

MS3. Structure solution on the fly (software) / Parallel data collection and structure analysis

Chairs: Manfred Weiss, Victor Lamzin

MS3-P1 Correcting for radiation damage in macromolecular crystallography

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Radiation damage is an unavoidable phenomenon that occurs during macromolecular crystallography (MX) experiments. It manifests itself in several ways including an overall decrease in reflection intensity of the diffraction pattern. Often these effects can be so severe that structure determination is not possible.

When data were routinely collected at room temperature, mathematical correction of reflection intensities to account for radiation damage was a common procedure [e.g. ref 1]. Radiation doses absorbed by cryocooled crystals are now much greater than they were previously, and the true behaviour of the reflection intensities is too complex to be described by a simple zero order correction.

Here we present two reflection intensity correction models. The first is a redundancy based model that extends previous models [2]. This model relies on portions of the data being highly multiplicitous so that the parameters of the model can be found by a weighted least squares fit. The remaining portions of low multiplicity can then be extrapolated later, by following the trends of the high multiplicity data. The extensions to the previous model include explicit dose parameterisation using RADDOSE-3D [3] and a new dose decay model [4] that captures the nonlinear behaviour of reflection intensities empirically.

The second model treats the crystal degradation and the reflection intensity observations as a stochastic (random) process. Explicitly we use a hidden Markov model to describe the data collection process. The model parameters that correspond to the maximum likelihood of observing the data can then be determined. This in turn allows for the reflection intensities to be determined from any given crystal state. The advantage of this model is that it does not rely on having high multiplicity data.

Both models have been used to correct highly damaged data collected from crystals of bovine pancreatic insulin. The resulting data reduction and refinement statistics will be compared.

References

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