Representation theoretic patterns in three dimensional cryo-electron microscopy

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Abstract: Three dimensional cryo-electron microscopy (3D cryo-EM, for short) is the problem of determining the three dimensional structure of a large molecule from the set of images, taken by an electron microscope, of randomly oriented and positioned identical molecular particles which are frozen in a thin layer of ice. A solution to this problem is of particular interest, since it promises to be an entirely general technique which does not require crystallization or other special preparation stages. Present approaches to the problem fail with particles that are too small, cryo-EM images that are too noisy or at resolutions where the signal-to-noise ratio becomes too small.

The focus of my talk is the *intrinsic reconstitution algorithm*, due to Singer and Shkolnisky, which constitutes a step for the solution of the 3D cryo-EM problem and whose main appealing property is its remarkable numerical stability to noise. My goal is to give an **introductory** explanation of the mathematical principles underlying this algorithmic approach, while hinting about how they apply to other fundamental problems in cryo-EM and beyond. Along the way, I will describe the mathematical model underlying the experimental set-up, specifying the main computational problems/technical difficulties that should be resolved as part of three dimensional structure determination from cryo-EM images.

Finally, to put things in a broader mathematical perspective, I will briefly mention the general picture: explaining how the intrinsic reconstitution algorithm can be recasted in the framework of categorical optimization, which is a novel paradigm for solving certain types of non-linear optimization problems by characterizing the solution as an object of a category instead of as an element of a set.

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