Abstract:

Cryo-electron microscopy (cryo-EM) is a microscopy technique used to discover the 3D structure of molecules from very noisy images. We discuss how algebra can describe two aspects of cryo-EM datasets. First, we’ll describe common lines datasets. Common lines are lines of intersection between cryo-EM images in 3D. They are a crucial ingredient in some 2D×3D reconstruction algorithms, and they can be characterized by polynomial equalities and inequalities. Second, we’ll discuss how 3D symmetries of a molecule can be detected from only 2D cryo-EM images, without performing full 3D reconstruction.