

# Simple Elastic Models of Protein Machines

Alexander S. Mikhailov

Fritz-Haber-Institut der Max-Planck-Gesellschaft, Germany

Tuesday, September 02, 2014, 14:00~15:00 D2F  
Seminar room

Protein machines, acting as enzymes, ion pumps, or molecular motors, and performing operations with different biomolecules, such as DNA or other proteins, play a fundamental role in biological cells. Once developed, their synthetic analogs may provide the basis for a new generation of nanotechnology. In this talk, some of the results of recent research in this field, undertaken in my group in Berlin, will be presented.

While chemical structures and equilibrium conformations of protein machines are known, full direct modeling of their molecular dynamics encounters serious difficulties. Even when supercomputers are employed, the dynamics of a single molecule cannot be followed for more than a microsecond, whereas one operation cycle of a molecular machine typically takes tens of milliseconds. Elastic-network models, proposed almost two decades ago, provide a reduced description which has turned out to be highly efficient and, at the same time, very simple. They are broadly used in the normal-mode analysis of experimental protein data and are furthermore applied to understand sensitivity of proteins with respect to local perturbations. A review of the applications, with the foreword by the Nobel prize laureate M. Karplus, can be found in the book [1].

The novel aspect in our research is that we have started to use nonlinear elastic models for dynamical simulations of molecular motors and other protein machines [2-5]. We have moreover begun to design synthetic machines based on such modeling principles [6,7].



Prof. Mikhailov is a theoretical physicist who has studied a broad range of complex phenomena, such as chaos, stochastic processes, pattern formation and networks in physics, chemistry and biology. He is a professor at the Fritz Haber Institute since 1995

<sup>1</sup> Q. Cui and I. Bahar (eds.), *Normal Mode Analysis: Theory and Applications to Biological and Chemical Systems*, Chapman & Hall/CRC, Boca Raton (2006).

<sup>2</sup> H. Flechsig and A. S. Mikhailov, "Tracing entire operation cycles of molecular motor hepatitis C virus helicase in structurally resolved dynamical simulations", *Proc. Natl. Acad. Sci.*, **107**, 20875 (2010)

<sup>3</sup> Y. Togashi, T. Yanagida, and A. S. Mikhailov, "Nonlinearity of mechanochemical motions in motor proteins", *PLOS Comput. Biol.*, **6**, e1000814 (2010).

<sup>4</sup> M. Düttmann, Y. Togashi, T. Yanagida, and A.S. Mikhailov, "Myosin-V as a mechanical sensor: An elastic network study", *biophys. j.* **102**, 542 (2012).

<sup>5</sup> M. Düttmann, M. Mittnenezweig, Y. Togashi, T. Yanagida, and A.S. Mikhailov "Complex intramolecular mechanics of G-actin - An elastic network study", *PLOS ONE*, **7**, e45859 (2012) (2012).

<sup>6</sup> Y. Togashi and A. S. Mikhailov "Nonlinear relaxation dynamics in elastic networks and design principles of molecular machines", *Proc. Natl. Acad. Sci.*, **104**, 8697 (2007).

<sup>7</sup> M.-J. Huang, R. Kapral, A. S. Mikhailov, and H.-Y. Chen "Coarse-grain simulations of active molecular machines in lipid bilayers", *J. Chem. Phys.*, **138**, 195101 (2013).