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Forced unfolding of protein domains determines cytoskeletal rheology JOHN CROCKER, BRENTON HOFFMAN, GLADYS MASSIERA, University of Pennsylvania — Cells have recently been shown to have a power-law dynamic shear modulus over wide frequency range; the value of the exponent being non-universal, varying from 0.1-0.25 depending on cell type. This observation has been interpreted as evidence for the Soft Glassy Rheology (SGR) model, a trap-type glass model with an effective granular temperature. We propose a simple, alternative model of cytoskeletal mechanics based on the thermally activated, forced unfolding of domains in proteins cross-linking a stressed semi-flexible polymer gel. It directly relates a cells mechanical response to biophysical parameters of the cytoskeletons molecular constituents. Simulations indicate that unfolding events in a random network display a collective self-organization, giving rise to an exponential distribution of crosslink stress that can reproduce cell viscoelasticity. The model suggests natural explanations for the observed correlation between cell rheology and intracellular static stress, including those previously explained using the tensegrity concept. Moreover, our model provides insight into potential mechanisms of mechanotransduction as well as cell shape sensing and maintenance.

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