Quantifying and comparing radiation damage in the Protein Data Bank

Elspeth F Garman, University of Oxford, UK

Structural biology relies on X-ray crystallography to provide much of the three dimensional information on proteins and other macromolecules that informs biological function [1], but radiation damage to the samples remains one of the major bottlenecks to accurate structure determined. The radiation damage can manifest as `global' changes resulting in the fading of the diffraction pattern with increasing dose, or as `specific' structural and chemical changes in the protein structures obtained. It is hence an important consideration when assessing the quality and biological veracity of crystal structures in repositories such as the Protein Data Bank (PDB). However, detection of radiation damage artefacts has traditionally proved very challenging. To address this, we have introduced the Bnet metric. Bnet summarises in a single value the extent of damage suffered by a crystal structure by comparing the B-factor values of damage-prone and non-damage-prone atoms in a similar local environment. After validating that Bnet successfully detects damage in 23 different crystal structures previously characterised as damaged, we have calculated Bnet values for 93,978 PDB crystal structures. Our metric highlights a range of damage features, many of which would remain unidentified by the other summary statistics typically calculated for PDB structures [2].
.

References:

[1] EF Garman (2014) Developments in X-ray Crystallographic Structure Determination of Biological Macromolecules. *Science* 343: 1102-1108

[2] KL Shelley & EF Garman (2022) Quantifying radiation damage in the Protein Data Bank. *Nature Communications* 13:1314- 1325