MS3. Structure solution on the fly (software) / Parallel data collection and structure analysis

Chairs: Manfred Weiss, Victor Lamzin

MS3-O1 DIMPLE: A difference map pipeline for the rapid screening of crystals on the beamline

Ronan Keegan[1], Marcin Wojdyr[1,2], Graeme Winter[2], Alun Ashton[2]

1. CCP4, Research Complex at Harwell, STFC Rutherford Appleton Laboratory, Didcot OX11 0FA, England
2. Diamond Light Source, Harwell Science and Innovation Campus, Didcot OX11 0DE, England

email: ronan.keegan@stfc.ac.uk

The ability to rapidly screen crystals is an essential requirement for efficient use of synchrotron beamlines when looking for potentially bound ligands. DIMPLE is an automated pipeline to make the process of screening crystals for bound ligands quick and efficient. It goes from a merged MTZ file and the known apo structure to a refined density map automatically and in a short space of time. The output presents the user with a set of images of the interesting pieces of density in the difference map unaccounted for by the apo structure. This allows a user to quickly decide if the crystal has a bound ligand present or not. When processing batches of crystals, such feedback allows the user to better decide what to measure next which leads to a more efficient use of the beam time. Recent developments have enhanced the pipeline to cover more complex cases, including changes in the space group and some changes in conformation. While the software is developed primarily for use at synchrotron beamlines during data acquisition, it is included in the CCP4 suite and can be used as well for in-house automation. Here we will also present a detailed analysis of the usage and success rate of DIMPLE on Diamond Light Source beamlines.

Keywords: Macromolecular Crystallography, Structure solution, ligands, CCP4, Diamond Light Source

MS3-O2 Automated structure solution from multiple data sets

Santosh Panjikar[1], Manfred Weiss[2], Victor Lamzin[3]

1. Australian Synchrotron, 800 Blackburn Road, Clayton, Melbourne
2. Helmholtz-Zentrum Berlin für Materialien und Energie,Berlin, Germany
3. EMBL-Hamburg, Germany

email: santosh.panjikar@synchrotron.org.au

Due to size and sensitivity of crystals and stronger X-ray source, it is often not possible to collect complete dataset and even if complete data set is collected from single crystal, it suffers from radiation damage (RD), which is detrimental for anomalous phasing. The advantage of combination of data sets has been well demonstrated and the combined datasets have been used from single or multiple crystals in order to improve multiplicity and anomalous signal (AS). The procedure requires time-consuming task to judge RD and isomorphism for selection of useful data sets for combination.

A number of python libraries have been used to design Auto-Rickshaw (AR) front and back-end engine for analysis, enabling users to choose dataset based on graphical plots from RD and AS along with input parameters necessary to invoke AR for SAD phasing. A graphical interface is generated on the fly for the beamline users. User can invoke AR job for combination of datasets on the local computer, resulting individual dataset are then uploaded along with the input parameters at the remote AR server for SAD phasing and link to the progress of each AR job is provided. This approach has been extended for MAD and SIRAS phasing.

In order to streamline, the above process has been automated that just requires directory path for the processed intensity data. Selection of the data is performed based on its unit cell and space group further followed by analysis of each dataset based on RD and AS. If the AS of individual dataset is above the threshold, then the dataset is pushed for post data analysis at the AR server otherwise the dataset is selected for clustering and scaling purpose. Similarly, each clustered and scaled data is analyzed and pushed further to AR server. In such automatic mode, in absence of sequence information, AR estimates input parameters on the fly. Complete data analysis is documented on the fly as PPTX file for readymade use for presentation.

The python based upfront AR module utilizes various crystallographic program such as XDSSTAT, XSCALE, POINTLESS, AIMLESS along with BLEND, which runs on a local beamline computer and evaluation of the dataset for experimental phasing using various crystallographic programs at the remote cluster (MASSIVE) or at the EMBL AR server.

AR development and workflow of the data analysis will be discussed along with long or short wavelength multiple datasets for S-SAD phasing.

Keywords: Auto-Rickshaw, experimental phasing, multiple data sets, S-SAD