Abstract Submitted for the 4CF13 Meeting of The American Physical Society

An approach to quantifying macromolecular transition pathways SEAN SEYLER, AVISHEK KUMAR, MICHAEL THORPE, OLIVER BECK-STEIN, Arizona State Univ — Fast transition path sampling methods can mitigate computational obstacles, though the question of whether they can replicate physical ensembles of transitions remains. We introduce a novel method for quantitatively measuring the similarity of transition paths, addressing a need in the computational biophysics community for techniques that facilitate the comparison of the multiplicity of transition path sampling methods. Using the Hausdorff and Fréchet path metrics, we quantify distances between piecewise-linear curves in protein configuration space. The dependence of these metrics on temperature (fluctuation size) and the number of particles (coarse-graining level) is tested using a toy model. We then apply our method to the closed/open conformational transition of the enzyme adenylate kinase by analyzing a sample of trajectories produced by a range of different methods. Hierarchical clustering of pairwise path comparisons can distinguish transitions produced by different sampling methods and also group qualitatively similar trajectories generated by variations of the same method. In summary, we present a method to quantitatively classify macromolecular transition pathways, which may assist in the future in evaluating the accuracy of transition path sampling methods.

> Sean Seyler Arizona State Univ

Date submitted: 03 Sep 2013

Electronic form version 1.4