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How much can we learn from athermal models of the mechanical response of biopolymer networks?

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Biopolymer networks of crosslinked, semiflexible filaments exhibit a wide variety of remarkable mechanical properties with distinct biological functionality. In recent years we have shown that network models of discrete, athermal filaments with deformable, yet static, crosslinkers to study the time-independent elastic properties of actin. Here I will summarise the key findings, including the effect of crosslink stiffness on nonlinear strain stiffening, to show that this athermal model captures all experimental trends. Inspired by this success, we now proceed with studying network viscoelasticity, and postulate that it arises solely from the independent unbinding and rebinding of crosslinkers. With a view on extracting the necessary insight to derive a constitutive law for polymer networks, we focus on a minimal system comprising two cross-linked filaments in a crosslinker heat bath. The simulations combine Grand Canonical Monte Carlo for the thermodynamically consistent dynamics of cross-linkers with athermal filament elasticity, including nonlinear elastic effects such as buckling.