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Analysis and Interpretation of Single Molecule Protein Unfolding Kinetics HERBERT LANNON, JASNA BRUJIC, New York University — The kinetics of protein unfolding under a stretching force has been extensively studied by atomic force microscopy (AFM) over the past decade [1]. Experimental artifacts at the single molecule level introduce uncertainties in the data analysis that have led to several competing physical models for the unfolding process. For example, the unfolding dynamics of the protein ubiquitin under constant force has been described by probability distributions as diverse as exponential [2,3], a sum of exponentials, log-normal [4], and more recently a function describing static disorder in the Arrhenius model [5]. A new method for data analysis is presented that utilizes maximum likelihood estimation (MLE) combined with other traditional statistical tests to unambiguously rank the consistency of these and other models with the experimental data. These techniques applied to the ubiquitin unfolding data shows that the probability of unfolding is best fit with a stretched exponential distribution, with important implications on the complexity of the mechanism of protein unfolding.

- [1] Carrion-Vazquez, et. al. Springer Series in Biophys. 2006
- [2] Fernandez et. al. Science 2004
- [3] Brujic et. al. Nat. Phys 2006
- [4] Garcia-Manyes et. al. Biophys. J. 2007
- [5] Kuo et. al. PNAS 2010

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