Enabling Extensibility of an MX Data Acquisition Platform with the Bluesky Python Library


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Recent years have seen a growth of new experiments (beyond the rotation, helical, and rastering data collections that comprise the standard protocols) becoming available at synchrotron macromolecular crystallography (MX) beamlines. To enable continued sustainable development of these new methods, such as serial crystallography via fixed target or extruders, time resolved experiments, and room temperature tray scans, we have recently adapted the Life Science Data Collection software (LSDC), developed for the AMX [1]and FMX [2] beamlines at NSLS-II, to use the Python-based Bluesky data acquisition system [3]. The Ophyd and Bluesky components of this system have been used to improve the abstraction and modularity of the existing data acquisition code which will enable users to have a consistent graphical user interface while performing new experiments intuitively as the standard protocols.

The recent move to use Bluesky has been instrumental in enabling the users of the NYX beamline (also at NSLS-II, but run independently by the New York Structural Biology Center) to perform experiments with LSDC. The NYX users, despite using different hardware (including robotic sample changer, detector, and motion controller), have the same user experience as AMX and FMX users, proving the effectiveness of the Bluesky system. Having established the principles of code abstraction into LSDC through Bluesky, we expect new MX experiments to become available to users in a sustainable and maintainable way, which will enable AMX, FMX, and NYX users to control an ever-increasing number of different types of experiments through the familiar LSDC experience.