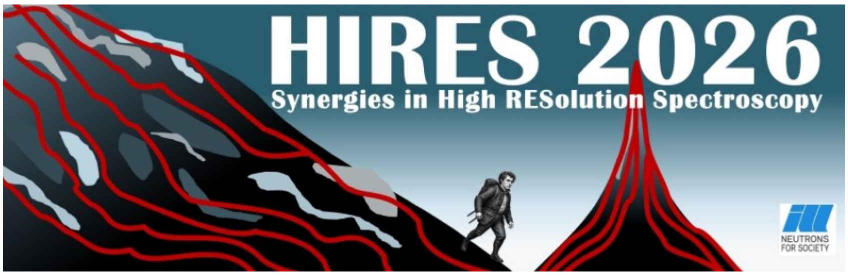

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Bending and thickness fluctuations of phospholipid membranes: joint SAXS/SAXS/NSE analysis with stochastic models

Scattering studies are among the few methods that can be used to analyze the structure and dynamics of phospholipid membranes at nanometer scales. However, the available structural information is indirect, as it consists of correlation functions: space-correlation functions for elastic scattering (e.g. SAXS or SANS), and space-time correlation functions for inelastic scattering (e.g. NSE). An essential and challenging aspect of any scattering study is therefore the development of models to convert scattering data into structural and dynamical insight. Here we report on a family of time-dependent stochastic models that can be used for the structural and dynamical analysis of bending and thickness fluctuations in phospholipid membranes, possibly with included proteins. The methods are illustrated with the joint SAXS/SANS/NSE analysis of unilamellar vesicles prepared from phospholipids extracted from porcine brain tissues [1], as well as on red blood cell membranes containing band3 proteins [2].

[1] C.J. Gommes, P. Dubey, A. Stadler, B. Wu, O. Czakkel, L. Porcar, S. Jaksch, H. Frielinghaus, O. Holderer, Gaussian model of fluctuating membrane and its scattering properties, Phys. Rev. E 110 (2024) 034608;
[2] C.J. Gommes, O. Matsarskaia, J. Pusterla, I. Graf von Westarp, B. Wu, O. Czakkel, A.M. Stadler, Model for small-angle scattering analysis of membranes with protein-like inclusions, J. Appl. Crystallogr. 58 (2025) 1571-1581.

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