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**Monte-Carlo simulations of single-molecule RNA pulling experiments** DAN LE, JUTTA LUETTMER-STRATHMANN, University of Akron, Department of Physics — In many viruses, genetic information is encoded in single-stranded ribonucleic acid (RNA) molecules. These molecules are very long chains with an interesting secondary structure that is still difficult to predict from the sequence of bases along the chain. In this work, we develop a coarse-grained lattice model for RNA with orientation-dependent interactions between hydrogen-bonded base pairs. We perform Monte Carlo simulations for several different chains to investigate chain conformations and determine the collapse transition. We determine force-extension curves under equilibrium conditions for tension forces applied to different segments of the chain. These simulated pulling experiments allow us to investigate the relationship between the mechanical response and the secondary structure of the chain.

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