

## “Reducing the Cost of Molecular Dynamics Simulations”

*Dr. Julija Zavadlav*

Computational Science and Engineering Laboratory, ETH Zürich CH-8092  
Switzerland

### **Abstract:**

To extend the Molecular Dynamics simulations to larger spatiotemporal length and time scales one can simplify the representation of the simulated system, i.e., perform a coarse-grained simulation. However, such models involve several often a priori made assumptions, i.e., the level of coarse-graining and the model complexity. We show how this issue can be addressed with Bayesian statistical framework [1] for the case of coarse-grained models of water [2]. Another route to cost reduction is to perform a multiscale simulation where the atomistic and coarse-grained representations are concurrently coupled. We showcase some recent applications: a protein embedded in an atomistic/supramolecular water [3] and a DNA molecule in a hybrid atomistic/implicit solvent [4].

[1] S. Wu, P. Angelikopoulos, G. Tauriello, C. Papadimitriou, and P. Koumoutsakos, *J. Chem. Phys.* 145, 244112, 2016.

[2] J. Zavadlav, G. Arampatzis, P. Koumoutsakos, *Sci. Rep.* 9, 99, 2019.

[3] J. Zavadlav, S. J. Marrink, M. Praprotnik, *Interface Focus*. 9, 20180075, 2019.

[4] J. Zavadlav, Jurij Sablić, Rudolf Podgornik, and M. Praprotnik, *Biophys. J.* 114 2352–2362 (2018)