Phasing ED data using the Molecular Replacement method

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Molecular replacement (MR) techniques have been developing rapidly in the field of Macromolecular X-ray Crystallography. The method has been the most successful approach to solving the phase problem with over 70% of X-ray structures in the PDB database having been determined this way. Recent developments have helped to reduce the reliance on sequence-based searches for homologues by sampling the entire PDB for good matches to the target phases or exploiting ab initio modeling techniques to generate approximations of the target structure based solely on the targets sequence. This has enabled the method to solve the phase problem in an expanding subset of the total number of X-ray diffraction experiments taking place.

These methods along with the sophisticated search and scoring techniques in programs like Phaser and Molrep are equally applicable to electron diffraction data. Indeed, MR is currently the only way to determine the phases of the target structure in a macromolecular ED experiment.

Here I present some of the latest developments from the CCP4 project in the area of Molecular Replacement along with a brief summary of the fundamentals of the technique.