240r Crystal Structure Determination from X-Ray Diffraction Data Using Triplet and Quartet Invariants

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Since the mid nineteen hundreds, analysis of X-ray diffraction data of crystals has been used extensively for the determination of molecular structure and properties. While the method is employed almost on a routine basis worldwide, it is often a major challenge to identify the three-dimensional structure that best fits the diffraction data. A key obstacle, in particular, is the identification of the phases of the diffracted rays from measurements of intensities alone. This problem is known as the "phase problem" in crystallography.

Traditional approaches to the crystallographic phase problem minimize merit functions of structural geometry to determine the missing phases [1]. To accurately model the diffraction physics, these merit functions are highly nonlinear and multimodal. As a result, phasing requires the solution of challenging global optimization problems. Trial-and-error, in combination with local search, has been used extensively to solve these optimization problems but is a tedious and difficult process, even for small molecules.

For centric structures, the phase problem has recently been approached via combinatorial optimization techniques that are guaranteed to find a global optimum of a minimal principle formulation of the phase problem [2, 3]. This methodology leaves no ambiguity regarding the correctness of the phases thus derived.

We study how the addition of quartet invariants to the phasing model affects the resolution limits of the previous work [2, 3], which only included triplet invariants. Phasing is accomplished with a polynomial-time binary Gaussian elimination algorithm. For a collection of structures, we show that our methodology leads to considerably more accurate solutions even when the X-ray diffraction data are available at lower resolutions. The quality of our structures also outperforms those of state-of-the-art crystallographic software. The results of this work lay the foundations of a new generation of crystallographic computing systems that will enable the determination of structures important in the understanding of life, materials science, and drug design.

References:

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