

Multiscale Computational Simulations of Cell Compaction in Collagen Gels

Edward A. Sander¹ & Victor H. Barocas²

¹Department of Biomedical Engineering, University of Iowa

²Department of Biomedical Engineering, University of Minnesota

Background: Multiscale mechanical interactions are important to characterize in tissues because they play an essential role in many biological processes that govern tissue physiology/ pathophysiology. To better understand these processes we have begun to model the effect of cell tractions on developing isometric tension in the surrounding fibers of a collagen gel. This behavior is approximated simply by partitioning the networks in the model into either collagen networks or contractile cellular networks. Contractile forces are generated within the model by incrementally reducing fiber reference length in the cellular networks, which results in the development of tension in the surrounding collagen.

Results: In a simple test case involving a rectangular finite element mesh containing 128 elements, half the elements were randomly assigned to be cellular networks with the remainder as collagen networks. The reference fiber lengths of cellular networks were incrementally shortened 0%, 20%, or 40%, followed by 50% uniaxial stretch. As expected, an increase in the amount of cell compaction resulted in a reduction in the nonlinearity of the stress-strain relationship due to a reduction in rotational freedom in the collagen networks under isometric tension. Cell compaction also resulted in a redistribution of forces and fiber stretches in the surrounding collagen networks.

Conclusion: Although the description of a cell was idealized the model produced results consistent with experimental observations. The development of such multiscale models will provide important insights on the role of mechanical environment in a number of biological contexts.

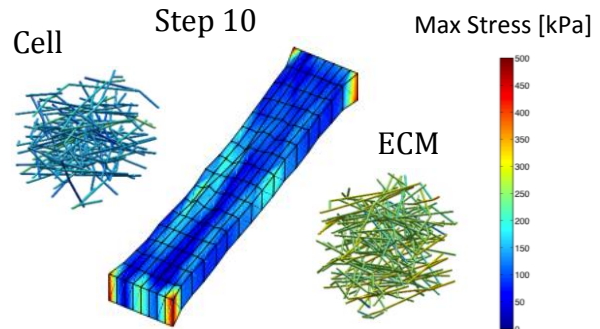
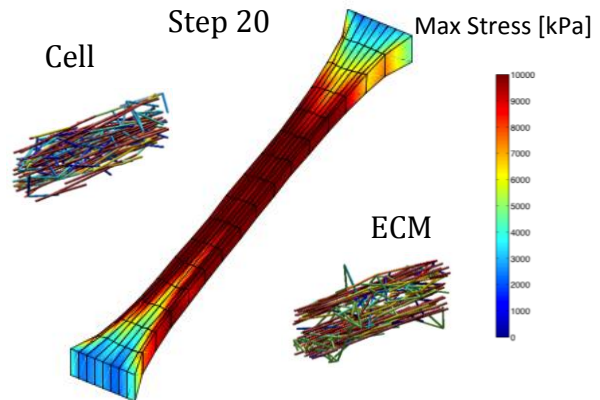
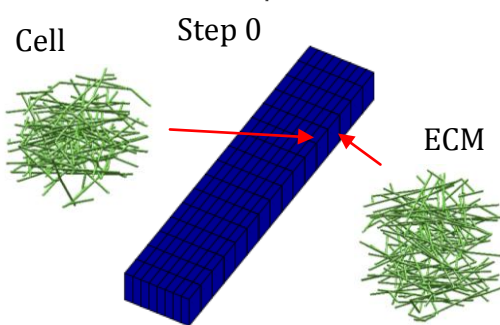
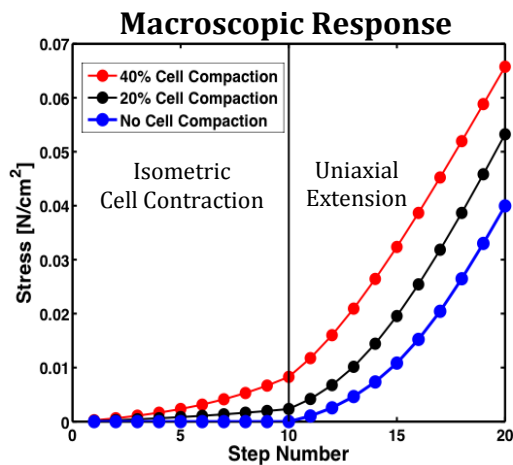


Fig. 1. Simulation results highlighting the macroscale and microscale response of the model when cell tractions are included.