

August 11-14th at the Crowne Plaza Hotel in downtown Knoxville, TN



Contribution ID: 89

Type: **Poster Only**

## Upgrades to the reduction and data analysis pipeline at Bio-SANS

Reduction and subsequent data analysis are the two fundamental steps to interpreting small angle neutron scattering data. At Bio-SANS, we have developed new analysis tools to streamline the data reduction and primary data analysis workflows. We have developed a new interactive, web-based analysis tool for solution scattering of biomolecules and extensible to soft matter polymer samples that provides interactive background subtraction integrated with pair distance distribution function calculation, Kratky and Guinier plots. The tool allows for quick interpretation of background subtracted data. We have also developed a new ensemble optimization genetic algorithm for SANS data to interpret SANS of flexible biomolecular systems. We have collaborated with SIBYLS beamline at ALS to host the genetic algorithm as part of the BilboMD workflow, for fast sampling of conformational space. In addition, we will present an overview of the future plans to improve the data pipeline at Bio-SANS, including live-data reduction, expansion of structure based contrast prediction (SCOMAP-XD), and multi-modal refinement with SAXS data.

### Topical Area

Biology and life sciences

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