The Canadian Macromolecular Crystallography Facility (CMCF) is a suite of two beamlines 08ID-1 and 08B1-1. Beamline 08ID-1, is an undulator beamline for studying small crystals and crystals with large unit cells, while beamline 08B1-1 is a bending-magnet beamline for high-throughput macromolecular crystallography with a high level of automation. The primary method of access to CMCF 08B1-1 will be remote, in what is commonly referred to in the field as “Mail-in” crystallography. We are developing a software system for automating both beamlines, with modules for beamline control, experiment control, data analysis, information management, and graphical user interaction. The system is developed using the Python programming language and makes use of popular open-source frameworks such as TWISTED, DJANGO and GTK+. Once completed, the system will allow automation of the macromolecular crystallography experiment from experiment setup to data analysis, thereby increasing the efficiency of the CMCF beamlines and reducing the need for user travel to the synchrotron.

### Remote Access and Automation

1. **UserLogs onto their CMCF LIMS web account**
2. **At Users home Lab**
3. **Beamline Staff retrieves Dry-Shipper from storage and loads Uni-Puck onto the automounter at the beamline, identifying the Pucks by barcode and updating the CMCF LIMS at each step. Staff then initiates a queue of automated data acquisition.**
4. **The beamline is equipped with a Stanford Automounter (SAM) robot which can hold up to 192 samples at a time, enough samples for a full shift of automated data acquisition and analysis by the EMM, BCM and DPM.**
5. **User Logs in to verify preliminary results, update experiment requests, inspect results and download data. Users can also see the status of their outgoing and incoming shipments.**

### Technologies

- Python
- GTK+
- TWISTED
- DJANGO