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Molecular replacement

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The CCP4 Study Weekend 2007 was held at the University of Reading. Its focus was on the most widely used macromolecular crystallographic phasing technique, molecular replacement (MR). As the number of three-dimensional structures in the PDB increases dramatically so does the popularity and applicability of this technique. Therefore, it was timely to organize this popular gathering on this technique. The meeting was a mixture of descriptions of latest developments in popular and well known software (*AMoRe*, *MOLREP*, *PHASER*), new algorithms and challenging case studies.

The topic of MR was previously visited at the 1992 and 2001 CCP4 Study Weekends, not surprisingly many old friends were welcomed back to bring the story up to date. The introductory session started by Phil Evans who outlined the ways and means of MR. He was followed by Stefano Trapatoni who described new algorithms on fast rotation functions implemented in the program *AMoRe*. Eleanor Dodson's lecture highlighted challenges of the technique and the importance of analysing the molecule under study even before starting to apply MR using bioinformatics techniques.

Model generation and preparation are arguably the most important steps in increasing the odds of a good solution. In the model generation session Geoff Barton described various bioinformatics techniques for the sequence alignment that is at the heart of the MR technique. Andrey Lebedev described the built-in model generation techniques in *MOLREP*. Marc Delaure gave a talk on the use of normal mode analysis to generate a series of search models for molecular replacement.

The final session of the first day was on validation of MR results and model completion. In this session talks by Gerard Bricogne, Serge Cohen and Paul Adams described how to validate the model and complete it using the packages *BUSTER*, *ARP/wARP* and *PHENIX*, respectively.

The second day was on electron microscopy (EM) and MR, case studies and MR pipelines. In the first session Jorge Navaza gave a talk on the use of techniques developed in MR for EM, while Yong Xiong talked about the use of EM models as a search model for MR. Kevin Cowtan described various techniques for fitting the three-dimensional coordinates of a molecule into an electron-density map.

In the session complicated cases Randy Read gave a talk on dealing with pseudo-translation, Michael Isupov and Adrian Lapthorn talked about challenging MR cases where the current MR software is not able to solve the structure automatically. They also described how an experienced user could overcome these problems. Peter Zwart's talk was on general pathologies in macromolecular crystallography and Judit Debrezceni talked about the case of twinned crystals and how can they be solved and analysed using the MR technique.

The final session was on recent developments on molecular replacement pipelines. In this session Lukasz Jaroszewski (JCSG MR pipeline), Martyn Winn (*MrBUMP*) and Fei Long (*BALBES*) described MR pipelines developed independently by different groups. Frank von Delft described the MR pipelines developed and used in his laboratory.

The scientific organisers would like to thank all the speakers who contributed to the study weekend, as well as the reviewers of the papers who helped to ensure the high quality of the proceedings.

The organization of the meeting would not have been possible without the efforts of Maeri Howard, Shirley Miller, Damian Jones and Tracey Kelly (Daresbury Laboratory), and the assistance of the University of Reading conference office.