Meeting the operational challenges of ever more automatous beamlines

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Structural Biology beamlines have been using robotic automation and remote access techniques for many years, allowing researchers to study 100 s of samples per day at the synchrotron without leaving their home laboratory. More recently, some MX beamlines have started to operate in a user-less mode: where samples are sent to the beamline and put into queues to be run without user intervention e.g Massif at ERSF [1] or XChem and VMXi at Diamond[2,3]. This has brought new challenges for beamline staff who are now responsible for managing a fast, efficient and error-free flow of samples and associated transport containers to and from the beamlines. At Diamond, we are expanding the existing functionality of the experimental database ISPyB[4] through the SynchWeb[5] interface to manage these new modes of operation. New hardware tools are also being developed to provide better sample tracking and a more efficient way to handle large numbers of samples.

References

[1] Bowler M.W., et.al., J. Sync. Rad., 2015, 22, 1540-1547

[2] VMXi: http://www.diamond.ac.uk/Beamlines/Mx/VMXi.html

[3] XChem: http://www.diamond.ac.uk/Beamlines/Mx/Fragment-Screening.html

[4] Delageniere S. et al, Bioinformatics, 2011, 27, 3186-92

[5] Fisher et al., J. Appl. Cryst,, 2015, 48, 927-932