

Conformational and Translational-Rotational Entropy from Molecular Ensembles [†]

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Entropy calculation is an important step in the postprocessing of molecular dynamics trajectories or predictive models. In recent years the nearest neighbor method proposed by Demchuk and coworkers [1] has emerged as a powerful method to deal in a flexible way with the dimensionality of the problem. Applications to most important biomolecular processes have been presented [2,3] and a specific development has concerned the computation of rotational-translational entropy which required in turn the definition of a metric in rotation-translation space [4]. Two programs have been developed to compute conformational and rotational-translational entropies from biomolecular ensembles [5]. Possible extensions of the method will be presented.

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