models, and data driven models. Classical constitutive models possess a fixed mathematical form that may be chosen with microstructural [1] or macroscopic [2] considerations in mind. These methods have the advantage of utilizing fewer material parameters than data driven models, and as a result it is straightforward to fit these material parameters to the mechanical test data. These models can also be constructed polyconvex a-priori, guaranteeing stability of the hyperelastic response. These models are often easy to implement and provide a good computational efficiency as they allow for closed form analytical calculations. On the other hand, complex structure of biological tissues makes it difficult to find the right mathematical form to represent strain energy functions such as exponential, polynomial, and power law forms that can be found in literature. A mathematical form chosen with a specific type of tissue in mind may not be successful in capturing the response of another type of soft tissue. This is especially a problem from the point of view of users, because choosing the right constitutive model may become a cumbersome process for an occasional user outside of mechanics community. We believe that biomechanics community needs an accurate yet flexible framework applicable to a wide range of soft tissues.

At this point, data driven models emerge as a novel approach to creating a unified model that is capable of predicting the mechanical response of various tissue classes [3]. In this study we propose a data driven constitutive framework based on B-Spline approximations. To this end, we start with the assumption of additive splitting of the strain energy function into volumetric, isotropic, and anisotropic components. We use B-Spline ansatz defined by the choice of control points and polynomial degree, in place of partial derivatives of the strain energy components. Our model allows the use of dispersion models from literature thanks to the employment of deformation invariants. Resulting framework communicates with the experimental data, adapts its control point values, therefore the B-Spline shape, by reducing the error between data and model prediction until a threshold value is reached. Thermodynamic consistency of the resulting free energy function is guaranteed with the use of simple optimization constraints imposed on the choice of B-spline control points [4]. We demonstrate the performance of our model on biological tissues of different characteristics: linea alba, myocardium, aneurismic aorta, and rectus sheath. Our model shows excellent fitting capabilities to the mentioned tissue data, utilizing a minimal number of control points. Finally, we compare the results of finite element simulations with our new model against the well-established Holzapfel-Ogden model [5]. The outcome of this work is a generic data-driven constitutive framework that can model any specific tissue given the data from uniaxial, biaxial, equibiaxial and shear experiments along with histological information from imaging techniques. We believe that this new method will bring the biomechanical simulations one step closer to everyday clinical use.

References:

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