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Extracting Models in Single Molecule Experiments STEVE PRESSE, Indiana University - Purdue University Indianapolis — Single molecule experiments can now monitor the journey of a protein from its assembly near a ribosome to its proteolytic demise. Ideally all single molecule data should be self-explanatory. However data originating from single molecule experiments is particularly challenging to interpret on account of fluctuations and noise at such small scales. Realistically, basic understanding comes from models carefully extracted from the noisy data. Statistical mechanics, and maximum entropy in particular, provide a powerful framework for accomplishing this task in a principled fashion. Here I will discuss our work in extracting conformational memory from single molecule force spectroscopy experiments on large biomolecules. One clear advantage of this method is that we let the data tend towards the correct model, we do not fit the data. I will show that the dynamical model of the single molecule dynamics which emerges from this analysis is often more textured and complex than could otherwise come from fitting the data to a pre-conceived model.

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