



Contribution ID: 82

Type: Poster

PyBlulce: Modular data acquisition software for long duration, scripted automation, and high speed protein crystallography experiments

Tuesday, September 20, 2022 5:14 PM (2 minutes)

In order to make new methods for protein crystallography experiments widely accessible at GM/CA@APS, the data acquisition program JBlulce was rewritten with improved modularity as the primary design goal. A comprehensive HTTP and Redis-based interface covering all levels of beamline functions enables a range of applications to control the beamline. This includes single use scripts for trying new methods, as well as a permanent GUI with decades of refinement built in which will be extended with new features including serial crystallography and automated planning. The API and plug-in architecture allow for more complex data collection modes by creating a shared framework to remove complexity. Automation is designed in a way to make it highly visible to the user and allow them to step in at any time. Viewing and analysis of data is decoupled from the data collection engine and adapts to any collection rate. And finally, a realistic beamline simulation with genuine EPICS, HTTP, SQL and Redis servers allows for most development to be done without a beamline.

Email address of presenting author

mhilgart@anl.gov

I agree to recordings of my presentation being made at NOBUGS 2022

Primary authors: HILGART, Mark (Argonne National Laboratory); Dr XU, Qingping (Argonne National Laboratory); Dr MAKAROV, Oleg (Argonne National Laboratory); Dr STEPANOV, Sergey (Argonne National Laboratory); Dr BECKER, Michael (Argonne National Laboratory); Dr VENUGOPALAN, Nagarajan (Argonne National Laboratory); Dr OGATA, Craig (Argonne National Laboratory); Dr KISSICK, David (Argonne National Laboratory); Dr FISCHETTI, Robert (Argonne National Laboratory)

Presenter: HILGART, Mark (Argonne National Laboratory)

Track Classification: NOBUGS 2022