Abstract:

Single-particle cryo-electron microscopy (cryo-EM) is an innovative technology for elucidating structures of biological molecules at atomic-scale resolution. In a cryo-EM experiment, tomographic projections of a molecule, taken at unknown viewing directions, are embedded in highly noisy images at unknown locations. The cryo-EM problem is to estimate the 3-D structure of a molecule from these noisy images.

Inspired by cryo-EM, the talk will focus on two estimation problems: *multi-reference alignment* and *blind deconvolution*. These problems abstract away much of the intricacies of cryo-EM, while retaining some of its essential features. In multi-reference alignment, we aim to estimate a signal from its noisy, rotated observations. While the rotations and the signal are unknown, the goal is only to estimate the signal. In the blind deconvolution problem, the goal is to estimate a signal from its convolution with an unknown, sparse signal in the presence of noise. Focusing on the low SNR regime, I will propose the *method of moments* as a computationally efficient estimation framework for both problems and will introduce its properties. In particular, I will show that the method of moments allows estimating the sought signal accurately in any noise level, provided sufficiently many observations are collected, with only one pass over the data. I will then argue that the same principles carry through to cryo-EM, show examples, and draw potential implications.