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Bayesian modeling of biomolecular structures

Bayesian inference provides a general framework for reasoning from limited information and is thus a powerful tool for analyzing scientific data. I will explain the foundations of Bayesian inference and use my research in biomolecular structure determination to demonstrate the strengths of Bayesian approaches. I will explain the challenges of inferring complex probabilistic models and show that these challenges can be met with the help of Markov chain Monte Carlo algorithms, allowing us to infer models of protein structures with thousands of conformational degrees of freedom from diverse data including measurements from nuclear magnetic resonance and cryo-electron microscopy. I will conclude with an outlook on ongoing and future research aiming to scale Bayesian structure modeling to cellular systems such as chromosomes and genomes.

Host: Dirk Görlich



Monday / 1.7.2019 / 11:00 Max Planck Institute for Biophysical Chemistry Ernst Abbe Seminar Room / Tower 2, 1st floor

