

Mechanical Engineering Department Seminar

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1130 Mechanical Engineering



Image-based Biomechanics and Biomechanical Imaging of Cell-Populated Collagen Gels

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Mechanical analysis of soft tissue is a major challenge in biomedical engineering today because of the large strain, tissue architecture (leading to complex constitutive relations), geometry, individual-to-individual variability, and other factors. In pursuing our long-term goal of understanding soft-tissue mechanics in healthy, diseased, injured, and healing tissue, we have begun with a simple model system, the cell-populated collagen gel. The gels are formed from highly (99%) hydrated networks of long, slender collagen fibers, populated with cells, typically fibroblasts or smooth-muscle cells. The network structure can vary with position, and since fibers are very stiff along their axis but bend and rotate easily, model systems can be produced that are nonlinear, anisotropic, and macroscopically (as well as microscopically) heterogeneous. We have developed a two-scale simulation code that maps the continuum-scale deformation field at each finite-element integration point to a fiber-scale network problem (typically using hundreds of fibers), then solves the network problem and maps the average stress in the micro-domain back to the macroscopic scale, on which a continuum average stress balance is solved. The code iterates between the two levels until both have converged. The model requires a network for each Gauss point; network data are obtained from polarized-light microscopy (PLM) of the sample, allowing us to specify the structural heterogeneity and anisotropy as inputs to the model. The talk will include examples of the method and how it is able to predict mechanical response at both scales in a biaxial stretching experiment. If time permits, biomechanical imaging will also be discussed. The rise of image-correlation methods has permitted determination of an entire strain field during a mechanical experiment. We have developed a scheme that partitions the domain into subdomains and calculates the linear elastic constants in each subdomain. In 2-D, the problem has two constraints per node (force balance in each direction) and six degrees of freedom per subdomain (six independent elastic constants), so the subdomains must be made up of multiple elements to ensure a well-posed error minimization problem. The problem is solved via the pseudo-inverse and provides an estimate of relative stiffness and anisotropy in different regions of the sample even though the linear elastic model is clearly a simplification. Tests on simulated data will be discussed, along with current experiments on collagen gels, unless they all fail.

Bio Victor Barocas is a Professor of Biomedical Engineering at UMN. He received his B.S. in Chemical Engineering and his M.S. in Chemical Engineering Practice from M.I.T., and he did his Ph.D. in Chemical Engineering at Minnesota. He was an Assistant Professor of Chemical Engineering at the University of Colorado at Boulder for three years before moving to the BME department here in 2000. He is interested in the mechanics of soft tissues, with particular emphasis on ocular tissues and engineered cardiovascular tissues.