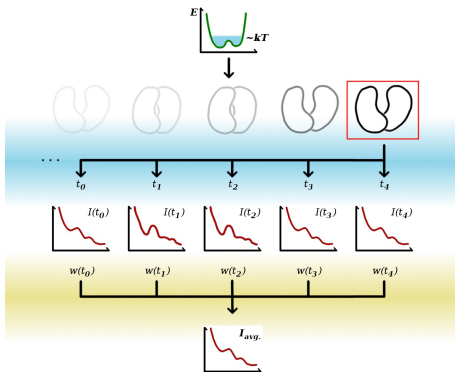


Guiding MD simulations with WAXS spectra - Preliminary Report

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Recent advances in Wide-angled X-ray Scattering techniques (WAXS) offer the ability to probe transient changes in protein conformations down to picosecond levels, [1] and at resolutions down to secondary structure levels where their fluctuations become apparent. [2] This information can be translated into constraints on conformational averages which are complementary to distance-based constraints such as NMR, and will assist in the characterisation of large-macromolecular complexes.

Improvements in computational techniques, such as explicit modelling of the solvent environment, [3] are increasing our understanding of the relationship between spectral features and underlying structural characteristics. Incorporation of WAXS-based constraints into MD-simulations will also guide the direction of simulation trajectories so as to avoid regions irrelevant to the states being studied. However, in order to convert the ensemble-average spectra into instantaneous forces, an understanding of the conformational averaging probed by WAXS is required. We show preliminary results of on-going efforts to integrate WAXS-prediction and WAXS-coupling tools into GROMACS.

This presentation shall include a brief discussion on our planned approach, its validation on trivial systems, and an analysis of how structural-features are linked to features in WAXS-spectra.

[1] R. Neutze and K. Moffat, *Curr. Opin. Struct. Biol.*, **2012**, 22, 651-659.

[2] L. Makowski *et al.*, *Biopolymers*, **2011**, 95, 531-542.

[3] S. Park, *et al.*, *J. Chem. Phys.*, **2009**, 130, 134114.