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Hyperelastic modeling of location-dependent human distal femoral cartilage mechanics

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ABSTRACT

Knee articular cartilage exhibits complex mechanical behavior, even under high strain rates, which poses a challenge to developing accurate and efficient cartilage models. In particular, the tissue's stress–strain response is non-linear and the stiffness of the response is location-dependent. Hyperelastic models such as those of Alan Gent and others have increasingly found use in soft tissue biomechanics. Recently, a hyperelastic statistical chain network model representing the transverse isotropy of the collagen matrix in the superficial tangential zone has been developed. The model successfully simulated the 100% strain/s unconfined compression response of human proximal tibial cartilage. Moreover, spatial variations in the tangent modulus to the nominal stress–strain curve taken at 10% strain were reflected in the variability of a single parameter of the model. Given the success of the model, we desired to determine whether these outcomes are equally applicable to healthy human distal femoral cartilage so that a complete model of tibiofemoral joint cartilage can be developed. The transversely isotropic model was employed along with two other hyperelastic chain network models to determine which model best simulated unconfined compression data for healthy distal femoral cartilage. The transversely isotropic model fit the data excellently ($R^2=0.999$). The model was subsequently simplified to depend on a single parameter and reapplied to the dataset. The modified model maintained an excellent fit to the data ($R^2=0.999$), and its single parameter varied in a statistically similar regional pattern ($p<0.05$) to the experimentally-obtained elastic modulus of the tissue. Outcomes suggest that this model is suitable for modeling the spatially-varying, non-linear mechanics of healthy human distal femoral cartilage. Implementation of this constitutive relation within computational models of the knee will provide novel insight into the relationship between joint mechanics, cartilage loading, and knee osteoarthritis development.

1. Introduction

Knee osteoarthritis (OA)[1] afflicts 14% of the US population over the age of 26 and 37% of the population over age 60, yet it remains a poorly understood disease [1]. Computational knee models afford a powerful research tool for investigating how the disease initiates and progresses [2–4]. Computational studies in which joint kinematics and kinetics are systematically varied and the effect on cartilage stress is determined can indicate which loading patterns are most likely to initiate and/or promote OA. However, the effectiveness of these models depends on the accuracy of the constitutive relations describing the many structures making up the knee. In the case of OA, in which the articular cartilage (AC)[2] is heavily affected, the AC material model is particularly important [5].

Selection of a material model requires balancing multiple criteria, such as correct mechanical response for loading conditions of interest, use of parameters with physical meaning that reveal insights into underlying mechanisms, and computational efficiency, e.g, short running time and minimal number of

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[1] OA: osteoarthritis.

[2] AC: articular cartilage.

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parameters [6,7]. For the study of OA, appropriate loading conditions are those associated with walking and other activities of daily living [8,9]. During level-ground walking knee cartilage undergoes compressive strains at a relatively high strain rate of 1 strain/s and peak strains near 20% [10,11], which can be challenging deformation parameters for popular AC models, e.g., the linear biphasic model and its derivatives [6,12,13].

The interaction of the three primary constituents of AC—collagen fibrils, large proteoglycan aggregates, and water containing mobile ions—gives rise to the tissue's mechanical response [14,15]. At equilibrium, the negatively-charged proteoglycans create a swelling pressure in the tissue, which is counteracted by tensile forces in the collagen network [16,17]. When compressed, fluid stress rises causing fluid to flow out of the tissue until equilibrium is re-established [18,19]. Fluid flow is resisted by electrostatic interactions with the proteoglycans and the physical impediments of the collagen matrix, producing a complex viscous response [18,20]. However, for the very short loading times that characterize typical human activity negligible fluid flow occurs. In this case, the tissue deforms nearly isochorically, with the amount of deformation governed by the mechanics of the collagen matrix [13,21–23]. Thus, the high strain-rate loading response of healthy AC may be successfully modeled by focusing on the short-term elasticity of the collagen network, without incorporating viscous effects or the contribution of proteoglycans.

The collagen network is characterized by non-linear elasticity [24], suggesting that a non-linear elastic model, such as a hyperelastic statistical chain network model, could be used to model the high strain-rate loading response of AC. Current linear elastic model are limited in their ability to fully represent the collagen network [19,25]. In contrast, hyperelastic statistical chain network models have successfully modeled high strain-rate, finite deformations of biological tissues containing collagen, such as aortic valve, skin, myocardium, tendon, and ligament [26–29]. The physical structure of these models is analogous to the collagen network that forms the backbone of the cartilage matrix [30,31]. These models require a small number of physically-meaningful parameters, enabling them to be executed in short computational times [26,32–34]. Taken together, these findings indicate that a statistical chain network model would be a viable model for high-strain rate loading of human knee cartilage. Other similar approaches to non-linear elasticity requiring a limited number of parameters to capture the full three-dimensional response of soft tissues are also becoming increasingly popular in soft tissue biomechanics. Although there are several notable models in this group, it behooves us to mention Alan Gent's elegant 1996 model [35].

Recently, it was determined that a transversely isotropic eight-chain network with freely jointed chains could simulate the 1 strain/s uniaxial compression response of healthy human tibial plateau cartilage with high accuracy ($R^2=0.999$) [32]. The transverse isotropy of the model reflects the anisotropy of the superficial tangential zone (STZ)[3] of cartilage [31,36], which is the zone that most influences the mechanical response of the AC matrix [21]. High accuracy was maintained when the model was reduced to dependence on a single parameter that related to the volume density of the solid collagen matrix. Furthermore, experimentally-determined regional variations in the tissue's linear elastic modulus at 10% strain were captured by this single parameter. Consequently this material model would be highly useful for evaluating the role of regional loading patterns on the development of OA [9,37,38]. It is plausible that a similar model would be equally effective at modeling the femoral cartilage of the knee.

With the above facts in mind, we currently aimed to evaluate three statistical chain-network models, including the transversely isotropic eight-chain network of freely-jointed chains, against healthy human distal femoral cartilage. The goal was to provide a complete material model for healthy human tibiofemoral joint cartilage that can be readily implemented into whole-knee computational modeling schemes. The first aim of the study was to determine which of three statistical chain network models could successfully model the uniaxial compression response of distal femoral AC. We hypothesized that the transversely-isotropic eight-chain network model, which was successful in representing regional tibial cartilage behaviors, would be the most successful of the three models. The second aim was to determine whether the model that best fit the data could represent the regional mechanical properties of the femoral AC via a single parameter. We hypothesized that variations in C_R, the parameter that reflects the chain density of the material, would match documented regional variations in the elastic tangent modulus at 10% nominal strain of the AC.

2. Methods

2.1. Material models

Three material models were evaluated for this study: the eight-chain isotropic network with freely-jointed chains (FJC)[4] [39], the eight-chain isotropic network with MacKintosh chains (MAC)[5] [33,40], and the eight-chain transversely isotropic network with freely-jointed chains (TI)[6] [32]. Each model can be described by (1) the constitutive relation used to model a single chain molecule, i.e., a single collagen fibril, and (2) the manner in which the chains are assembled together to the material network, i.e., the cartilage solid matrix. The following sections briefly describe two chain models (the freely-jointed chain and the MacKintosh chain), two network models (the eight-chain isotropic network and the eight-chain transversely isotropic network), how they were combined into the three chain-network models (FJC, MAC, TI) of interest, and how those models were implemented for the case of uniaxial compression.

2.1.1. Mechanical response of single collagen fibril

The freely-jointed chain [41] and the MacKintosh chain [40] represent two common chain models. These chains are suitable for the large, non-linear deformations that typically occur in biological tissues. The chains are considered entropy springs: each chain seeks the conformation that results in maximal entropy. Elongating the chain decreases its entropy and increases its strain energy. The freely-jointed chain can be modeled as N rigid links of length l (Fig. 1a). One end of the chain is fixed at the origin and the other end occupies a volume dv at a location $\boldsymbol{r}$ with probability $p(\boldsymbol{r})$:

$$\ln\ p(\boldsymbol{r}) = p_0 - N\left(\frac{r}{Nl}\beta_r + \ln\frac{\beta_r}{\sinh\ \beta_r}\right) \tag{1}$$

where p_0 is a constant, $r=|\boldsymbol{r}|$, $\beta_r=\mathscr{L}^{-1}(r/Nl)$, and $\mathscr{L}(x)=\coth x-1/x$ is the Langevin function. The inverse Langevin is commonly computed from the Padé approximation [42]:

$$\mathscr{L}^{-1}(x) = x\frac{(3-x^2)}{(1-x^2)} + O(x^6) \tag{2}$$

[3] STZ: superficial tangential zone.

[4] FJC: isotropic eight-chain network with freely-jointed chains.

[5] MAC: isotropic eight-chain network with MacKintosh chains.

[6] TI: transversely-isotropic eight-chain network with freely-jointed chains.