Viewing Directions Estimation in cryo-EM Using Synchronization

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A central stage in recovering the structure of large proteins (3D density maps) from their 2D cryo-electron microscopy (cryo-EM) images, is to determine a three-dimensional model of the protein given many of its 2D projection images. The direction from which each image was taken is unknown, and the images are small and extremely noisy. The goal is to determine the direction from which each image was taken, and then to combine the images into a three-dimensional model of the molecule.
We present an algorithm for determining the viewing directions of all cryo-EM images at once, which is robust to extreme levels of noise. The algorithm is based on formulating the problem as a synchronization problem, that is, we estimate the relative spatial configuration of pairs of images, and then estimate a global assignment of orientations that satisfies all pairwise relations. Information about the spatial relation of pairs of images is extracted from common lines between triplets of images. These noisy pairwise relations are combined into a single consistent orientations assignment, by constructing a matrix whose entries encode the pairwise relations. This matrix is shown to have rank 3, and its non-trivial eigenspace is shown to reveal the projection orientation of each image. In particular, we show that the non-trivial eigenvectors encode the rotation matrix that corresponds to each image.
No prior knowledge is required.

This is a joint work with Amit Singer from Princeton University.