Molecular Replacement with Powder Diffraction Data

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As more and more protein folds become known, the molecular replacement (MR) method[1] becomes a more attractive method for structure solution. We will demonstrate that synchrotron powder data are sufficient to solve the simple MR problem of finding the position and orientation of the origin of the unit cell with respect to a single protein molecule. A series of examples of small proteins (including lysozyme, trypsin, myoglobin, thaumatin and apoferritin) that cover symmetries from cubic down to monoclinic will be described.

The challenges encountered in more complex molecular replacement problems depend on both the quality of the search model and experimental data. For single-crystal experiments, the data are effectively error free and this essentially reduces to a question of model quality. The peak overlap problem can be so severe for powder experiments that significant gains are possible when peak overlaps are accounted for. The effects of both counting statistics and instrumental resolution on the likely success of a molecular replacement approach with powder data will also be discussed. While the finding that powder data are sufficient for simple molecular replacement problems is not surprising in view of the complexity of small molecule structures that are now be solved from such data, the routine applicability to macromolecular structures remains to be established.

[1] Rossman M. G., *Acta., Cryst.,* 1990, **A46**, 73-82.

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