Sparse Approximations of Protein Structure Given Noisy Random Projections

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Abstract

Single-particle electron microscopy is a modern technique that biophysicists employ to learn the structure of proteins. It yields data that consist of noisy random projections of the protein structure of interest in random directions, with the added complication that the projection angles cannot be observed. In order to reconstruct a three–dimensional model, the projection directions need to be estimated by use of an ad-hoc starting estimate for the unknown particle. In this paper, we propose methodology that does not rely on any knowledge of the angles, in order to construct an objective data–dependent low–resolution approximation to the unknown structure, that can serve as such a starting estimate. The approach assumes that the protein admits a suitable sparse represenation, and employs L^1-regularisation using Least Angle Regression as well as notions from shape theory to tackle the peculiar challenges involved in the associated inverse problem. We illustrate the approach by application to the reconstruction of an E. Coli protein component called the *Klenow fragment*.

Keywords: *Deconvolution; Electron Microscopy; Nearly Black Object; Real Projective Plane; Single Particles; Statistical Tomography.*