

Visualizing Projection Algorithms with Application to Protein Reconstruction

Matthew K. Tam, University of Newcastle

The ability to visualize an algorithm is immensely useful tool for better understanding its behavior and building intuition. Many non-convex applications of "projection algorithms" lack sufficient theoretical justification to explain their experimentally observed good performance. In such applications, the role of visualization is a key for both improving understanding and guiding future work. In this talk, I will focus on the role of visualization in a recent application of the Douglas-Rachford method to the protein conformation determination problem.

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