Using molecular replacement to exploit multiple crystal forms

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Abstract

One of the most powerful methods for phase improvement is to average multiple copies of density, either from different crystal forms or from non-crystallographic symmetry within a single crystal form.

To initiate averaging, it is necessary to have both initial phases for all density maps and the rotation/translation operators relating the various copies of density. Although it has been appreciated for some time that molecular replacement can help achieve both of these requirements, this approach has not been adopted as widely as it should be. We are aiming to make the tools much more convenient and, if possible, automatic.

Molecular replacement can be used in a variety of ways:

- solve a second crystal form using copies of density cut out from the map of the first crystal form
- define NCS operators within a single crystal form by finding the operators that superimpose copies of density
- superimpose a poor model on density isolated from a single image in an experimental map

One surprising use of these tools is to find a recalcitrant copy in a difficult molecular replacement problem. Often it is possible to find some, but not all, copies when using a poor model to solve the structure of a crystal with non-crystallographic symmetry. It turns out that, despite model bias, the model-phased density for a previously-placed copy provides a more sensitive model than the atomic model for finding subsequent copies.

The use of such tools in recent structure determinations will be presented.